

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:51:14 ; Search time 5.46546 Seconds  
(without alignment)  
1149.648 Million cell updates/sec

Title: US-10-644-277-149  
Perfect score: 405  
Sequence: 1 QPDAINAPVTCYNFTNRKI.....QKVVQDSMDHLDKQTQPKT 76

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5 COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PCFUS COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	405	100.0	76	1	US-08-716-188-2
2	405	100.0	76	1	US-08-615-232A-5
3	405	100.0	76	2	US-08-470-323-5
4	405	100.0	76	2	US-09-195-457-5
5	405	100.0	76	2	US-09-291-038-5
6	405	100.0	76	2	US-09-043-861-31
7	405	100.0	78	1	US-08-330-163-12
8	405	100.0	78	1	US-08-482-111-12
9	405	100.0	78	2	US-09-567-225-14
10	405	100.0	99	1	US-08-127-499A-35
11	405	100.0	99	1	US-08-482-847-35
12	405	100.0	99	1	US-08-347-492B-8
13	405	100.0	99	1	US-08-480-449-19
14	405	100.0	99	1	US-08-479-126B-5
15	405	100.0	99	1	US-08-421-144A-5
16	405	100.0	99	1	US-08-726-830A-5
17	405	100.0	99	1	US-08-660-542-19
18	405	100.0	99	1	US-08-798-143-8
19	405	100.0	99	2	US-07-927-391-24
20	405	100.0	99	2	US-08-995-156A-5
21	405	100.0	99	2	US-09-044-856A-5
22	405	100.0	99	2	US-09-044-855A-5
23	405	100.0	99	2	US-08-679-493A-152
24	405	100.0	99	2	US-08-479-603-19
25	405	100.0	99	2	US-09-419-281-5
26	405	100.0	99	2	US-09-366-887A-10
27	405	100.0	99	2	US-08-939-107-19

28	405	100.0	99	2	US-09-545-894-5	Sequence 5, Appli
29	405	100.0	99	2	US-09-067-447B-19	Sequence 19, Appl
30	405	100.0	99	2	US-08-517-204-10	Sequence 10, Appl
31	405	100.0	99	2	US-08-437-306-2	Sequence 2, Appli
32	405	100.0	99	2	US-08-479-620-19	Sequence 19, Appl
33	405	100.0	99	2	US-10-054-967-5	Sequence 5, Appli
34	405	100.0	99	2	US-10-141-965-5	Sequence 5, Appli
35	405	100.0	99	4	PCT-US96-10087-5	Sequence 5, Appli
36	405	100.0	99	6	5212073-2	Patent No. 5212073
37	400	98.8	76	1	US-07-956-862A-1	Sequence 1, Appli
38	400	98.8	76	1	US-08-250-958-1	Sequence 1, Appli
39	400	98.8	76	1	US-08-235-659-1	Sequence 1, Appli
40	398	98.8	78	4	PCT-US95-00605-1	Sequence 1, Appli
41	398	98.3	99	2	US-09-834-795A-28	Sequence 28, Appl
42	362	89.4	68	2	US-09-463-458A-30	Sequence 30, Appl
43	362	89.4	69	2	US-09-463-458A-31	Sequence 31, Appl
44	362	89.4	69	2	US-09-463-458A-32	Sequence 32, Appl
45	358	88.4	68	2	US-09-463-458A-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1  
US-08-716-188-2  
; Sequence 2, Application US/08716188  
; Patent No. 5908629  
; GENERAL INFORMATION:  
; APPLICANT: KELLY, RODNEY W  
; TITLE OF INVENTION: USE OF MCP-1 FOR INDUCING RIPENING OF  
; TITLE OF INVENTION: THE CERVIX  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/716,188  
; FILING DATE: 30-SEP-1996  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB95/00733  
; FILING DATE: 31-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9406463.1  
; FILING DATE: 31-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 117-219  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 76 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-716-188-2

Query Match 100.0%; Score 405; DB 1; Length 76;  
Best Local Similarity 100.0%; Pred. No. 7.3e-47;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QPDAINAPVTCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Qy 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 2
US-08-615-232A-5
; Sequence 5, Application US/08615232A
; Patent No. 5993814
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,232A
; FILING DATE: 13-AUG-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9318984
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: GB 9408602
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 550-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 5:
; LENGTH: 76 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-615-232A-5

Query Match 100.0%; Score 405; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 7.3e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QPDAINAPVTCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Qy 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 3
US-08-470-323-5
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; Sequence 5, Application US/08470323A
; Patent No. 6031080
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; FILE REFERENCE: 550-33
; CURRENT APPLICATION NUMBER: US/08/470,323A
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: PCT/GB94/02006
; EARLIER FILING DATE: 1994-09-14
; EARLIER APPLICATION NUMBER: GB 9318984.3
; EARLIER FILING DATE: 1993-09-14
; EARLIER APPLICATION NUMBER: GB 94086902.2
; EARLIER FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 76
; TYPE: PRT
; ORGANISM: human
; US-08-470-323-5

Query Match 100.0%; Score 405; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 7.3e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Qy 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 4
US-09-195-457-5
; Sequence 5, Application US/09195457
; Patent No. 6605702
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; FILE REFERENCE: 550-33
; CURRENT APPLICATION NUMBER: US/09/195,457
; CURRENT FILING DATE: 1998-11-18
; CURRENT APPLICATION NUMBER: 08/470,323
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/GB94/02006
; PRIOR FILING DATE: 1994-09-14
; PRIOR APPLICATION NUMBER: GB 9318984.3
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: GB 94086902.2
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 76
; TYPE: PRT
; ORGANISM: human
; US-09-195-457-5

Query Match 100.0%; Score 405; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 7.3e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
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Qy 61 QDSMDHLDKQTTPKT 76
Db 61 QDSMDHLDKQTTPKT 76

RESULT 5
US-09-291-038-5
; Sequence 5, Application US/09291038
; Patent No. 6635251
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; JOSE, PETER J.
; GRIFFITHS-JOHNSON, DAVID A.
; HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P. C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/291,038
; FILING DATE: 14-Apr-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,232A
; FILING DATE: 13-AUG-1996
; APPLICATION NUMBER: GB 9318984
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: GB 9408602
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 550-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-291-038-5
Query Match 100.0%; Score 405; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 7.3e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNFTNRKISVQLASVYRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
Db 1 QPDAINAPVTCYNFTNRKISVQLASVYRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

Qy 61 QDSMDHLDKQTTPKT 76
Db 61 QDSMDHLDKQTTPKT 76

RESULT 6
US-09-043-861-31
; Sequence 31, Application US/09043861
; Patent No. 6793917
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; GENERAL INFORMATION:
; APPLICANT: IMAI, Toshio
; APPLICANT: YOSHIDA, Tetsuya
; APPLICANT: YOSHIE, Osamu
; TITLE OF INVENTION: TYPE CC CHEMOKINE-LIKE PROTEIN
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/043,861
; FILING DATE: 27-MAR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP96/02801
; FILING DATE: 27-SEP-1996
; APPLICATION DATA:
; APPLICATION NUMBER: JP 56044/1996
; FILING DATE: 13-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 249457/1995
; FILING DATE: 27-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wegner, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 74129/432
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-043-861-31
Query Match 100.0%; Score 405; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 7.3e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNFTNRKISVQLASVYRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
Db 1 QPDAINAPVTCYNFTNRKISVQLASVYRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

Qy 61 QDSMDHLDKQTTPKT 76
Db 61 QDSMDHLDKQTTPKT 76

RESULT 7
US-08-330-163-12
; Sequence 12, Application US/08330163
; Patent No. 5656724
; GENERAL INFORMATION:
; APPLICANT: Daly, Thomas J.
; APPLICANT: Larosa, Gregory J.
; TITLE OF INVENTION: Chemokine-Like Proteins and Methods of
; TITLE OF INVENTION: Use
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
```





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; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,499A
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/102/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
;
US-08-127-499A-35

Query Match 100.0%; Score 405; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQRLASVYRRITSSKCPKEAVIFKTIYAKEICADPKQKWV 60
Db 24 QPDAINAPVTCYNTNRKISVQRLASVYRRITSSKCPKEAVIFKTIYAKEICADPKQKWV 83
Qy 61 QDSMDHLDKQTQTPKT 76
Db 84 QDSMDHLDKQTQTPKT 99

RESULT 11
US-08-842-847-35
; Sequence 35, Application US/08482847
; Patent No. 5556757
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,847
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
;
US-08-482-847-35

Query Match 100.0%; Score 405; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQRLASVYRRITSSKCPKEAVIFKTIYAKEICADPKQKWV 60
Db 24 QPDAINAPVTCYNTNRKISVQRLASVYRRITSSKCPKEAVIFKTIYAKEICADPKQKWV 83
Qy 61 QDSMDHLDKQTQTPKT 76
Db 84 QDSMDHLDKQTQTPKT 99

RESULT 12
US-08-347-492B-8
; Sequence 8, Application US/08347492B
; Patent No. 5602008
; GENERAL INFORMATION:
; APPLICANT: Wilde, Craig G.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR
; TITLE OF INVENTION: PRODUCTION AND USES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,492B
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/303,241
; FILING DATE: 07-SEP-1994
; APPLICATION NUMBER: 08/320,011
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
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/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: peptide  
/ IMMEDIATE SOURCE:  
/ LIBRARY: GENBANK  
/ CLONE: GI 487124  
/ US-08-347-492B-8

Query Match 100.0%; Score 405; DB 1; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1e-46;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60  
DB 24 QPDAINAPVTCYNTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 83

QY 61 QDSMDHLDKQTQTPKT 76  
DB 84 QDSMDHLDKQTQTPKT 99

RESULT 13  
US-08-480-449-19  
; Sequence 19, Application US/08480449  
; Patent No. 5688927  
; GENERAL INFORMATION:  
; APPLICANT: Godiska, Ronald  
; APPLICANT: Gray, Patrick W.  
; TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480.449  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gass, David A.  
; REGISTRATION NUMBER: 38,153  
; REFERENCE/DOCKET NUMBER: 27866/32779  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 99 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: "Hu MCP-1"  
; US-08-480-449-19

Query Match 100.0%; Score 405; DB 1; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1e-46;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

DB 24 QPDAINAPVTCYNTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 83

QY 61 QDSMDHLDKQTQTPKT 76  
DB 84 QDSMDHLDKQTQTPKT 99

RESULT 14  
US-08-479-126B-5  
; Sequence 5, Application US/08479126B  
; Patent No. 5866373  
; GENERAL INFORMATION:  
; APPLICANT: LI, HAODONG  
; APPLICANT: RUBEN, STEVEN M  
; APPLICANT: SUTTON, GRANGER G III  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN MONOCYTE  
; TITLE OF INVENTION: CHEMOTACTIC PROTEIN-4 (AS AMENDED)  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/479.126B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/424,425  
; FILING DATE: 21-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/05384  
; FILING DATE: 16-MAY-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0340001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 99 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-479-126B-5

Query Match 100.0%; Score 405; DB 1; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1e-46;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60  
DB 24 QPDAINAPVTCYNTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 83

QY 61 QDSMDHLDKQTQTPKT 76  
DB 84 QDSMDHLDKQTQTPKT 99

RESULT 15  
US-08-421-144A-5  
; Sequence 5, Application US/08421144A  
; Patent No. 5874211  
; GENERAL INFORMATION:

APPLICANT: BANDMAN, OLGA  
APPLICANT: COLEMAN, ROGER  
APPLICANT: STUART, SUSAN G.  
TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/421,144A  
FILING DATE: 13-APR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33954  
REFERENCE/DOCKET NUMBER: PF-0031 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-421-144A-5

Query Match 100.0%; Score 405; DB 1; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1e-46;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QPDAINAPVTCVNTNRKISVQRSLASVRRITSSKCPKEAVIFKTIIVAKEICADPKOKWV 60  
Db 24 QPDAINAPVTCVNTNRKISVQRSLASVRRITSSKCPKEAVIFKTIIVAKEICADPKOKWV 83  
Qy 61 QDSMDHLDKQTQPKT 76  
Db 84 QDSMDHLDKQTQPKT 99

Search completed: February 3, 2006, 09:53:35  
Job time : 6.56546 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 3, 2006, 09:53:49 ; Search time 16.4394 Seconds  
(without alignment)  
1931.640 Million cell updates/sec

Title: US-10-644-277-149  
Perfect score: 405  
Sequence: 1 QPDAINAPVTCYNFTNRKI.....QKWQDSMDHLKQTQTPKT 76

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pcp:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pcp:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pcp:\*  
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6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pcp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	405	100.0	76	3	US-09-195-457-5
2	405	100.0	76	3	US-09-792-793A-20
3	405	100.0	76	4	US-10-339-778-3
4	405	100.0	76	4	US-10-276-971-1
5	405	100.0	76	4	US-10-375-209A-20
6	405	100.0	76	4	US-10-332-038A-5
7	405	100.0	76	4	US-10-668-733-7
8	405	100.0	76	4	US-10-668-733-14
9	405	100.0	76	4	US-10-393-804A-1
10	405	100.0	76	4	US-10-243-795-7
11	405	100.0	76	5	US-10-872-198-102
12	405	100.0	76	5	US-10-839-017-8
13	405	100.0	76	5	US-10-644-277-149
14	405	100.0	76	5	US-10-332-039A-5
15	405	100.0	76	5	US-10-833-656-3
16	405	100.0	76	5	US-10-822-134-5
17	405	100.0	76	5	US-10-981-936-42
18	405	100.0	76	6	US-11-021-951-102
19	405	100.0	78	4	US-10-803-960-14
20	405	100.0	98	4	US-10-449-831A-210
21	405	100.0	99	2	US-08-927-939-16
22	405	100.0	99	4	US-10-057-275-9
23	405	100.0	99	4	US-10-033-067-4
24	405	100.0	99	4	US-10-141-965-5
25	405	100.0	99	4	US-10-146-496-9
26	405	100.0	99	4	US-10-054-967-5
27	405	100.0	99	4	US-10-293-705-8

28	405	100.0	99	4	US-10-170-385-395	Sequence 395, Appl
29	405	100.0	99	4	US-10-116-275-222	Sequence 222, Appl
30	405	100.0	99	4	US-10-440-464-62	Sequence 62, Appl
31	405	100.0	99	4	US-10-764-649-18	Sequence 18, Appl
32	405	100.0	99	5	US-10-733-878-515	Sequence 515, Appl
33	405	100.0	99	5	US-10-852-335A-141	Sequence 141, Appl
34	405	100.0	99	5	US-10-852-335A-148	Sequence 148, Appl
35	405	100.0	99	5	US-10-833-656-1	Sequence 1, Appl
36	405	100.0	99	5	US-10-773-446-130	Sequence 130, Appl
37	405	100.0	99	5	US-10-818-952-19	Sequence 19, Appl
38	405	100.0	99	6	US-11-035-998-5	Sequence 5, Appl
39	405	100.0	122	4	US-10-339-778-2	Sequence 2, Appl
40	405	100.0	133	4	US-10-449-831A-214	Sequence 214, Appl
41	405	100.0	325	3	US-09-792-793A-71	Sequence 71, Appl
42	405	100.0	325	4	US-10-375-209A-71	Sequence 71, Appl
43	405	100.0	327	3	US-09-792-793A-72	Sequence 72, Appl
44	405	100.0	327	4	US-10-375-209A-72	Sequence 72, Appl
45	405	100.0	332	3	US-09-792-793A-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1

US-09-195-457-5  
; Sequence 5, Application US/09195457  
; Patent No. US20020081623A1  
; GENERAL INFORMATION:  
; APPLICANT: WILLIAMS, TIMOTHY J.  
; APPLICANT: JOSE, PETER J.  
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.  
; APPLICANT: HSUAN, JOHN J.  
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE  
; FILE REFERENCE: 550-33  
; CURRENT APPLICATION NUMBER: US/09/195,457  
; PRIOR FILING DATE: 1998-11-18  
; PRIOR APPLICATION NUMBER: 08/470,323  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: PCT/GB94/02006  
; PRIOR FILING DATE: 1994-09-14  
; PRIOR APPLICATION NUMBER: GB 9318984.3  
; PRIOR FILING DATE: 1993-09-14  
; PRIOR APPLICATION NUMBER: GB 94086902.2  
; PRIOR FILING DATE: 1994-04-29  
; NUMBER OF SEQ ID NOS: 11  
; SEQ ID NO 5  
; LENGTH: 76  
; TYPE: PRT  
; ORGANISM: human  
US-09-195-457-5

Query Match 100.0%; Score 405; DB 3; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.4e-41;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QPDAINAPVTCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKICADPKQKWV	60
Db	1	QPDAINAPVTCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKICADPKQKWV	60
Qy	61	QDSMDHLKQTQTPKT	76
Db	61	QDSMDHLKQTQTPKT	76

RESULT 2

US-09-792-793A-20  
; Sequence 20, Application US/09792793A  
; Patent No. US20020168370A1  
; GENERAL INFORMATION:  
; APPLICANT: McDonald, John R.  
; APPLICANT: Cogging, Philip  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND OTHER INFLAMMATORY CONDITIONS AND DISORDERS

FILE REFERENCE: 25020-601D  
CURRENT APPLICATION NUMBER: US/09/792,793A  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 20  
LENGTH: 76  
TYPE: PRT  
ORGANISM: homo sapien  
FEATURE:  
OTHER INFORMATION: Human Chemokine Polypeptide: MCP-1  
US-09-792-793A-20

Query Match 100.0%; Score 405; DB 3; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.4e-41;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60  
DB 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76  
DB 61 QDSMDHLDKQTQTPKT 76

RESULT 3  
US-10-339-778-3  
Sequence 3, Application US/10339778  
Publication No. US20030129214A1  
GENERAL INFORMATION:  
APPLICANT: Bornstein, P.  
TITLE OF INVENTION: METHODS OF ENHANCING THE BIOCOMPATIBILITY OF AN IMPLANTABLE MEDICAL DEVICE  
FILE REFERENCE: UMOTL-1-20275  
CURRENT APPLICATION NUMBER: US/10/339,778  
CURRENT FILING DATE: 2003-01-09  
PRIOR FILING DATE: 2002-01-10  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 3  
LENGTH: 76  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-339-778-3

Query Match 100.0%; Score 405; DB 4; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.4e-41;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60  
DB 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76  
DB 61 QDSMDHLDKQTQTPKT 76

RESULT 4  
US-10-276-971-1  
Sequence 1, Application US/10276971  
Publication No. US20030162737A1  
GENERAL INFORMATION:  
APPLICANT: Egaehira Kensei  
APPLICANT: Yoshikazu Yonemitsu  
APPLICANT: Katsuo Sueishi  
APPLICANT: Yasuhiro Ikeda  
APPLICANT: Yoshiyuki Inada  
TITLE OF INVENTION: Preventatives and Remedies for Pulmonary Hypertension  
FILE REFERENCE: 2733 US0P

CURRENT APPLICATION NUMBER: US/10/276,971  
CURRENT FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 4  
SEQ ID NO 1  
LENGTH: 76  
TYPE: PRT  
ORGANISM: Human  
US-10-276-971-1

Query Match 100.0%; Score 405; DB 4; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.4e-41;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60  
DB 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76  
DB 61 QDSMDHLDKQTQTPKT 76

RESULT 5  
US-10-375-209A-20  
Sequence 20, Application US/10375209A  
Publication No. US20030215421A1  
GENERAL INFORMATION:  
APPLICANT: McDonald, John R.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND OTHER INFLAMMATORY CONDITIONS AND DISORDERS  
FILE REFERENCE: 25020-601E  
CURRENT APPLICATION NUMBER: US/10/375,209A  
CURRENT FILING DATE: 2003-02-24  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 20  
LENGTH: 76  
TYPE: PRT  
ORGANISM: homo sapien  
FEATURE:  
OTHER INFORMATION: Human Chemokine Polypeptide: MCP-1  
US-10-375-209A-20

Query Match 100.0%; Score 405; DB 4; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.4e-41;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60  
DB 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76  
DB 61 QDSMDHLDKQTQTPKT 76

RESULT 6  
US-10-332-038A-5  
Sequence 5, Application US/10332038A  
Publication No. US20040077835A1  
GENERAL INFORMATION:  
APPLICANT: Gryphon Therapeutics, Inc.  
APPLICANT: Offord, Robin  
APPLICANT: Gaertner, Hubert  
APPLICANT: Hartley, Oliver  
TITLE OF INVENTION: Chemokine Receptor Modulators, Production and Use  
FILE REFERENCE: 03504.271  
CURRENT APPLICATION NUMBER: US/10/332,038A  
CURRENT FILING DATE: 2003-05-06  
PRIOR APPLICATION NUMBER: US 60/217,683  
PRIOR FILING DATE: 2000-07-12  
NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 76  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-332-038A-5

Query Match 100.0%; Score 405; DB 4; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.4e-41;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60  
Db 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

Qy 61 QDSMDHLDKQTQTPKT 76  
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 7  
US-10-668-733-7  
; Sequence 7, Application US/10668733  
; Publication No. US20040138422A1  
; GENERAL INFORMATION:  
; APPLICANT: Demotz et al.  
; TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS  
; FILE REFERENCE: 29964/38772A  
; CURRENT APPLICATION NUMBER: US/10/668,733  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: US 60/412,866  
; PRIOR FILING DATE: 2002-09-23  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 76  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
; NAME/KEY: misc feature  
; LOCATION: (75)-(75)  
; OTHER INFORMATION: The Lysine at position 75 is biotinylated  
US-10-668-733-7

Query Match 100.0%; Score 405; DB 4; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.4e-41;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60  
Db 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

Qy 61 QDSMDHLDKQTQTPKT 76  
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 8  
US-10-668-733-14  
; Sequence 14, Application US/10668733  
; Publication No. US20040138422A1  
; GENERAL INFORMATION:  
; APPLICANT: Demotz et al.  
; TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS  
; FILE REFERENCE: 29964/38772A  
; CURRENT APPLICATION NUMBER: US/10/668,733  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: US 60/412,866  
; PRIOR FILING DATE: 2002-09-23  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 14  
; LENGTH: 76  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-10-668-733-14

Query Match 100.0%; Score 405; DB 4; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.4e-41;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60  
Db 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

Qy 61 QDSMDHLDKQTQTPKT 76  
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 9  
US-10-393-804A-1  
; Sequence 1, Application US/10393804A  
; Publication No. US20040185450A1  
; GENERAL INFORMATION:  
; APPLICANT: Heavner, George  
; APPLICANT: Das, Anuk  
; TITLE OF INVENTION: MCP-1 MUTANT PROTEINS, ANTIBODIES, COMPOSITIONS, METHODS AND USES  
; FILE REFERENCE: CEN0290NP  
; CURRENT APPLICATION NUMBER: US/10/393,804A  
; CURRENT FILING DATE: 2003-03-21  
; PRIOR APPLICATION NUMBER: 60/367,932  
; PRIOR FILING DATE: 2002-03-26  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 76  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-393-804A-1

Query Match 100.0%; Score 405; DB 4; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.4e-41;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60  
Db 1 QPDAINAPVTCYCNFTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

Qy 61 QDSMDHLDKQTQTPKT 76  
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 10  
US-10-243-795-7  
; Sequence 7, Application US/10243795  
; Publication No. US20040197303A1  
; GENERAL INFORMATION:  
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.  
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES  
; FILE REFERENCE: 59296.00003  
; CURRENT APPLICATION NUMBER: US/10/243,795  
; CURRENT FILING DATE: 2002-09-13  
; NUMBER OF SEQ ID NOS: 1640  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 76  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

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US-10-243-795-7
Query Match      100.0%; Score 405; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.4e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Qy 61 QDSMDHLDKQTPTPT 76
Db 61 QDSMDHLDKQTPTPT 76

RESULT 11
US-10-872-198-102
; Sequence 102, Application US/10872198
; Publication No. US20050002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VORTSMEIER
; APPLICANT: Ulrich Kettling
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.0002U4
; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR FILING DATE: 2004-05-18
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 102
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-198-102

Query Match      100.0%; Score 405; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.4e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Qy 61 QDSMDHLDKQTPTPT 76
Db 61 QDSMDHLDKQTPTPT 76

RESULT 12
US-10-839-017-8
; Sequence 8, Application US/10839017
; Publication No. US20050058635A1
; GENERAL INFORMATION:
; APPLICANT: DEMUTH, HANS-ULRICH
; APPLICANT: HOFFMANN, TORSTEN
; APPLICANT: NIESTROJ, ANDRE J.
; APPLICANT: SCHILLING, STEPHAN
; TITLE OF INVENTION: USE OF EFFECTORS OF GLUTAMINYL CYCLASE
; FILE REFERENCE: 20488-53

US-10-243-795-7
; CURRENT APPLICATION NUMBER: US/10/839,017
; CURRENT FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,043
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/512,038
; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/468,014
; PRIOR FILING DATE: 2003-05-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-839-017-8

Query Match      100.0%; Score 405; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.4e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Qy 61 QDSMDHLDKQTPTPT 76
Db 61 QDSMDHLDKQTPTPT 76

RESULT 13
US-10-644-277-149
; Sequence 149, Application US/10644277
; Publication No. US20050058639A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean M.
; APPLICANT: Haak-Frendscho, Mary
; APPLICANT: Foord, Orit
; APPLICANT: Liang, Meina L.
; APPLICANT: Ahluwalia, Kiran
; APPLICANT: Bhakta, Sunil
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
; FILE REFERENCE: ABGENIX.091A
; CURRENT APPLICATION NUMBER: US/10/644,277
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 60/404,802
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homosapien
US-10-644-277-149

Query Match      100.0%; Score 405; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.4e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Qy 61 QDSMDHLDKQTPTPT 76
Db 61 QDSMDHLDKQTPTPT 76

RESULT 14
US-10-332-039A-5
; Sequence 5, Application US/10332039A
; Publication No. US20050089970A1
; GENERAL INFORMATION:
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OM protein - protein search, using sw model

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Title: US-10-644-277-149

Perfect score: 405

Sequence: 1 QPDAINAPVTCYNFTNRKI.....QKWQDSMDHLDKQTQTPKT 76

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Gapop 10.0 , Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 88029

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### Database :

Published Applications AA New:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep.\*  
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3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
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8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	405	100.0	99	7 US-11-043-788-8	Sequence 8, Appli
2	273	67.4	74	6 US-10-509-292-1	Sequence 1, Appli
3	273	67.4	97	6 US-10-995-561-900	Sequence 900, App
4	218	53.8	65	7 US-11-043-788-9	Sequence 9, Appli
5	176.5	43.6	73	6 US-10-329-472-7	Sequence 7, Appli
6	145.5	35.9	93	7 US-11-186-284-179	Sequence 179, App
7	133.5	33.0	92	7 US-11-224-076-3	Sequence 3, Appli
8	125	30.9	134	6 US-10-329-472-2	Sequence 2, Appli
9	125	30.9	134	6 US-10-821-234-1597	Sequence 1597, App
10	122.5	30.2	66	7 US-11-175-690-287	Sequence 287, App
11	122.5	30.2	68	7 US-11-175-690-285	Sequence 285, App
12	122.5	30.2	68	7 US-11-175-690-286	Sequence 286, App
13	122.5	30.2	672	7 US-11-175-690-200	Sequence 200, App
14	122.5	30.2	688	7 US-11-175-690-198	Sequence 198, App
15	122.5	30.2	693	7 US-11-175-690-199	Sequence 199, App
16	118.5	29.3	94	6 US-10-131-826A-322	Sequence 322, App
17	99.5	24.6	254	6 US-10-997-747-3	Sequence 3, Appli
18	84.5	20.9	122	6 US-10-512-109-13	Sequence 13, Appli
19	78.5	19.4	28	6 US-10-509-292-44	Sequence 44, Appli
20	76	18.8	21	6 US-10-509-292-23	Sequence 23, Appli
21	76	18.8	28	6 US-10-509-292-42	Sequence 42, Appli
22	76	18.8	28	6 US-10-509-292-43	Sequence 43, Appli
23	76	18.8	28	6 US-10-509-292-45	Sequence 45, Appli
24	71	17.5	20	6 US-10-509-292-24	Sequence 24, Appli
25	70	17.3	19	6 US-10-509-292-25	Sequence 25, Appli

26	70	17.3	99	7 US-11-186-284-87	Sequence 87, Appli
27	68	16.8	67	6 US-10-945-674A-3	Sequence 3, Appli
28	66	16.3	89	7 US-11-028-922A-7	Sequence 7, Appli
29	65	16.0	18	6 US-10-509-292-26	Sequence 26, Appli
30	65	16.0	21	6 US-10-509-292-17	Sequence 17, Appli
31	61.5	15.2	67	6 US-10-945-674A-8	Sequence 8, Appli
32	61	15.1	67	6 US-10-945-674A-5	Sequence 5, Appli
33	61	15.1	67	6 US-10-945-674A-6	Sequence 6, Appli
34	61	15.1	67	6 US-10-945-674A-9	Sequence 9, Appli
35	61	15.1	67	6 US-10-945-674A-12	Sequence 12, Appli
36	61	15.1	67	7 US-11-136-097-6	Sequence 5, Appli
37	61	15.1	68	7 US-11-028-922A-5	Sequence 5, Appli
38	61	15.1	72	7 US-11-136-097-7	Sequence 7, Appli
39	61	15.1	89	7 US-11-028-922A-6	Sequence 6, Appli
40	60.5	14.9	67	6 US-10-945-674A-4	Sequence 4, Appli
41	60	14.8	18	6 US-10-509-292-14	Sequence 14, Appli
42	60	14.8	19	6 US-10-509-292-15	Sequence 15, Appli
43	60	14.8	20	6 US-10-509-292-16	Sequence 16, Appli
44	60	14.8	27	6 US-10-509-292-46	Sequence 46, Appli
45	60	14.8	27	6 US-10-509-292-47	Sequence 47, Appli

#### ALIGNMENTS

##### RESULT 1

US-11-043-788-8

; Sequence 8, Application US/11043788

; Publication No. US20060014166A1

; GENERAL INFORMATION:

; APPLICANT: Compugen Ltd

; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS

; FILE OF INVENTION: THEREOF FOR DIAGNOSIS OF ENDOMETRIOSIS

; FILE REFERENCE: 1847.1006

; CURRENT APPLICATION NUMBER: US/11/043,788

; CURRENT FILING DATE: 2005-01-27

; NUMBER OF SEQ ID NOS: 506

; SEQ ID NO 8

; LENGTH: 99

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-043-788-8

Query Match 100.0%; Score 405; DB 7; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3e-45;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QPDAINAPVTCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKETCADPKOKWV	60
Db	24	QPDAINAPVTCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKETCADPKOKWV	83

Qy	61	QDSMDHLDKQTQTPKT	76
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Db	84	QDSMDHLDKQTQTPKT	99
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##### RESULT 2

US-10-509-292-1

; Sequence 1, Application US/10509292

; Publication No. US20050287159A1

; GENERAL INFORMATION:

; APPLICANT: Mercia Pharma LLC

; TITLE OF INVENTION: Methods and Compositions for Treating and Preventing Botaxin

; FILE OF INVENTION: Mediated Inflammatory Conditions

; FILE REFERENCE: MERPH.001

; CURRENT APPLICATION NUMBER: US/10/509,292

; CURRENT FILING DATE: 2004-09-23

; PRIOR APPLICATION NUMBER: US 60/367,591

; PRIOR FILING DATE: 2002-03-25

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1

; LENGTH: 74



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; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-179

Query Match      35.9%; Score 145.5; DB 7; Length 93;
Best Local Similarity 40.3%; Pred. No. 5.6e-12;
Matches 27; Conservative 16; Mismatches 23; Indels 1; Gaps 1;

Qy 2 PDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWVQ 61
Db 25 PLAADTPTACCFSTYTSRQIPQNFITADYFE-TSSQCKSPSVIFLTGRGQVCADPSEEWVQ 83
Qy 62 DSMDHL 68
Db 84 KYVSDLE 90

RESULT 7
US-11-224-076-3
; Sequence 3, Application US/11224076
; Publication No. US2006008882A1
; GENERAL INFORMATION:
; APPLICANT: Wei et al.
; FILE REFERENCE: Chemokine Alpha-5
; CURRENT APPLICATION NUMBER: US/11/224,076
; PRIOR FILING DATE: 2005-09-13
; PRIOR APPLICATION NUMBER: US/10/114,482
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 09/195,106
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/066,369
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-224-076-3

Query Match      33.0%; Score 133.5; DB 7; Length 92;
Best Local Similarity 37.3%; Pred. No. 1.9e-10;
Matches 25; Conservative 16; Mismatches 25; Indels 1; Gaps 1;

Qy 2 PDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWVQ 61
Db 25 PIGSDPTSCCFSTYTSRKIRNFVMDYFE-TSSLCSPQAVVFLTKGRQICADPSEEPVN 83
Qy 62 DSMDHL 68
Db 84 EYVNDLE 90

RESULT 8
US-10-329-472-2
; Sequence 2, Application US/10329472
; Publication No. US2005024488A1
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: Human Chemokine Beta-9
; FILE REFERENCE: PFI31P2DI

; CURRENT APPLICATION NUMBER: US/10/329,472
; CURRENT FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: US 08/793,381
; PRIOR FILING DATE: 1997-05-19
; PRIOR APPLICATION NUMBER: PCT/US95/06260
; PRIOR FILING DATE: 1996-02-29
; PRIOR APPLICATION NUMBER: US 08/294,251
; PRIOR FILING DATE: 1994-08-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-329-472-2

Query Match      30.9%; Score 125; DB 6; Length 134;
Best Local Similarity 41.2%; Pred. No. 3.6e-09;
Matches 28; Conservative 12; Mismatches 24; Indels 4; Gaps 3;

Qy 11 CCYNFTNRKISVQRLASVRRITSS-KCPKEAVIF--KTIIVAKEICADPKQKWQDSMDHL 67
Db 31 CCLKYSQKIPAKVVRYSYRKQEPSLGCISIPAILFLPKRSQAEICADPKELWVQQLMQHL 90
Qy 68 DKQTQTPK 75
Db 91 DK-TPSPQ 97

RESULT 9
US-10-821-234-1597
; Sequence 1597, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1597
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1597

Query Match      30.9%; Score 125; DB 6; Length 134;
Best Local Similarity 41.2%; Pred. No. 3.6e-09;
Matches 28; Conservative 12; Mismatches 24; Indels 4; Gaps 3;

Qy 11 CCYNFTNRKISVQRLASVRRITSS-KCPKEAVIF--KTIIVAKEICADPKQKWQDSMDHL 67
Db 31 CCLKYSQKIPAKVVRYSYRKQEPSLGCISIPAILFLPKRSQAEICADPKELWVQQLMQHL 90
Qy 68 DKQTQTPK 75
Db 91 DK-TPSPQ 97

RESULT 10
US-11-175-690-287
; Sequence 287, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseeltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
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QY 8 PVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWQD 62  
DB 7 PSECCFTYTTYKIQRIMDYIE-TNSQCSKPGIVFITKRGHSVCTNPSPDKWQD 60

RESULT 12

US-11-175-690-286  
; Sequence 286, Application US/11175690  
; Publication No. US20060014254A1  
; GENERAL INFORMATION:  
; APPLICANT: Haseltine et al.  
; FILE REFERENCE: PF605  
; CURRENT APPLICATION NUMBER: US/11/175,690  
; CURRENT FILING DATE: 2005-07-07  
; PRIOR APPLICATION NUMBER: PCT/US04/001369  
; PRIOR FILING DATE: 2004-01-20  
; PRIOR APPLICATION NUMBER: US 60/441,305  
; PRIOR FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: US 60/453,201  
; PRIOR FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: US 60/467,222  
; PRIOR FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: US 60/472,816  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: US 60/476,267  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/505,172  
; PRIOR FILING DATE: 2003-09-24  
; PRIOR APPLICATION NUMBER: US 60/506,746  
; NUMBER OF SEQ ID NOS: 568  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 286  
; LENGTH: 68  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-175-690-286

Query Match 30.2%; Score 122.5; DB 7; Length 68;  
Best Local Similarity 40.0%; Pred. No. 3.5e-09;  
Matches 22; Conservative 9; Mismatches 23; Indels 1; Gaps 1;

QY 8 PVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWQD 62  
DB 7 PSECCFTYTTYKIQRIMDYIE-TNSQCSKPGIVFITKRGHSVCTNPSPDKWQD 60

RESULT 13

US-11-175-690-200  
; Sequence 200, Application US/11175690  
; Publication No. US20060014254A1  
; GENERAL INFORMATION:  
; APPLICANT: Haseltine et al.  
; FILE REFERENCE: PF605  
; CURRENT APPLICATION NUMBER: US/11/175,690  
; CURRENT FILING DATE: 2005-07-07  
; PRIOR APPLICATION NUMBER: PCT/US04/001369  
; PRIOR FILING DATE: 2004-01-20  
; PRIOR APPLICATION NUMBER: US 60/441,305  
; PRIOR FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: US 60/453,201  
; PRIOR FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: US 60/467,222  
; PRIOR FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: US 60/472,816  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: US 60/476,267  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/505,172  
; PRIOR FILING DATE: 2003-09-24  
; PRIOR APPLICATION NUMBER: US 60/506,746

; CURRENT APPLICATION NUMBER: US/11/175,690  
; CURRENT FILING DATE: 2005-07-07  
; PRIOR APPLICATION NUMBER: PCT/US04/001369  
; PRIOR FILING DATE: 2004-01-20  
; PRIOR APPLICATION NUMBER: US 60/441,305  
; PRIOR FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: US 60/453,201  
; PRIOR FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: US 60/467,222  
; PRIOR FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: US 60/472,816  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: US 60/476,267  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/505,172  
; PRIOR FILING DATE: 2003-09-24  
; PRIOR APPLICATION NUMBER: US 60/506,746  
; PRIOR FILING DATE: 2003-09-30  
; NUMBER OF SEQ ID NOS: 568  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 287  
; LENGTH: 66  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-175-690-287

Query Match 30.2%; Score 122.5; DB 7; Length 66;  
Best Local Similarity 40.0%; Pred. No. 3.4e-09;  
Matches 22; Conservative 9; Mismatches 23; Indels 1; Gaps 1;

QY 8 PVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWQD 62  
DB 5 PSECCFTYTTYKIQRIMDYIE-TNSQCSKPGIVFITKRGHSVCTNPSPDKWQD 58

RESULT 11

US-11-175-690-285  
; Sequence 285, Application US/11175690  
; Publication No. US20060014254A1  
; GENERAL INFORMATION:  
; APPLICANT: Haseltine et al.  
; FILE REFERENCE: PF605  
; CURRENT APPLICATION NUMBER: US/11/175,690  
; CURRENT FILING DATE: 2005-07-07  
; PRIOR APPLICATION NUMBER: PCT/US04/001369  
; PRIOR FILING DATE: 2004-01-20  
; PRIOR APPLICATION NUMBER: US 60/441,305  
; PRIOR FILING DATE: 2003-01-22  
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; PRIOR FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: US 60/467,222  
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; PRIOR APPLICATION NUMBER: US 60/476,267  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/505,172  
; PRIOR FILING DATE: 2003-09-24  
; PRIOR APPLICATION NUMBER: US 60/506,746  
; PRIOR FILING DATE: 2003-09-30  
; NUMBER OF SEQ ID NOS: 568  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 285  
; LENGTH: 68  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-175-690-285

Query Match 30.2%; Score 122.5; DB 7; Length 68;  
Best Local Similarity 40.0%; Pred. No. 3.5e-09;  
Matches 22; Conservative 9; Mismatches 23; Indels 1; Gaps 1;

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; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 200
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-200

Query Match      30.2%; Score 122.5; DB 7; Length 672;
Best Local Similarity 40.0%; Pred. No. 4.7e-08;
Matches 22; Conservative 9; Mismatches 23; Indels 1; Gaps 1;

Qy      8 PVTCCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKWQD 62
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      26 PSECCTTYTYKIPRQIMDYIE-TNSQCSKPGIVFITKRGHSVCTNPSPDKWQD 79

RESULT 14
US-11-175-690-198
; Sequence 198, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 198
; LENGTH: 688
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-198

Query Match      30.2%; Score 122.5; DB 7; Length 688;
Best Local Similarity 40.0%; Pred. No. 4.8e-08;
Matches 22; Conservative 9; Mismatches 23; Indels 1; Gaps 1;

Qy      8 PVTCCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKWQD 62
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      26 PSECCTTYTYKIPRQIMDYIE-TNSQCSKPGIVFITKRGHSVCTNPSPDKWQD 79

RESULT 15
US-11-175-690-199
; Sequence 199, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
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; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 199
; LENGTH: 693
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-199

Query Match      30.2%; Score 122.5; DB 7; Length 693;
Best Local Similarity 40.0%; Pred. No. 4.8e-08;
Matches 22; Conservative 9; Mismatches 23; Indels 1; Gaps 1;

Qy      8 PVTCCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKWQD 62
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Search completed: February 3, 2006, 10:00:35  
Job time : 3.06569 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 6, 2006, 14:21:14 ; Search time 196 Seconds

(without alignments)

35.868 Million cell updates/sec

Title: US-10-644-277-149\_COPY\_20\_35

Perfect score: 73

Sequence: 1 ISVQLASVRRITSSK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A\_Geneseq21.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	73	100.0	23	4	AAV72689 Human mon
3	73	100.0	24	4	AAV72682 Human mon
4	73	100.0	26	4	AAV72683 Human mon
5	73	100.0	26	8	ADM71779 Chemokine
6	73	100.0	26	8	ADM71742 Chemokine
7	73	100.0	26	8	ADM71778 Chemokine
8	73	100.0	35	8	ADM71727 Chemokine
9	73	100.0	35	8	ADM71718 Chemokine
10	73	100.0	35	8	ADM71720 Chemokine
11	73	100.0	35	8	ADM71736 Chemokine
12	73	100.0	35	8	ADM71741 Chemokine
13	73	100.0	35	8	ADM71725 Chemokine
14	73	100.0	35	8	ADM71726 Chemokine
15	73	100.0	35	8	ADM71719 Chemokine
16	73	100.0	35	8	ADM71723 Chemokine
17	73	100.0	35	8	ADM71730 Chemokine
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21	73	100.0	35	8	ADM71735 Chemokine
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23	73	100.0	35	8	ADM71733 Chemokine
24	73	100.0	35	8	ADM71780 Chemokine

25	73	100.0	35	8	ADM71721	Chemokine
26	73	100.0	35	8	ADM71724	Chemokine
27	73	100.0	35	8	ADM71731	Chemokine
28	73	100.0	35	8	ADM71739	Chemokine
29	73	100.0	35	8	ADM71729	Chemokine
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32	73	100.0	35	8	ADM71738	Chemokine
33	73	100.0	41	8	ADM71745	Chemokine
34	73	100.0	41	8	ADM71783	Chemokine
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38	73	100.0	68	2	AAW13597	Monocyte
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40	73	100.0	68	2	AAW95035	MCP-1 ana
41	73	100.0	68	2	AAW95036	MCP-1 ana
42	73	100.0	68	8	ADN36565	Chemokine
43	73	100.0	68	8	ADN36567	Chemokine
44	73	100.0	69	2	ADN36562	Monocyte
45	73	100.0	69	2	ADN36567	Chemokine
46	73	100.0	69	7	ADD14999	Truncated
47	73	100.0	69	8	ADN36567	Chemokine
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50	73	100.0	74	8	ADU04446	Human mon
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99	73	100.0	76	9	AEA16549	Aea16549 Human mon	172	56	76.7	74	5	AAO14141	AAO14141 Human eot
100	73	100.0	76	9	AE92582	Aeb92582 Glutamin	173	56	76.7	74	7	ADC89677	ADC89677 Human eot
101	73	100.0	77	2	AAR6859	Aar6859 Mature MC	174	56	76.7	74	7	ADF42623	Adf42623 Mature hu
102	73	100.0	77	2	AY14222	Aay14222 Chemokine	175	56	76.7	74	8	ADJ66688	Adj66688 Human mat
103	73	100.0	77	2	ADC9671	Adc9671 Human MCP	176	56	76.7	74	8	ADO32082	Ado32082 Eotaxin p
104	73	100.0	77	7	ADC9672	Adc9672 Human MCP	177	56	76.7	74	8	ADR40246	Adr40246 Human mat
105	73	100.0	91	8	ADN36564	Adn36564 Chemokine	178	56	76.7	74	8	ADSI19902	Adsi19902 Modified
106	73	100.0	92	8	ADN36566	Adn36566 Chemokine	179	56	76.7	74	8	ADSI19899	Adsi19899 Modified
107	73	100.0	98	1	ADJ36261	Adj36261 Self-coal	180	56	76.7	74	8	ADSI19906	Adsi19906 Human che
108	73	100.0	99	1	AAP95387	Aap95387 Human mon	181	56	76.7	74	8	ADR90676	Adr90676 Human eot
109	73	100.0	99	2	AAR06398	Aar06398 Human MCP	182	56	76.7	74	8	ADSI18178	Adsi18178 Mature hu
110	73	100.0	99	2	AAR28663	Aar28663 MCF_3/20	183	56	76.7	74	9	ADV90271	Adv90271 Protease-
111	73	100.0	99	2	AAR73914	Aar73914 Human mon	184	56	76.7	82	2	AAW44721	Aaw44721 Amino aci
112	73	100.0	99	2	AAR70800	Aar70800 Chemoattr	185	56	76.7	82	2	AAW00667	Aaw00667 Pancreas
113	73	100.0	99	2	AAW40174	Aaw40174 Macrophag	186	56	76.7	82	2	AAW00667	Aaw00667 Pancreas
114	73	100.0	99	2	AY26176	Aay26176 Monocyte	187	56	76.7	82	2	AAW44721	Aaw44721 Amino aci
115	73	100.0	99	2	AY48391	Aay48391 Human pro	188	56	76.7	82	2	AAW10099	Aaw10099 Human eot
116	73	100.0	99	3	AAB15785	Aab15785 Human che	189	56	76.7	82	2	AAW10099	Aaw10099 Human eot
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118	73	100.0	99	5	AAM52440	Aam52440 HIV_Nef1	191	56	76.7	82	2	AAW10099	Aaw10099 Human eot
119	73	100.0	99	5	AAU77179	Aau77179 Human sma	192	56	76.7	82	2	AAW10099	Aaw10099 Human eot
120	73	100.0	99	5	ABU80901	Abu80901 Human MCP	193	56	76.7	82	2	AAW10099	Aaw10099 Human eot
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122	73	100.0	99	5	ADG47764	Adg47764 Monocyte	195	56	76.7	82	2	AAW10099	Aaw10099 Human eot
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126	73	100.0	99	7	ADN95634	Adn95634 Human BEC	199	56	76.7	82	2	AAW10099	Aaw10099 Human eot
127	73	100.0	99	7	ADN95618	Adn95618 Human mon	200	56	76.7	82	2	AAW10099	Aaw10099 Human eot
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130	73	100.0	99	8	ADN04746	Adn04746 Antipeori	203	56	76.7	82	2	AAW10099	Aaw10099 Human eot
131	73	100.0	99	8	ADP75932	Adp75932 Chemokine	204	56	76.7	82	2	AAW10099	Aaw10099 Human eot
132	73	100.0	99	8	ADQ76210	Adq76210 Chemokine	205	56	76.7	82	2	AAW10099	Aaw10099 Human eot
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134	73	100.0	99	8	ADR05376	Adr05376 Human mon	207	56	76.7	82	2	AAW10099	Aaw10099 Human eot
135	73	100.0	99	8	ADR40231	Adr40231 Human eot	208	56	76.7	82	2	AAW10099	Aaw10099 Human eot
136	73	100.0	99	8	ADP24779	Adp24779 PRO poly	209	56	76.7	82	2	AAW10099	Aaw10099 Human eot
137	73	100.0	99	8	ADS16435	Ads16435 Human cyt	210	56	76.7	82	2	AAW10099	Aaw10099 Human eot
138	73	100.0	99	8	ADU04444	Adu04444 Human sma	211	56	76.7	82	2	AAW10099	Aaw10099 Human eot
139	73	100.0	99	8	ADT75242	Adt75242 Human mon	212	56	76.7	82	2	AAW10099	Aaw10099 Human eot
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141	73	100.0	99	9	ADV70217	Adv70217 Tumor-ass	214	56	76.7	82	2	AAW10099	Aaw10099 Human eot
142	73	100.0	99	9	ADV70224	Adv70224 Tumor-ass	215	56	76.7	82	2	AAW10099	Aaw10099 Human eot
143	73	100.0	99	9	AEA89981	Aea89981 Human mon	216	56	76.7	82	2	AAW10099	Aaw10099 Human eot
144	73	100.0	99	9	AE894408	Aeb94408 Human C-C	217	56	76.7	82	2	AAW10099	Aaw10099 Human eot
145	73	100.0	99	9	ABE70237	Aeb70237 Small ind	218	56	76.7	82	2	AAW10099	Aaw10099 Human eot
146	73	100.0	122	7	ADU14997	Adu14997 Self-coal	219	56	76.7	82	2	AAW10099	Aaw10099 Human eot
147	73	100.0	133	8	ADJ36265	Adj36265 Self-coal	220	56	76.7	82	2	AAW10099	Aaw10099 Human eot
148	73	100.0	325	3	AAV69049	Aay69049 A chemoki	221	56	76.7	82	2	AAW10099	Aaw10099 Human eot
149	73	100.0	327	3	AAV69050	Aay69050 A chemoki	222	56	76.7	82	2	AAW10099	Aaw10099 Human eot
150	73	100.0	331	9	AD258561	Adz58561 Mature hu	223	56	76.7	82	2	AAW10099	Aaw10099 Human eot
151	73	100.0	332	3	AAV69051	Aay69051 A chemoki	224	56	76.7	82	2	AAW10099	Aaw10099 Human eot
152	73	100.0	23	4	AAV72692	Aay72692 Human mon	225	56	76.7	82	2	AAW10099	Aaw10099 Human eot
153	68	93.2	23	4	ABG11504	Abg11504 Novel hum	226	56	76.7	82	2	AAW10099	Aaw10099 Human eot
154	67	91.8	44	4	AAV72693	Aay72693 Human mon	227	56	76.7	82	2	AAW10099	Aaw10099 Human eot
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156	63	86.3	19	4	AAV72696	Aay72696 Human mon	229	56	76.7	82	2	AAW10099	Aaw10099 Human eot
157	63	86.3	23	4	AAV72690	Aay72690 Human mon	230	56	76.7	82	2	AAW10099	Aaw10099 Human eot
158	63	86.3	76	2	AAV72697	Aay72697 Human mon	231	56	76.7	82	2	AAW10099	Aaw10099 Human eot
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162	58	79.5	23	4	AAV72684	Aay72684 Human mon	235	56	76.7	82	2	AAW10099	Aaw10099 Human eot
163	56	76.7	37	8	ABE80908	Aeb80908 Human eot	236	56	76.7	82	2	AAW10099	Aaw10099 Human eot
164	56	76.7	37	8	ADR40241	Adr40241 Human eot	237	56	76.7	82	2	AAW10099	Aaw10099 Human eot
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166	56	76.7	73	7	ADN08877	Adn08877 Eotaxin c	239	56	76.7	82	2	AAW10099	Aaw10099 Human eot
167	56	76.7	73	9	ADW22565	Adw22565 Human mat	240	56	76.7	82	2	AAW10099	Aaw10099 Human eot
168	56	76.7	74	3	AAV69023	Aay69023 Amino aci	241	56	76.7	82	2	AAW10099	Aaw10099 Human eot
169	56	76.7	74	5	AAO20001	Aao20001 74-mer pr	242	56	76.7	82	2	AAW10099	Aaw10099 Human eot
170	56	76.7	74	5	AAO20008	Aao20008 Human che	243	56	76.7	82	2	AAW10099	Aaw10099 Human eot

244	47	64.4	76	9	AEb92585	Glutaminy
245	47	64.4	77	2	Ay14224	Chemokine
246	47	64.4	77	3	Ay69064	Amino aci
247	47	64.4	91	8	ADN36560	Chemokine
248	47	64.4	92	8	ADN36562	Chemokine
249	47	64.4	99	2	AAR70801	Chemoattr
250	47	64.4	99	3	AAB15787	Human che
251	47	64.4	99	5	AAO19999	99-mex pr
252	47	64.4	99	5	ABP65245	Hypoxia-r
253	47	64.4	99	5	ADZ58696	Human MCP
254	47	64.4	99	7	ADC78915	Human MCP
255	47	64.4	99	7	ADP65189	Human sma
256	47	64.4	99	8	ADJ66686	Human MCP
257	47	64.4	99	8	ADQ32080	Chemokine
258	47	64.4	99	8	ADO47924	Human che
259	47	64.4	99	8	ADP24078	PRO poly
260	47	64.4	99	9	ADW20994	Human MCP
261	47	64.4	109	4	AAU27814	FULL-leng
262	47	64.4	109	5	AAU52441	HIV Nef1
263	47	64.4	109	5	AAO21490	Small ind
264	47	64.4	110	5	ABB80904	Human MCP
265	47	64.4	110	8	ADR40234	Human eot
266	47	64.4	133	8	ADU24453	Novel glu
267	47	64.4	137	2	AAZ29893	Human MCP
268	47	64.4	143	4	AAO12965	Human pol
269	47	64.4	151	2	AAZ29898	Human MCP
270	47	64.4	325	3	AAZ69052	A chemoki
271	47	64.4	327	3	AAZ69053	DNA encod
272	47	64.4	332	3	AAZ69054	A chemoki
273	47	64.4	348	2	AAZ29903	Human MCP
274	47	64.4	359	2	AAZ29913	Human MCP
275	47	64.4	361	2	AAZ29912	Human MCP
276	47	64.4	471	5	AAZ29958	MCP3-HIV
277	47	64.4	601	2	AAZ29901	Human IP-
278	47	64.4	931	5	AAE23965	MCP3-gp16
279	46	63.0	70	5	AAO19998	70-mex pr
280	46	63.0	70	8	ADJ66685	Human mat
281	46	63.0	70	8	ADO32079	Botaxin m
282	46	63.0	70	9	ADW20993	Botaxin m
283	46	63.0	148	7	ADD46369	Rat Prote
284	45	61.6	92	5	ABB80905	Murine MC
285	45	61.6	92	8	ADR40235	Mouse eot
286	45	61.6	97	2	AAR70803	Growth fa
287	45	61.6	97	5	ADZ58695	Mouse MCP
288	45	61.6	156	2	AAZ29907	Murine MCP
289	45	61.6	171	2	AAZ29909	Murine MC
290	44	60.3	71	2	AAO7238	Truncated
291	44	60.3	71	2	AAO7234	Truncated
292	44	60.3	72	2	AAR70804	Chemoattr
293	44	60.3	76	3	AAZ69031	Amino aci
294	44	60.3	76	5	AAG78390	Human che
295	44	60.3	76	5	AAG68353	Human mon
296	44	60.3	76	5	AAO21099	Protein o
297	44	60.3	76	5	AAO21109	MCP-2 che
298	44	60.3	76	6	ABB95533	Amino aci
299	44	60.3	76	7	ADC98686	Human MCP
300	44	60.3	76	7	ADC89674	Human MCP
301	44	60.3	76	7	ADE80844	MCP2 chem
302	44	60.3	76	7	ADE80873	MCP2 chem
303	44	60.3	76	8	ADU24448	Novel glu
304	44	60.3	76	8	ADU46723	CCL8, sub
305	44	60.3	76	9	ADZ71379	N-termina
306	44	60.3	76	9	AEA41185	MCP-2 gly
307	44	60.3	76	9	AEA41185	MCP-2 gly
308	44	60.3	76	9	ABE92581	Glutaminy
309	44	60.3	77	3	AAB15786	Human che
310	44	60.3	77	5	ABB80903	Human MCP
311	44	60.3	77	5	AAG78395	Mouse/hum
312	44	60.3	77	5	AAG68358	Chimeric
313	44	60.3	77	6	ABB99538	Amino aci
314	44	60.3	77	8	ADR40233	Human eot
315	44	60.3	78	7	ADC98691	Human mmd
316	44	60.3	94	5	ANG78393	Mouse/hum

317	44	60.3	94	5	AAG68356	Chimeric
318	44	60.3	94	6	ABB99536	Amino aci
319	44	60.3	94	7	ADC98689	Human mcl
320	44	60.3	95	4	ABB11828	Human che
321	44	60.3	99	2	AAZ07237	Wild type
322	44	60.3	99	2	AAZ07233	C-C chemo
323	44	60.3	99	2	AAZ05300	Human MCP
324	44	60.3	99	5	ADZ58702	Human MCP
325	44	60.3	99	8	ADQ20008	Human eot
326	44	60.3	99	8	ADP55086	Human PRO
327	44	60.3	109	2	AAR24353	Cytokine
328	44	60.3	109	2	AAR26655	Human bet
329	44	60.3	109	2	AAW42072	Human MC
330	44	60.3	109	5	ABP65253	Hypoxia-r
331	44	60.3	109	5	ABG35167	Reference
332	44	60.3	109	5	ABG35169	Polymorph
333	44	60.3	109	5	ABG35168	Polymorph
334	44	60.3	109	5	ADZ58742	Human MCP
335	44	60.3	109	7	ADZ58765	Human MCP
336	44	60.3	109	8	ABM81857	Tumour-as
337	43	58.9	9	2	AAZ14255	Chemokine
338	43	58.9	9	3	AAZ15842	Human che
339	43	58.9	10	2	AAZ14280	Chemokine
340	43	58.9	10	3	AAZ15835	Human che
341	43	58.9	15	2	AAZ14234	Chemokine
342	43	58.9	15	3	AAZ18354	Human che
343	43	58.9	15	3	AAZ15852	Human che
344	43	58.9	15	3	AAZ15772	Human che
345	43	58.9	16	3	AAZ15857	Human che
346	43	58.9	17	2	AAZ14273	Chemokine
347	43	58.9	17	2	AAZ14258	Chemokine
348	43	58.9	17	2	AAZ14286	Chemokine
349	43	58.9	17	3	AAZ15841	Human che
350	42	57.5	14	4	AAZ72697	Human mon
351	42	57.5	301	6	AAZ93760	Human nov
352	42	57.5	301	6	ABU00303	Human pro
353	42	57.5	352	4	ABG03657	Novel hum
354	42	57.5	771	6	AAU65531	Propionib
355	42	57.5	771	6	ABM62050	Propionib
356	42	57.5	1480	6	ABM65520	Propionib
357	41	56.2	18	4	AAZ72700	Human mon
358	41	56.2	18	4	AAZ72696	Human mon
359	41	56.2	321	7	ABO79927	Pseudomon
360	41	56.2	356	7	ABO83985	Pseudomon
361	41	56.2	919	8	ADL26748	Human syn
362	41	56.2	931	4	ABG18567	Novel hum
363	41	56.2	1908	4	ABG18569	Novel hum
364	40	54.8	475	9	ABE39330	L. pneumo
365	40	54.8	491	9	ABE35895	L. pneumo
366	40	54.8	492	8	ADK67290	Acidovor
367	39	53.4	12	8	ADS18308	Human eot
368	39	53.4	12	8	ADS18307	Human eot
369	39	53.4	12	8	ADS18309	Human eot
370	39	53.4	375	9	ABE54572	Vibrio vu
371	39	53.4	1307	8	ADU02646	Novel hum
372	38	52.1	14	4	AAZ72699	Human mon
373	38	52.1	44	7	ADF70122	Acma-type
374	38	52.1	179	8	ADZ74488	Plant ful
375	38	52.1	223	7	ADC87129	Human GPC
376	38	52.1	311	4	ADG73016	Olfactory
377	38	52.1	342	4	AAZ72843	Human olf
378	38	52.1	423	5	AAE22839	Human pho
379	38	52.1	547	7	ABM85898	Rice abio
380	38	52.1	564	9	AEA20320	Novel hum
381	38	52.1	802	5	AAE22843	Human pho
382	38	52.1	818	7	ADB61634	Human 818
383	38	52.1	1026	5	ABB07497	Human lip
384	38	52.1	1045	7	ADC10174	Human NOV
385	37	50.7	14	4	AAZ72698	Human mon
386	37	50.7	197	6	ABU29465	Protein e
387	37	50.7	198	7	ADH86543	Enterococ
388	37	50.7	241	1	AAZ90060	N-termina
389	37	50.7	241	2	AAZ26128	Flagellin

390	37	50.7	248	5	ABB06152	Abb06152 Human NS	463	36	49.3	762	4	AAB94398	Aab94398 Human pro
391	37	50.7	317	1	AAP70303	Aap70303 Sequence	464	36	49.3	789	6	ABU23388	Abu23388 Protein e
392	37	50.7	349	4	AAB49636	Aab49636 Escherich	465	36	49.3	844	8	AD061905	Ad061905 Transcrip
393	37	50.7	369	1	AAP70309	Aap70309 Sequence	466	36	49.3	905	4	ABG05208	Abg05208 Novel hum
394	37	50.7	387	1	AAP70307	Aap70307 Sequence	467	36	49.3	1003	4	ABG23021	Abg23021 Novel hum
395	37	50.7	395	1	AAP70308	Aap70308 Sequence	468	36	49.3	1022	6	ABU27718	Abu27718 Protein e
396	37	50.7	414	1	AAP70313	Aap70313 Sequence	469	36	49.3	1134	6	ABU45323	Abu45323 Protein e
397	37	50.7	425	1	AAP70315	Aap70315 Sequence	470	36	49.3	1148	4	AU434541	Au434541 E. coli c
398	37	50.7	436	4	AAB49637	Aab49637 Escherich	471	36	49.3	1148	4	AU382333	Au382333 Salmonell
399	37	50.7	446	1	AAP70314	Aap70314 Sequence	472	36	49.3	1148	6	AU47974	Au47974 Protein e
400	37	50.7	476	8	ADX71308	Adx71308 Plant ful	473	36	49.3	1148	6	ABU31825	Abu31825 Protein e
401	37	50.7	498	1	AAP70302	Aap70302 Sequence	474	36	49.3	1148	6	ABU28601	Abu28601 Protein e
402	37	50.7	498	4	AAB49641	Aab49641 Escherich	475	36	49.3	1152	6	ABM67058	Abm67058 Photorhab
403	37	50.7	500	2	AAR90303	Aar90303 Thioresox	476	36	49.3	1154	7	ABO61207	Abu61207 Klebsiell
404	37	50.7	527	9	ABM96031	Abm96031 M. xanthu	477	36	49.3	1166	6	ABU40581	Abu40581 Protein e
405	37	50.7	550	9	ABE91490	Abm91490 Microbial	478	36	49.3	1172	5	AU96983	Au96983 Human tra
406	37	50.7	565	4	AAB49642	Aab49642 Escherich	479	36	49.3	1172	5	AU97451	Au97451 Human tra
407	37	50.7	568	4	AAB49639	Aab49639 Escherich	480	36	49.3	1172	8	ADL16938	Adl16938 Human tra
408	37	50.7	570	4	AAB49640	Aab49640 Escherich	481	36	49.3	1173	7	ADF07680	Adf07680 Bacterial
409	37	50.7	588	4	AAB49638	Aab49638 Escherich	482	36	49.3	1204	9	ADU98137	Adu98137 Human ion
410	37	50.7	595	3	AAI52370	Aay52370 Escherich	483	36	49.3	1211	8	ADRO9085	Aaol9088 Human pro
411	37	50.7	605	4	AAB49643	Aab49643 Escherich	484	36	49.3	1235	5	ADCI0052	Adci10052 Human NOV
412	37	50.7	1078	4	ABG21954	Abg21954 Novel hum	485	36	49.3	1237	5	AEE21180	Aee21180 Human TRI
413	37	50.7	1265	5	ABP73331	Abp73331 Candida a	486	36	49.3	1262	4	ABG20674	Abg20674 Novel hum
414	37	50.7	1309	4	ABG30366	Abg30366 Novel hum	487	36	49.3	1262	4	ABR82700	AbR82700 Human cal
415	37	50.7	1443	8	ADN21466	Adn21466 Bacterial	488	36	49.3	1322	7	ABR82701	AbR82701 Human KIA
416	36.5	50.0	220	4	AAU53626	Aam53626 Propionib	489	36	49.3	1349	7	ABR82701	AbR82701 Human the
417	36.5	50.0	220	6	ABM50145	Abm50145 Propionib	490	36	49.3	1430	8	ADS10713	AdS10713 Novel hum
418	36	49.3	23	4	AAU00933	Aau00933 VH ligand	491	36	49.3	1507	4	ABG30343	Abg30343 Novel hum
419	36	49.3	44	4	AAU21881	Aam21881 Peptide #	492	36	49.3	1585	4	ABG10815	Abg10815 Novel hum
420	36	49.3	44	4	ABB44250	Abb44250 Peptide #	493	36	49.3	1585	4	ABG06075	Abg06075 Novel hum
421	36	49.3	44	4	AAW77987	Aam77987 Human bon	494	36	49.3	1598	4	ABG09655	Abg09655 Novel hum
422	36	49.3	44	4	AAW65289	Aam65289 Human bra	495	36	49.3	1598	4	ABG06618	Abg06618 Novel hum
423	36	49.3	44	5	ABG47003	Abg47003 Human pep	496	36	49.3	1614	2	AAR75917	Aar75917 Polycyveti
424	36	49.3	54	4	AAU45504	Aau45504 Propionib	497	36	49.3	1614	2	AAR87538	Aar87538 Polycyveti
425	36	49.3	54	6	ABM42023	Abm42023 Propionib	498	36	49.3	1647	4	ABG04001	Abg04001 Novel hum
426	36	49.3	57	4	AAU56117	Aau56117 Propionib	499	36	49.3	1647	4	ADJ35146	Adj35146 Xylanase
427	36	49.3	57	6	ABM52636	Abm52636 Propionib	500	36	49.3	3001	5	AAE18944	Aae18944 Human PKD
428	36	49.3	118	4	AAAG66777	Aag66777 Human ILF	501	36	49.3	3313	4	AU301134	Au301134 Novel hum
429	36	49.3	131	4	ABG16963	Abg16963 Novel hum	502	36	49.3	3313	4	AAU30134	Au30134 Novel hum
430	36	49.3	149	4	AAO05874	Aao05874 Human pol	503	36	49.3	3858	5	ABP69242	Abp69242 Human pol
431	36	49.3	158	8	ADY06335	Ady06335 Plant ful	504	36	49.3	4292	4	ABG17060	Abg17060 Novel hum
432	36	49.3	159	8	ADY22993	Ady22993 Plant ful	505	36	49.3	4299	6	AAW52622	Aaw52622 Human NOV
433	36	49.3	209	8	AAW39178	Aaw39178 Human PKD	506	36	49.3	4302	2	AAW00870	Aaw00870 Polycyveti
434	36	49.3	209	8	ABO58792	AbO58792 Human gen	507	36	49.3	4302	2	AAW33396	Aaw33396 Human PKD
435	36	49.3	217	8	ADT56318	Adt56318 Plant pol	508	36	49.3	4302	2	AAW23830	Aaw23830 Human PKD
436	36	49.3	223	3	AAW24244	Aaw24244 Arabidops	509	36	49.3	4302	7	AAI00392	Aai00392 Human pol
437	36	49.3	228	8	ABR86058	AbR86058 Aspergill	510	36	49.3	4302	9	ADX08181	Adx08181 Cyclin-de
438	36	49.3	257	9	ABM94771	Abm94771 M. xanthu	511	36	49.3	4303	2	AAU90302	Aau90302 Polycyveti
439	36	49.3	281	8	ADX67927	Adx67927 Plant ful	512	36	49.3	4303	3	AAU95558	Aay95558 Human pol
440	36	49.3	282	7	ABM87880	Abm87880 Rice abio	513	36	49.3	4303	3	AAE18943	Aae18943 Human PKD
441	36	49.3	290	5	ABB92940	Abb92940 Herbicida	514	36	49.3	4303	5	AAE18934	Aae18934 Human PKD
442	36	49.3	331	4	ABB59867	Abb59867 Drosophil	515	36	49.3	4303	5	AAE18935	Aae18935 Human PKD
443	36	49.3	331	4	ABO08051	AbO08051 Fly polyv	516	36	49.3	4303	5	AAE18937	Aae18937 Human PKD
444	36	49.3	331	8	ADU008051	Adu008051 Protein e	517	36	49.3	4303	5	AAE18929	Aae18929 Human PKD
445	36	49.3	345	6	ABU48718	Abu48718 Photorhab	518	36	49.3	4303	5	AAE18939	Aae18939 Human PKD
446	36	49.3	348	6	ABM67677	Abm67677 Photorhab	519	36	49.3	4303	5	AAE18942	Aae18942 Human PKD
447	36	49.3	355	5	ADI117237	Adi117237 Human NOV	520	36	49.3	4303	5	AAE18932	Aae18932 Human PKD
448	36	49.3	417	7	ABO70979	AbO70979 Pseudomon	521	36	49.3	4303	5	AAE18938	Aae18938 Human PKD
449	36	49.3	447	4	ABG30346	Abg30346 Novel hum	522	36	49.3	4303	5	AAE18940	Aae18940 Human PKD
450	36	49.3	462	5	ADI117234	Adi117234 Human NOV	523	36	49.3	4303	5	AAE18941	Aae18941 Human PKD
451	36	49.3	479	7	ABO79945	AbO79945 Pseudomon	524	36	49.3	4303	5	AAE18936	Aae18936 Human PKD
452	36	49.3	489	7	ADC37575	Adc37575 Human nuc	525	36	49.3	4303	8	ADN07621	Adn07621 Human pol
453	36	49.3	496	5	ADI117235	Adi117235 Human NOV	526	36	49.3	4303	9	ADW79338	Adw79338 Human pol
454	36	49.3	496	7	ADJ70341	Adj70341 Human hea	527	36	49.3	4304	5	AAE18951	Aae18951 Human PKD
455	36	49.3	521	5	ADI17233	Adi17233 Human NOV	528	36	49.3	4304	5	AAE18933	Aae18933 Human PKD
456	36	49.3	521	9	ADY15832	Ady15832 PRO polyv	529	36	49.3	4339	2	AAR75916	Aar75916 Polycyveti
457	36	49.3	531	8	ADT60843	Adt60843 Plant pol	530	36	49.3	4339	2	AAR87539	Aar87539 Polycyveti
458	36	49.3	542	4	AAAB94571	AaB94571 Human pro	531	36	49.3	4725	4	ABG23837	Abg23837 Novel hum
459	36	49.3	590	7	ABO74701	AbO74701 Pseudomon	532	36	49.3	4977	4	ABG17057	Abg17057 Novel hum
460	36	49.3	643	4	ABB11071	Abb11071 Human pol	533	36	49.3	6685	4	ABG23030	Abg23030 Novel hum
461	36	49.3	664	4	ABG04272	Abg04272 Novel hum	534	35.5	48.6	37	4	ABB39431	Abb39431 Peptide #
462	36	49.3	664	4	ABG05550	Abg05550 Novel hum	535	35.5	48.6	37	4	AAM32956	Aam32956 Peptide #

536	35.5	48.6	37	4	ABB24203	Abb24203 Protein #
537	35.5	48.6	37	4	Aam72725	Aam72725 Human bon
538	35.5	48.6	37	4	Aam60112	Aam60112 Human bra
539	35.5	48.6	37	4	ABG54423	ABG54423 Human liv
540	35.5	48.6	37	5	ABG42549	ABG42549 Human pep
541	35.5	48.6	64	3	AAY95578	Aay95578 Human che
542	35.5	48.6	64	5	AAE15784	Aae15784 Human che
543	35.5	48.6	65	3	AAY95577	Aay95577 Human che
544	35.5	48.6	65	3	AAE15783	Aae15783 Human che
545	35.5	48.6	66	3	AAY95567	Aay95567 Human che
546	35.5	48.6	66	5	AAE15782	Aae15782 Human che
547	35.5	48.6	67	3	AAY95566	Aay95566 Human che
548	35.5	48.6	67	5	AAE15781	Aae15781 Human che
549	35.5	48.6	68	5	AAE15780	Aae15780 Human che
550	35.5	48.6	69	3	AAY95565	Aay95565 Human che
551	35.5	48.6	69	5	AAE15779	Aae15779 Human che
552	35.5	48.6	70	3	AAY95564	Aay95564 Human che
553	35.5	48.6	70	5	AAE15778	Aae15778 Human che
554	35.5	48.6	71	2	AAW22675	Aaw22675 Drol3+ ch
555	35.5	48.6	71	3	AAY95563	Aay95563 Human che
556	35.5	48.6	71	5	AAE15785	Aae15785 Human che
557	35.5	48.6	72	3	AAY95562	Aay95562 Human che
558	35.5	48.6	72	3	AAY95576	Aay95576 Human che
559	35.5	48.6	72	5	AAE15786	Aae15786 Human che
560	35.5	48.6	73	3	AAY95575	Aay95575 Human che
561	35.5	48.6	73	5	AAE15787	Aae15787 Human che
562	35.5	48.6	74	5	AAE15788	Aae15788 Human che
563	35.5	48.6	74	7	ADE80851	Ade80851 MCP4 chem
564	35.5	48.6	74	7	ADE80851	Ade80851 MCP4 chem
565	35.5	48.6	75	2	AAW22673	Aaw22673 Bac 3 che
566	35.5	48.6	75	2	AAW56690	Aaw56690 Chemokine
567	35.5	48.6	75	3	AAE15789	Aae15789 Human che
568	35.5	48.6	75	3	AAE15789	Aae15789 Human che
569	35.5	48.6	75	3	AAE15789	Aae15789 Human che
570	35.5	48.6	75	7	ADC89676	Adc89676 Human MCP
571	35.5	48.6	75	7	ADC89676	Adc89676 Human MCP
572	35.5	48.6	76	3	AAY95573	Aay95573 Human che
573	35.5	48.6	77	2	AAW22672	Aaw22672 Bac 2 che
574	35.5	48.6	77	3	AAY95572	Aay95572 Human che
575	35.5	48.6	78	3	AAY95571	Aay95571 Human che
576	35.5	48.6	79	2	AAW22674	Aaw22674 Drol1/2 c
577	35.5	48.6	79	3	AAY95570	Aay95570 Human che
578	35.5	48.6	80	3	AAY95569	Aay95569 Human che
579	35.5	48.6	81	3	AAY95568	Aay95568 Human che
580	35.5	48.6	82	2	AAW22671	Aaw22671 Bac 1 che
581	35.5	48.6	82	2	AAW17665	Aaw17665 Stem cell
582	35.5	48.6	98	2	AAY93087	Aay93087 Human che
583	35.5	48.6	98	2	AAW22670	Aaw22670 Human che
584	35.5	48.6	98	2	AAW30191	Aaw30191 Monocyte
585	35.5	48.6	98	2	AAW56087	Aaw56087 Human mon
586	35.5	48.6	98	2	AAW41164	Aaw41164 Human che
587	35.5	48.6	98	3	AB15831	Aab15831 Human che
588	35.5	48.6	98	3	AB15808	Aab15808 Human che
589	35.5	48.6	98	3	AAY95534	Aay95534 Human che
590	35.5	48.6	98	4	AAE15795	Aae15795 Amino aci
591	35.5	48.6	98	5	AAO19997	Aao19997 Protein o
592	35.5	48.6	98	5	AAE15751	Aae15751 Human che
593	35.5	48.6	98	5	AAY77180	Aay77180 Human che
594	35.5	48.6	98	7	ADD46371	Add46371 Human Pro
595	35.5	48.6	98	7	ADN39903	Adn39903 Cancer/an
596	35.5	48.6	98	8	ADJ66672	Adj66672 Human che
597	35.5	48.6	98	8	ADO32066	Ado32066 Chemokine
598	35.5	48.6	98	8	ADQ20884	Adq20884 Human sof
599	35.5	48.6	98	9	ADM20982	Adm20982 Human che
600	35.5	48.6	106	4	ABG13572	Abg13572 Novel hum
601	35	47.9	18	4	RAY72701	Ray72701 Human mon
602	35	47.9	72	4	AAU39893	Aau39893 Propionib
603	35	47.9	72	6	ABM36412	Abm36412 Propionib
604	35	47.9	83	6	ABU39737	Abu39737 Protein e
605	35	47.9	85	4	AAU50390	Aau50390 Propionib
606	35	47.9	85	6	ABM46909	Abm46909 Propionib
607	35	47.9	121	5	ABP34551	Abp34551 Human ORF
608	35	47.9	121	9	ABM91642	Abm91642 M. xanthu

609	35	47.9	129	7	ABO79747	AbO79747
610	35	47.9	141	2	AAy19767	Aay19767 SEQ ID NO
611	35	47.9	146	8	ADx73014	Adx73014 Plant ful
612	35	47.9	209	8	ADs29805	Ads29805 Bacterial
613	35	47.9	219	4	ABb69309	Abb69309 Drosophil
614	35	47.9	260	8	ADx91046	Adx91046 Plant ful
615	35	47.9	274	9	ABm92570	Abm92570 M. xanthu
616	35	47.9	283	8	ADn21526	Adn21526 Bacterial
617	35	47.9	287	5	ABb49876	Abb49876 Listeria
618	35	47.9	287	6	AAE33353	Aae33353 Listeria
619	35	47.9	334	4	ABb70737	Abb70737 Drosophil
620	35	47.9	343	5	ABp73327	Abp73327 Candida a
621	35	47.9	344	2	AAx47213	Aax47213 Lipase mo
622	35	47.9	352	6	ABO14679	AbO14679 Novel hum
623	35	47.9	353	7	ADM26624	Adm26624 Hyperther
624	35	47.9	358	6	ABR62336	AbR62336 Thermoasc
625	35	47.9	358	8	ADx94179	Adx94179 Plant ful
626	35	47.9	415	7	ADf07717	Adf07717 Bacterial
627	35	47.9	424	6	ABO14680	AbO14680 Novel hum
628	35	47.9	450	7	ADM05405	Adm05405 Human pro
629	35	47.9	450	9	AEb39376	Aeb39376 L. pneumo
630	35	47.9	453	9	AEb35942	Aeb35942 L. pneumo
631	35	47.9	455	6	ABM68247	Abm68247 Photorhab
632	35	47.9	466	5	ADi17236	Adi17236 Murine NO
633	35	47.9	469	6	ABO14678	AbO14678 Novel hum
634	35	47.9	469	6	ABR61426	AbR61426 Syrian ha
635	35	47.9	469	7	ADJ68407	AdJ68407 Human hea
636	35	47.9	469	8	ADN03839	Adn03839 Antipsori
637	35	47.9	469	8	ADQ30583	Adq30583 Pancreas
638	35	47.9	469	9	ADY54941	Ady54941 Chronic v
639	35	47.9	470	7	ADJ69473	AdJ69473 Human hea
640	35	47.9	470	8	ABM80386	Abm80386 Tumour-as
641	35	47.9	473	8	ADN19556	Adn19556 Bacterial
642	35	47.9	485	8	ADU07677	Adu07677 Amino aci
643	35	47.9	490	4	ABG07778	Abg07778 Novel hum
644	35	47.9	490	4	ABG08484	AbG08484 Novel hum
645	35	47.9	505	6	ABU33273	Abu33273 Protein e
646	35	47.9	506	9	AEb36481	Aeb36481 L. pneumo
647	35	47.9	506	9	AEb39884	Aeb39884 L. pneumo
648	35	47.9	507	8	ADN20926	Adn20926 Bacterial
649	35	47.9	515	8	ADx94287	Adx94287 Plant ful
650	35	47.9	550	8	ADx66701	Adx66701 Plant ful
651	35	47.9	552	8	ADx93413	Adx93413 Plant ful
652	35	47.9	646	4	ABG25254	AbG25254 Novel hum
653	35	47.9	702	4	ABG18349	Abg18349 Novel hum
654	35	47.9	716	4	ABG35880	AbG35880 Novel hum
655	35	47.9	730	6	ABU29945	Abu29945 Protein e
656	35	47.9	730	7	ADC95125	Adc95125 E. faeciu
657	35	47.9	749	4	ABG05779	AbG05779 Novel hum
658	35	47.9	808	8	ADL33463	Adl33463 Feetuca a
659	35	47.9	808	8	ADOG3031	AdoG3031 Transcrip
660	35	47.9	811	4	ABG29434	AbG29434 Novel hum
661	35	47.9	924	4	ABG25166	AbG25166 Novel hum
662	35	47.9	1257	7	ABO68544	AbO68544 Pseudomon
663	35	47.9	1402	5	ABP66040	AbP66040 Bifidobac
664	35	47.9	1717	4	ABG20672	AbG20672 Novel hum
665	34.5	47.3	211	3	AAG41341	Aag41341 Arabidops
666	34.5	47.3	219	3	AAG41340	Aag41340 Arabidops
667	34.5	47.3	221	3	AAG41339	Aag41339 Arabidops
668	34.5	47.3	431	8	ADN18521	Adn18521 Bacterial
669	34	46.6	18	9	ADV22825	Adv22825 HCV H77 1
670	34	46.6	22	2	AAU84628	Aau84628 HCV HepC1
671	34	46.6	30	5	AAU84627	Aau84627 HCV HepC1
672	34	46.6	30	5	AAU84627	Aau84627 HCV HepC1
673	34	46.6	48	8	ADU04144	AdU04144 HCV type
674	34	46.6	58	7	ADC23277	Adc23277 Conserved
675	34	46.6	58	7	ADC23101	Adc23101 Conserved
676	34	46.6	72	4	AAm85498	Aam85498 Human imm
677	34	46.6	72	5	ABU04170	Abu04170 HCV secon
678	34	46.6	73	8	ABM80911	Abm80911 Murine eo
679	34	46.6	73	8	ADR40245	Adr40245 Mouse mat
680	34	46.6	82	8	ADU04116	Adu04116 HCV type
681	34	46.6	83	6	ABU23471	Abu23471 Protein e

682	34	46.6	84	4	AU42321	Propionib	755	34	46.6	9	ADW71301	Adw71301	Hepatitis
683	34	46.6	84	6	ABM3840	Propionib	756	34	46.6	8	ADL72980	Adl72980	Hepatitis
684	34	46.6	84	7	ADK17255	Mouse eot	757	34	46.6	421	ADL72980	Adl72980	Hepatitis
685	34	46.6	91	5	ABB77256	HCV bait	758	34	46.6	435	ADL72980	Adl72980	Hepatitis
686	34	46.6	91	7	ABO80300	Pseudomon	759	34	46.6	440	ABG25855	Novel hum	Abg25855
687	34	46.6	96	7	ADK17286	Virus-dlik	760	34	46.6	441	ABG25855	Novel hum	Abg25855
688	34	46.6	97	5	ABG94306	Mouse eot	761	34	46.6	442	ABG25855	Novel hum	Abg25855
689	34	46.6	97	5	ABB80897	Mouse eot	762	34	46.6	443	ABG25855	Novel hum	Abg25855
690	34	46.6	97	5	ABG80618	Mouse che	763	34	46.6	444	ABG25855	Novel hum	Abg25855
691	34	46.6	97	8	ADK17213	Mouse eot	764	34	46.6	445	ABG25855	Novel hum	Abg25855
692	34	46.6	97	8	ADR40228	Mouse eot	765	34	46.6	446	ABG25855	Novel hum	Abg25855
693	34	46.6	98	5	ABB80898	Murine eo	766	34	46.6	447	ABG25855	Novel hum	Abg25855
694	34	46.6	98	8	ADR40229	Mouse ful	767	34	46.6	448	ABG25855	Novel hum	Abg25855
695	34	46.6	105	3	AAG33281	Zea mays	768	34	46.6	449	ABG25855	Novel hum	Abg25855
696	34	46.6	125	3	AAG33280	Zea mays	769	34	46.6	450	ABG25855	Novel hum	Abg25855
697	34	46.6	144	2	AAR33398	HC-J1 E2/	770	34	46.6	451	ABG25855	Novel hum	Abg25855
698	34	46.6	145	7	ADF59171	Human pol	771	34	46.6	452	ABG25855	Novel hum	Abg25855
699	34	46.6	146	8	ADK171954	Plant ful	772	34	46.6	453	ABG25855	Novel hum	Abg25855
700	34	46.6	156	4	AAB84198	Anino aci	773	34	46.6	454	ABG25855	Novel hum	Abg25855
701	34	46.6	165	4	ABB69534	Human pro	774	34	46.6	455	ABG25855	Novel hum	Abg25855
702	34	46.6	166	4	ABB69534	Human pro	775	34	46.6	456	ABG25855	Novel hum	Abg25855
703	34	46.6	174	2	AAR34441	Sequence	776	34	46.6	457	ABG25855	Novel hum	Abg25855
704	34	46.6	208	6	ABU35518	Protein e	777	34	46.6	458	ABG25855	Novel hum	Abg25855
705	34	46.6	239	4	AAG66305	Human cor	778	34	46.6	459	ABG25855	Novel hum	Abg25855
706	34	46.6	246	6	AABU93224	Protein e	779	34	46.6	460	ABG25855	Novel hum	Abg25855
707	34	46.6	250	5	AABU93220	Hepatitis	780	34	46.6	461	ABG25855	Novel hum	Abg25855
708	34	46.6	266	3	ABAB42726	Human ORF	781	34	46.6	462	ABG25855	Novel hum	Abg25855
709	34	46.6	271	3	AAU57069	Calbindin	782	34	46.6	463	ABG25855	Novel hum	Abg25855
710	34	46.6	271	4	AAE00445	HCV E2-63	783	34	46.6	464	ABG25855	Novel hum	Abg25855
711	34	46.6	271	4	AAE00445	HCV E2-63	784	34	46.6	465	ABG25855	Novel hum	Abg25855
712	34	46.6	271	7	ADB70324	Calretini	785	34	46.6	466	ABG25855	Novel hum	Abg25855
713	34	46.6	271	7	ADBE63979	Human pro	786	34	46.6	467	ABG25855	Novel hum	Abg25855
714	34	46.6	271	7	ADBE63983	Human pro	787	34	46.6	468	ABG25855	Novel hum	Abg25855
715	34	46.6	271	8	ADJ37103	Human mal	788	34	46.6	469	ABG25855	Novel hum	Abg25855
716	34	46.6	271	8	ADJ37103	Human mal	789	34	46.6	470	ABG25855	Novel hum	Abg25855
717	34	46.6	279	5	ABP53576	Human NOV	790	34	46.6	471	ABG25855	Novel hum	Abg25855
718	34	46.6	280	4	ABG17374	Novel hum	791	34	46.6	472	ABG25855	Novel hum	Abg25855
719	34	46.6	280	6	ABO00771	Polypepti	792	34	46.6	473	ABG25855	Novel hum	Abg25855
720	34	46.6	294	7	ABO80718	Pseudomon	793	34	46.6	474	ABG25855	Novel hum	Abg25855
721	34	46.6	301	8	ADRO8563	Human pro	794	34	46.6	475	ABG25855	Novel hum	Abg25855
722	34	46.6	309	2	AAW00929	Recombina	795	34	46.6	476	ABG25855	Novel hum	Abg25855
723	34	46.6	315	2	AAW45330	Anti-HCV	796	34	46.6	477	ABG25855	Novel hum	Abg25855
724	34	46.6	325	6	ABM67429	Phototrab	797	34	46.6	478	ABG25855	Novel hum	Abg25855
725	34	46.6	332	2	AAW45330	Phototrab	798	34	46.6	479	ABG25855	Novel hum	Abg25855
726	34	46.6	335	6	ABU27791	Protein e	799	34	46.6	480	ABG25855	Novel hum	Abg25855
727	34	46.6	337	2	AAW79217	pHCV351-e	800	34	46.6	481	ABG25855	Novel hum	Abg25855
728	34	46.6	342	6	ABO00448	Novel hum	801	34	46.6	482	ABG25855	Novel hum	Abg25855
729	34	46.6	342	7	ADD71112	Human int	802	34	46.6	483	ABG25855	Novel hum	Abg25855
730	34	46.6	349	6	ABU33151	Protein e	803	34	46.6	484	ABG25855	Novel hum	Abg25855
731	34	46.6	350	5	AAE19891	Hepatitis	804	34	46.6	485	ABG25855	Novel hum	Abg25855
732	34	46.6	350	7	ABW00342	Hepatitis	805	34	46.6	486	ABG25855	Novel hum	Abg25855
733	34	46.6	355	6	ABW23392	Protein e	806	34	46.6	487	ABG25855	Novel hum	Abg25855
734	34	46.6	356	6	ABM68241	Phototrab	807	34	46.6	488	ABG25855	Novel hum	Abg25855
735	34	46.6	363	6	ABP55567	Hepatitis	808	34	46.6	489	ABG25855	Novel hum	Abg25855
736	34	46.6	363	6	AAE32880	Hepatitis	809	34	46.6	490	ABG25855	Novel hum	Abg25855
737	34	46.6	367	2	AAW40115	APP-HCV-E	810	34	46.6	491	ABG25855	Novel hum	Abg25855
738	34	46.6	367	2	AAW79218	pHCV167-e	811	34	46.6	492	ABG25855	Novel hum	Abg25855
739	34	46.6	367	7	ADF07756	pHCV422-e	812	34	46.6	493	ABG25855	Novel hum	Abg25855
740	34	46.6	377	9	ABE54574	Vibriu vu	813	34	46.6	494	ABG25855	Novel hum	Abg25855
741	34	46.6	383	9	ABE54574	Vibriu vu	814	34	46.6	495	ABG25855	Novel hum	Abg25855
742	34	46.6	388	6	ABW70493	Phototrab	815	34	46.6	496	ABG25855	Novel hum	Abg25855
743	34	46.6	391	6	ABU23061	Protein e	816	34	46.6	497	ABG25855	Novel hum	Abg25855
744	34	46.6	397	2	AAW79220	pHCV419-e	817	34	46.6	498	ABG25855	Novel hum	Abg25855
745	34	46.6	399	2	AAW40117	HGH-HCV-E	818	34	46.6	499	ABG25855	Novel hum	Abg25855
746	34	46.6	401	2	AAW21970	APP riba	819	34	46.6	500	ABG25855	Novel hum	Abg25855
747	34	46.6	401	2	AAW55033	Actinobac	820	34	46.6	501	ABG25855	Novel hum	Abg25855
748	34	46.6	402	2	AAW34440	Sequence	821	34	46.6	502	ABG25855	Novel hum	Abg25855
749	34	46.6	402	2	AAW34439	Sequence	822	34	46.6	503	ABG25855	Novel hum	Abg25855
750	34	46.6	409	2	AAW33995	H77 E2/NS	823	34	46.6	504	ABG25855	Novel hum	Abg25855
751	34	46.6	409	2	AAW33996	H90 E2/NS	824	34	46.6	505	ABG25855	Novel hum	Abg25855
752	34	46.6	410	2	AAW33996	H90 E2/NS	825	34	46.6	506	ABG25855	Novel hum	Abg25855
753	34	46.6	417	2	AAW79227	pHCV423-e	826	34	46.6	507	ABG25855	Novel hum	Abg25855
754	34	46.6	421	8	ADJ10452	HCV E2 pr	827	34	46.6	508	ABG25855	Novel hum	Abg25855

828	34	46.6	1997	5	AAU84802	Aau84802	HCV HepC	901	33	45.2	176	4	AAU20983	Aau20983	Human nov
829	34	46.6	2984	4	AAE00449	Aae00449	Hepatitis	902	33	45.2	183	3	AAU44884	Aay44884	Corn tran
830	34	46.6	2984	4	AAE00447	Aae00447	Hepatitis	903	33	45.2	187	3	ABO71281	AbO71281	Pseudomon
831	34	46.6	2984	4	AAE00447	Aae00447	Hepatitis	904	33	45.2	198	8	ADY04356	AdY04356	Plant ful
832	34	46.6	3002	7	ADM24822	Adm24822	Hepatitis	905	33	45.2	199	3	AAG24245	Aag24245	Arabidops
833	34	46.6	3011	2	AAE22154	Aae22154	NANBV Hut	906	33	45.2	204	8	ADY13976	AdY13976	Plant ful
834	34	46.6	3011	2	AAE40119	Aae40119	HCV genom	907	33	45.2	208	7	ABM74197	Abm74197	DNA clone
835	34	46.6	3011	2	AAE66595	Aae66595	Hepatitis	908	33	45.2	223	7	ABM89886	Abm89886	Rice abio
836	34	46.6	3011	2	AAE79232	Aae79232	HCV sequ	909	33	45.2	235	7	ADI21207	Adi21207	Novel hum
837	34	46.6	3011	2	AAE77397	Aae77397	Hepatitis	910	33	45.2	236	7	ADC33168	Adc33168	Human nov
838	34	46.6	3011	2	AAE77398	Aae77398	Hepatitis	911	33	45.2	244	2	AAV37743	Aay37743	Amino aci
839	34	46.6	3011	2	AAE98020	Aae98020	Infectiou	912	33	45.2	245	6	ABU01853	Abu01853	S. pneumo
840	34	46.6	3011	4	AAE59173	Aae59173	Protein e	913	33	45.2	245	6	ABU46119	Abu46119	Protein e
841	34	46.6	3011	4	AAE31169	Aae31169	Amino aci	914	33	45.2	245	8	ADK46984	Adk46984	Streptoco
842	34	46.6	3011	5	AAU92920	Aau92920	Hepatitis	915	33	45.2	254	8	ADR94587	Adr94587	Novel S.
843	34	46.6	3011	5	AAU84597	Aau84597	HCV polyp	916	33	45.2	254	9	AEA58457	Aea58457	Streptoco
844	34	46.6	3011	5	AAU79221	Aau79221	Hepatitis	917	33	45.2	261	8	ADX70691	Adx70691	Plant ful
845	34	46.6	3011	5	AAE19888	Aae19888	Hepatitis	918	33	45.2	268	6	ABU40461	Abu40461	Protein e
846	34	46.6	3011	6	AAO26784	Aao26784	Protein d	919	33	45.2	273	4	ABG09597	Abg09597	Novel hum
847	34	46.6	3011	6	ABP71460	Abp71460	Amino aci	920	33	45.2	277	4	ABG09597	Abg09597	Novel hum
848	34	46.6	3011	6	ABU61849	Abu61849	HCV-H. 8/	921	33	45.2	286	8	ADL05360	Adl05360	M. catarr
849	34	46.6	3011	7	ABW00339	Abw00339	Hepatitis	922	33	45.2	286	6	ABU08215	Abu08215	Human syn
850	34	46.6	3011	8	ADH79949	Adh79949	E2 HCV en	923	33	45.2	287	6	ABU08214	Abu08214	Human Zep
851	34	46.6	3011	8	ADJ56744	Adj56744	Hepatitis	924	33	45.2	287	8	ADO19757	Ado19757	Human PRO
852	34	46.6	3011	8	ADJ64256	Adj64256	Hepatitis	925	33	45.2	287	9	ADY16389	Ady16389	PRO polyp
853	34	46.6	3011	8	ADL72983	Adl72983	Hepatitis	926	33	45.2	287	9	ADZ77616	Adz77616	Human SNA
854	34	46.6	3011	9	ADX40785	Adx40785	HCV polym	927	33	45.2	288	4	ABG04313	Abg04313	Novel hum
855	34	46.6	3011	9	ADX40784	Adx40784	HCV polym	928	33	45.2	289	3	AAG32624	Aag32624	Arabidops
856	34	46.6	3011	9	ADX40802	Adx40802	HCV polym	929	33	45.2	289	3	AAG52306	Aag52306	Arabidops
857	34	46.6	3011	9	AEA06142	Aea06142	Full leng	930	33	45.2	292	3	AAG52305	Aag52305	Arabidops
858	34	46.6	3011	9	AEA62080	Aea62080	Hepatitis	931	33	45.2	292	3	AAG32623	Aag32623	Arabidops
859	34	46.6	3011	9	AEA62088	Aea62088	Hepatitis	932	33	45.2	294	7	ABO65908	AbO65908	Klebsiell
860	34	46.6	3011	9	AEA62078	Aea62078	Hepatitis	933	33	45.2	296	7	ABO81296	AbO81296	Pseudomon
861	34	46.6	3011	9	ABE17053	AbE17053	Hepatitis	934	33	45.2	300	4	AAU65033	Aau65033	Propionib
862	34	46.6	3012	5	AAU99289	Aau99289	Hepatitis	935	33	45.2	300	6	ABM61552	Abm61552	Eucalyptu
863	34	46.6	3012	6	ABU61848	Abu61848	HCV H77 c	936	33	45.2	309	3	AAB25283	Aab25283	Bacterial
864	34	46.6	3180	6	ABG73195	Abg73195	MKO-Z vir	937	33	45.2	313	8	ADM42776	Adm42776	Murine ca
865	34	46.6	3194	6	ABU31122	Abu31122	Protein e	938	33	45.2	315	8	ADT60334	Adt60334	Plant poi
866	34	46.6	3194	6	ABU31122	Abu31122	Protein e	939	33	45.2	317	8	ADI53718	Adi53718	Streptomy
867	34	46.6	3208	7	ADD67948	Add67948	Hepatitis	940	33	45.2	318	8	ADI53717	Adi53717	Streptomy
868	34	46.6	3261	9	ADV23776	Adv23776	Hepatitis	941	33	45.2	346	8	ADS43166	AdS43166	Bacterial
869	34	46.6	3835	4	AAU83167	Aau83167	Amino aci	942	33	45.2	350	7	ABO77322	AbO77322	Pseudomon
870	34	46.6	5985	5	AAU84799	Aau84799	HCV HepC1	943	33	45.2	351	3	AAG32622	Aag32622	Arabidops
871	34	46.6	19938	6	ABN98398	Abn98398	Streptomy	944	33	45.2	351	3	AAG52304	Aag52304	Arabidops
872	33.5	45.9	652	4	ABB58621	Abb58621	Drosophil	945	33	45.2	351	4	AAB96657	Aab96657	Putative
873	33.5	45.9	652	4	ABB65548	Abb65548	Drosophil	946	33	45.2	351	5	ABB92959	Abb92959	Herbicida
874	33.5	45.9	657	4	AAE94585	Aae94585	Human pro	947	33	45.2	351	8	ABO77297	AbO77297	Plant pol
875	33.5	45.9	1208	4	AAE95292	Aae95292	Human pro	948	33	45.2	351	7	ABO80171	AbO80171	Pseudomon
876	33.5	45.9	1208	8	ADQ96328	Adq96328	T cell ac	949	33	45.2	366	7	ADU02767	Adu02767	Novel hum
877	33.5	45.9	1208	9	ADY15794	Ady15794	PRO polyp	950	33	45.2	395	8	ADX76039	Adx76039	Plant ful
878	33.5	45.9	1208	9	ADY15792	Ady15792	PRO polyp	951	33	45.2	396	4	ABG13640	Abg13640	Novel hum
879	33.5	45.9	1213	5	AAO22597	Aao22597	1213-mer	952	33	45.2	435	3	AAG52270	Aag52270	Arabidops
880	33	45.2	9	9	ADZ37635	Adz37635	Human kin	953	33	45.2	436	9	ABE12240	AbE12240	Thale cre
881	33	45.2	15	3	AAE15818	Aae15818	Human che	954	33	45.2	437	2	AAV34786	Aay34786	Amino aci
882	33	45.2	58	4	AAU55086	Aau55086	Propionib	955	33	45.2	447	8	ADN99753	Adn99753	Novel hum
883	33	45.2	58	6	ABM51605	Abm51605	Propionib	956	33	45.2	450	3	AAG52269	Aag52269	Arabidops
884	33	45.2	76	4	AAE82738	Aae82738	Human imm	957	33	45.2	457	7	ADC31549	Adc31549	Human nov
885	33	45.2	84	4	ABG25360	Abg25360	Novel hum	958	33	45.2	457	8	ADN19823	Adn19823	Bacterial
886	33	45.2	107	3	AAE41543	Aae41543	Human ORF	959	33	45.2	458	5	ABB931883	Abb931883	Herbicida
887	33	45.2	112	8	ADM42760	Adm42760	Murine ca	960	33	45.2	481	3	AAG22093	Aag22093	Arabidops
888	33	45.2	119	6	ABM71531	Abm71531	Staphyloc	961	33	45.2	500	4	AAW93943	Aaw93943	Human pol
889	33	45.2	134	7	ABO75832	AbO75832	Pseudomon	962	33	45.2	500	8	ABG95660	Abg95660	Human nuc
890	33	45.2	135	7	ABO70109	AbO70109	Pseudomon	963	33	45.2	500	8	ADH44816	Adh44816	Human KRZ
891	33	45.2	137	4	AAW91823	Aaw91823	Human imm	964	33	45.2	500	8	ADL32095	Adl32095	Human pro
892	33	45.2	140	3	AAE44885	Aae44885	Corn tran	965	33	45.2	501	4	AAU66224	Aau66224	Propionib
893	33	45.2	146	7	ABO76760	AbO76760	Pseudomon	966	33	45.2	501	6	ABM62743	Abm62743	Propionib
894	33	45.2	148	2	AAE62755	Aae62755	Sefid sequ	967	33	45.2	511	5	ABB84430	Abb84430	Human neu
895	33	45.2	148	2	AAW23574	Aaw23574	Salmonell	968	33	45.2	521	5	ADI16762	Adi16762	Human NOV
896	33	45.2	148	7	ABO79792	AbO79792	Pseudomon	969	33	45.2	521	8	ADN42416	Adn42416	Human nov
897	33	45.2	150	8	ADY11798	Ady11798	Plant ful	970	33	45.2	522	9	AEA20030	Aea20030	Novel hum
898	33	45.2	151	9	AAE98545	Aae98545	HPV (onco	971	33	45.2	523	3	AAG52268	Aag52268	Arabidops
899	33	45.2	166	4	AAE72587	Aae72587	Human OR-	972	33	45.2	542	3	AAV44905	Aay44905	Human pot
900	33	45.2	166	4	AAG72308	Aag72308	Human OR	973	33	45.2	548	5	ADI16976	Adi16976	Murine NO



974	33	45.2	552	4	AAU15074	Aau15074	Protein e
975	33	45.2	552	5	ABP73260	Abp73260	Candida a
976	33	45.2	554	3	AAG22092	Agag22092	Arabidops
977	33	45.2	574	3	AAG22091	Agag22091	Arabidops
978	33	45.2	624	8	ADN24288	Adn24288	Bacterial
979	33	45.2	656	8	ADG22363	Adg22363	Cyanophag
980	33	45.2	657	8	ADT05651	Adt05651	Haemophil
981	33	45.2	714	4	AAU15107	Aau15107	Protein e
982	33	45.2	714	5	ABP73232	Abp73232	Candida a
983	33	45.2	718	4	AAU39123	Aau39123	Propionib
984	33	45.2	718	6	AEM35642	Aem35642	Propionib
985	33	45.2	753	4	ABM50093	Abm50093	GB1 prote
986	33	45.2	783	7	ABM88922	Abm88922	Rice abio
987	33	45.2	819	4	ABB71266	Abb71266	Drosophill
988	33	45.2	843	8	AD523575	Ad523575	Bacterial
989	33	45.2	844	9	ADY93057	Ady93057	Adenylyate
990	33	45.2	878	5	ABG93380	Abg93380	C. albica
991	33	45.2	878	5	ABP73678	Abp73678	Candida a
992	33	45.2	886	4	ABG15346	Abg15346	Novel hum
993	33	45.2	965	8	ADN24287	Adn24287	Bacterial
994	33	45.2	1033	6	ABU35225	Abu35225	Protein e
995	33	45.2	1046	8	ADL04690	Adl04690	M. catarr
996	33	45.2	1114	4	ABB71505	Abb71505	Drosophill
997	33	45.2	1123	9	ADZ10462	Adz10462	P. gingiv
998	33	45.2	1130	9	ABE42540	Abe42540	L. pneumo
999	33	45.2	1148	6	ABU50517	Abu50517	Protein e
1000	33	45.2	1158	2	AAU34576	Aau34576	Porphormy

## ALIGNMENTS

RESULT 1	
AAB15851	
ID AAB15851 standard; peptide; 23 AA.	
XX	
AC AAB15851;	
XX	
DT 17-JAN-2001 (first entry)	
XX	
DE Chemokine derived peptide SEQ ID NO: 103.	
XX	
DE Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;	
KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;	
KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;	
KW basophil-mediated disease; myocardial infarction; acute ischaemia;	
KW rheumatoid arthritis; contraception.	
XX	
OS Unidentified.	
XX	
PN WO200042071-A2.	
XX	
PD 20-JUL-2000.	
XX	
PF 12-JAN-2000; 2000WO-US000821.	
XX	
PR 12-JAN-1999; 99US-00229071.	
PR 17-MAR-1999; 99US-00271192.	
PR 01-DEC-1999; 99US-00452406.	
XX	
PA (NEOR-) NEORX CORP.	
XX	
PI Grainger DJ, Tatalick LM;	
XX	
DR WPI; 2000-499101/44.	
XX	
XX New peptide 3, amide and heterocyclic compounds and saccharide conjugates	
PT used for inhibiting chemokine induced activity and for treating e.g.	
PT stroke, vascular diseases, autoimmune diseases and tumor growth.	
XX	
PS Disclosure; Page 387; 387pp; English.	
XX	
CC The present invention concerns the identification of a number of	

CC	chemokines which can be used to produce derivatives, agonists and
CC	antagonists which are then useful in disease treatment. The chemokines
CC	include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.
CC	These chemokine derivatives can be used to treat diseases such as
CC	autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and
CC	AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated
CC	diseases, endotoxaemia, myocardial infarction, acute ischaemia and
CC	rheumatoid arthritis, and can be used to prevent strokes and as
CC	contraceptives. The coding sequences for the chemokines can be used in
CC	gene therapy for the same diseases, as well as in the production of
CC	animal models
XX	
XX	Sequence 23 AA;
XX	Query Match 100.0%; Score 73; DB 3; Length 23;
XX	Best Local Similarity 100.0%; Pred. No. 4.3e-06;
XX	Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ISVQRLASVRRITSSK 16
DB	
	8 ISVQRLASVRRITSSK 23
RESULT 2	
AAAY72689	AAAY72689 standard; peptide; 23 AA.
ID	AAAY72689
XX	
AC	AAAY72689;
XX	
DT	31-MAY-2001 (first entry)
XX	
DE	Human monocyte chemoattractant protein-1 (MCP-1) fragment #6.
XX	
XX	Human; monocyte chemoattractant protein-1; MCP-1; therapy;
KW	atherosclerotic plaque; autoimmune disease; asthma; inhibitor;
KW	ligand-protein binding; rheumatoid arthritis.
OS	Homo sapiens.
PN	W0200114886-A2.
XX	
PD	01-MAR-2001.
XX	
PF	23-AUG-2000; 2000WO-US023346.
XX	
PR	23-AUG-1999; 99US-0150230P.
PR	23-AUG-1999; 99US-0150318P.
PR	03-SEP-1999; 99US-0152421P.
XX	
PA	(POLA-) POLARIS PHARM INC.
XX	
PI	Jenson JC, Sworin M;
XX	
DR	WPI; 2001-211321/21.
XX	
PT	Identifying inhibitors of binding between a protein and a ligand,
PT	comprises preparing analogs of a lead compound which inhibit binding,
PT	combining analog, ligand, protein and assaying inhibition of ligand-
PT	protein binding.
XX	
PS	Disclosure; Fig 3; 45pp; English.
XX	
CC	The invention relates to identification of compounds which inhibit the
CC	binding between a target protein and a macromolecular ligand. These
CC	compounds comprise a targeting group, an attaching group and optionally a
CC	linker group. They are capable of covalently binding to the surface of a
CC	target protein in sufficient proximity to the target protein/ligand
CC	binding site in order to inhibit binding of ligand with the target
CC	protein. The compounds of the invention serve as potent inhibitors and
CC	are useful as drugs which can inhibit protein/macromolecular ligand
CC	binding or can serve as leads to optimize biological activity or some
CC	other pharmacologically relevant property. The compounds are also useful
CC	for detecting target protein in a sample or assessing the quantity of



CC target protein in a sample which is useful for diagnosing a disease  
 CC characterised by over or under abundance of target protein in a tissue or  
 CC blood sample. They are also used to assess whether the individual  
 CC expresses target protein or its polymorphic form, where the compound has  
 CC greater affinity for target protein than its polymorphic form or vice  
 CC versa. The present sequence is a fragment of human monocyte  
 CC chemoattractant protein-1 (MCP-1). This sequence functions as a  
 CC degradable targeting group and inhibits the binding between MCP-1 and its  
 CC receptor. Hence this peptide can be useful as drugs in the treatment of  
 CC atherosclerotic plaque and autoimmune diseases such as asthma and  
 CC rheumatoid arthritis  
 XX  
 SQ Sequence 23 AA;

Query Match 100.0%; Score 73; DB 4; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQLASRYRITSSK 16  
 |||||  
 DB 8 ISVQLASRYRITSSK 23

## RESULT 3

AY72682  
 ID AAY72682 standard; peptide; 24 AA.

XX  
 AC AAY72682;

DT 31-MAY-2001 (first entry)

DE Human monocyte chemoattractant protein-1 (MCP-1) fragment #3.

XX Human; monocyte chemoattractant protein-1; MCP-1; therapy;  
 KW atherosclerotic plaque; autoimmune disease; asthma; inhibitor;  
 KW ligand-protein binding; rheumatoid arthritis.

XX Homo sapiens.

XX WO200114886-A2.

XX 01-MAR-2001.

XX 23-AUG-2000; 2000WO-US023346.

XX 23-AUG-1999; 99US-0150230P.

XX 23-AUG-1999; 99US-0150318P.

XX 03-SEP-1999; 99US-0152421P.

XX (POLA-) POLARIS PHARM INC.

XX Jenson JC, Sworin M;

XX WPI; 2001-211321/21.

XX Identifying inhibitors of binding between a protein and a ligand,  
 PT comprises preparing analogs of a lead compound which inhibit binding,  
 PT combining analog, ligand, protein and assaying inhibition of ligand-  
 PT protein binding.

XX Disclosure; Page 12; 45pp; English.

XX The invention relates to identification of compounds which inhibit the  
 CC binding between a target protein and a macromolecular ligand. These  
 CC compounds comprise a targeting group, an attaching group and optionally a  
 CC linker group. They are capable of covalently binding to the surface of a  
 CC target protein in sufficient proximity to the target protein/ligand  
 CC binding site in order to inhibit binding of ligand with the target  
 CC protein. The compounds of the invention serve as potent inhibitors and  
 CC are useful as drugs which can inhibit protein/macromolecular ligand  
 CC binding or can serve as leads to optimise biological activity or some  
 CC other pharmacologically relevant property. The compounds are also useful  
 CC for detecting target protein in a sample or assessing the quantity of

CC target protein in a sample which is useful for diagnosing a disease  
 CC characterised by over or under abundance of target protein in a tissue or  
 CC blood sample. They are also used to assess whether the individual  
 CC expresses target protein or its polymorphic form, where the compound has  
 CC greater affinity for target protein than its polymorphic form or vice  
 CC versa. The present sequence is a fragment of human monocyte  
 CC chemoattractant protein-1 (MCP-1). This sequence functions as a  
 CC degradable targeting group and inhibits the binding between MCP-1 and its  
 CC receptor. Hence this peptide can be useful as drugs in the treatment of  
 CC atherosclerotic plaque and autoimmune diseases such as asthma and  
 CC rheumatoid arthritis  
 XX  
 SQ Sequence 24 AA;

Query Match 100.0%; Score 73; DB 4; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQLASRYRITSSK 16  
 |||||  
 DB 9 ISVQLASRYRITSSK 24

## RESULT 4

AY72683  
 ID AAY72683 standard; peptide; 26 AA.

XX  
 AC AAY72683;

DT 31-MAY-2001 (first entry)

DE Human monocyte chemoattractant protein-1 (MCP-1) fragment #4.

XX Human; monocyte chemoattractant protein-1; MCP-1; therapy;  
 KW atherosclerotic plaque; autoimmune disease; asthma; inhibitor;  
 KW ligand-protein binding; rheumatoid arthritis; cyclic.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Disulfide-bond 2..26 /note= "Forms a cyclic structure"

XX WO200114886-A2.

XX 01-MAR-2001.

XX 23-AUG-2000; 2000WO-US023346.

XX 23-AUG-1999; 99US-0150230P.

XX 23-AUG-1999; 99US-0150318P.

XX 03-SEP-1999; 99US-0152421P.

XX (POLA-) POLARIS PHARM INC.

XX Jenson JC, Sworin M;

XX WPI; 2001-211321/21.

XX Identifying inhibitors of binding between a protein and a ligand,  
 PT comprises preparing analogs of a lead compound which inhibit binding,  
 PT combining analog, ligand, protein and assaying inhibition of ligand-  
 PT protein binding.

XX Disclosure; Page 12; 45pp; English.

XX The invention relates to identification of compounds which inhibit the  
 CC binding between a target protein and a macromolecular ligand. These  
 CC compounds comprise a targeting group, an attaching group and optionally a  
 CC linker group. They are capable of covalently binding to the surface of a  
 CC target protein in sufficient proximity to the target protein/ligand  
 CC binding site in order to inhibit binding of ligand with the target  
 CC protein. The compounds of the invention serve as potent inhibitors and

are useful as drugs which can inhibit protein/macromolecular ligand binding or can serve as leads to optimise biological activity or some other pharmacologically relevant property. The compounds are also useful for detecting target protein in a sample or assessing the quantity of target protein in a sample which is useful for diagnosing a disease characterised by over or under abundance of target protein in a tissue or blood sample. They are also used to assess whether the individual expresses target protein or its polymorphic form, where the compound has greater affinity for target protein than its polymorphic form or vice versa. The present sequence is a disulphide cyclised fragment of human monocyte chemoattractant protein-1 (MCP-1). This sequence functions as a degradable targeting group and inhibits the binding between MCP-1 and its receptor. Hence this peptide can be useful as drugs in the treatment of atherosclerotic plaque and autoimmune diseases such as asthma and rheumatoid arthritis

Sequence 26 AA;

Query Match 100.0%; Score 73; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 4.9e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQLASVRRITSSK 16  
| | | | | | | | | | | | | | | | | |  
Db 10 ISVQLASVRRITSSK 25

RESULT 5

ADW17179

ID ADW17179 standard; peptide; 26 AA.

XX AC ADW17179;

XX 17-JUN-2004 (first entry)

DE Chemokine analog, 963, SEQ ID 1412.

XX Chemokine analog; Chemokine; interleukin-8; IL-8;  
KW Interferon Inducible Protein-10; IP-10; CXCL 10;  
KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;  
KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;  
KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;  
KW infectious disease; inflammatory condition; graft rejection;  
KW bacterial infection; viral infection; vascular condition;  
KW atherosclerosis; restenosis; systemic lupus erythematosus;  
KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;  
KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;  
KW Immunosuppressive; Dermatological; Antiinflammatory; cyclic.

XX OS Synthetic.

XX FH Location/Qualifiers

FT Key Modified-site 1 /note= "RNH-Ala"

FT FT Misc-difference 3

FT FT Modified-site 9 /note= "Any amino acid"

FT FT Modified-site 26 /note= "The residue at this position forms a bond with Glu26 to form a cyclic peptide"

FT FT Modified-site 26 /note= "Glu(OH)-NH2. The residue at this position forms a bond with Lys9 to form a cyclic peptide"

FT FT W02004024088-A2.

XX 25-MAR-2004.

XX 11-SEP-2003; 2003WO-US028745.

XX 13-SEP-2002; 2002US-00243795.

XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.

PI Merzouk A, Wong D, Salari H;

XX WPI; 2004-329387/30.

DR Compound useful for treating cancer and cardiovascular disease, comprises structure of chemokine analogs such as interleukin-8 and interferon inducible protein-10.

XX Claim 1; SEQ ID NO 1412; 271pp; English.

PS The present invention relates to chemokine analogs (I, ADW70378-ADW72006), including interleukin (IL)-8 analogs, Interferon inducible Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation, Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309 analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28 analogs. (I) are useful for treating a disease or disorder by administering (I) to a patient. The disease or disorder is chosen from autoimmune diseases, cancer, chronic inflammation, cardiovascular disease or infectious disease. The administration increases the hemocrit, assist in mobilizing stem cells, in vaccine production or in gene therapy, which are also useful for modulating the activity of chemokine receptor, which involves contacting the chemokine receptor with (I), for mobilizing intracellular calcium in a patient, which involves administering (I) to a patient in need of such treatment. (I) are also useful for protecting haematopoietic cells in a patient undergoing treatment with cytotoxic agent, by administering (I) to the patient, where the survival of white blood cells or leukocytes is increased. (I) are also useful for maintaining cells capable of divisions in a quiescent state cells in a patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, vascular conditions (e.g. atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 26 AA;

Query Match 100.0%; Score 73; DB 8; Length 26;

Best Local Similarity 100.0%; Pred. No. 4.9e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQLASVRRITSSK 16

| | | | | | | | | | | | | | | | | |  
Db 10 ISVQLASVRRITSSK 25

RESULT 6

ADW17142

ID ADW17142 standard; peptide; 26 AA.

XX AC ADW17142;

XX 17-JUN-2004 (first entry)

DE Chemokine analog, 926, SEQ ID 1375.

XX Chemokine analog; Chemokine; interleukin-8; IL-8;

KW Interferon Inducible Protein-10; IP-10; CXCL 10;

KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;

KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;

KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;

KW infectious disease; inflammatory condition; graft rejection;

KW bacterial infection; viral infection; vascular condition;

KW atherosclerosis; restenosis; systemic lupus erythematosus;

KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;

KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;

KW Immunosuppressive; Dermatological; Antiinflammatory.

```

XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "RNH-Ala"
XX FT Misc-difference 3 /note= "Any amino acid"
XX FT Modified-site 26 /note= "Glu- (OH) -NH2"
XX FT
XX PN WO2004024088-A2.
XX XX
XX PD 25-MAR-2004.
XX XX
XX PF 11-SEP-2003; 2003WO-US028745.
XX PR 13-SEP-2002; 2002US-00243795.
XX PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX PI Merzouk A, Wong D, Salari H;
XX XX WPI; 2004-329387/30.
XX DR
XX XX Compound useful for treating cancer and cardiovascular disease, comprises
XX FT structure of chemokine analogs such as interleukin-8 and interferon
XX FT inducible protein-10.
XX XX
XX PS Claim 1; SEQ ID NO 1375; 271pp; English.
XX XX
XX CC The present invention relates to chemokine analogs (I, ADM70378-
XX CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible
XX CC Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-
XX CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,
XX CC Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309
XX CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28
XX CC analogs. (I) are useful for treating a disease or disorder by
XX CC administering (I) to a patient. The disease or disorder is chosen from
XX CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease
XX CC or infectious diseases. The administration increases the hemocrit, assist
XX CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)
XX CC are also useful for modulating the activity of chemokine receptor, which
XX CC involves contacting the chemokine receptor with (I), for mobilizing
XX CC intracellular calcium in a patient, which involves administering (I) to a
XX CC patient in need of such treatment. (I) are also useful for protecting
XX CC haematopoietic cells in a patient undergoing treatment with cytotoxic
XX CC agent, by administering (I) to the patient, where the survival of white
XX CC blood cells or leukocytes is increased. (I) are also useful for
XX CC maintaining cells capable of divisions in a quiescent state cells in a
XX CC patient undergoing treatment with a cytotoxic agent, by administering (I)
XX CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a
XX CC patient by administering (I) to the patient. (I) are also useful for
XX CC treating or preventing inflammatory conditions, graft rejection,
XX CC bacterial infection, viral infection, vascular conditions (e.g.
XX CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-
XX CC reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell
XX CC mobilization, vaccine production and blood cell recovery following
XX CC chemotherapy. Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ
XX Sequence 26 AA;
XX
XX Query Match 100.0%; Score 73; DB 8; Length 26;
XX Best Local Similarity 100.0%; Pred. No. 4.9e-06;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 ISVQLASRYRRTSSK 16
XX |||||
XX Db 10 ISVQLASRYRRTSSK 25

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RESULT 7
ADM71778
ID ADM71778 standard; peptide; 26 AA.
XX AC ADM71778;
XX DT 17-JUN-2004 (first entry)
XX XX Chemokine analog, g62, SEQ ID 1411.
XX DE
XX KW Chemokine analog; Chemokine; interleukin-8; IL-8;
XX KW Interferon inducible Protein-10; IP-10; CXCL 10;
XX KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;
XX KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
XX KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
XX KW infectious disease; inflammatory condition; graft rejection;
XX KW bacterial infection; viral infection; vascular condition;
XX KW atherosclerosis; restenosis; systemic lupus erythematosus;
XX KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;
XX KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
XX KW Immunosuppressive; Dermatological; Antiinflammatory; cyclic.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "RNH-Ala"
XX FT Modified-site 2 /note= "The residue at this position forms a bond with
XX FT Glu26 to form a cyclic peptide"
XX FT Misc-difference 3 /note= "Any amino acid"
XX FT Modified-site 26 /note= "Glu- (OH) -NH2. The residue at this position forms
XX FT a bond with Lys2 to form a cyclic peptide"
XX PN WO2004024088-A2.
XX XX
XX PD 25-MAR-2004.
XX XX
XX PF 11-SEP-2003; 2003WO-US028745.
XX PR 13-SEP-2002; 2002US-00243795.
XX PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX PI Merzouk A, Wong D, Salari H;
XX XX WPI; 2004-329387/30.
XX DR
XX XX Compound useful for treating cancer and cardiovascular disease, comprises
XX FT structure of chemokine analogs such as interleukin-8 and interferon
XX FT inducible protein-10.
XX XX
XX PS Claim 1; SEQ ID NO 1411; 271pp; English.
XX XX
XX CC The present invention relates to chemokine analogs (I, ADM70378-
XX CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible
XX CC Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-
XX CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,
XX CC Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309
XX CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28
XX CC analogs. (I) are useful for treating a disease or disorder by
XX CC administering (I) to a patient. The disease or disorder is chosen from
XX CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease
XX CC or infectious diseases. The administration increases the hemocrit, assist
XX CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)
XX CC are also useful for modulating the activity of chemokine receptor, which
XX CC involves contacting the chemokine receptor with (I), for mobilizing
XX CC intracellular calcium in a patient, which involves administering (I) to a
XX CC patient in need of such treatment. (I) are also useful for protecting
XX CC haematopoietic cells in a patient undergoing treatment with cytotoxic
XX CC agent, by administering (I) to the patient, where the survival of white
XX CC blood cells or leukocytes is increased. (I) are also useful for
XX CC maintaining cells capable of divisions in a quiescent state cells in a
XX CC patient undergoing treatment with a cytotoxic agent, by administering (I)
XX CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a
XX CC patient by administering (I) to the patient. (I) are also useful for
XX CC treating or preventing inflammatory conditions, graft rejection,
XX CC bacterial infection, viral infection, vascular conditions (e.g.
XX CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-
XX CC reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell
XX CC mobilization, vaccine production and blood cell recovery following
XX CC chemotherapy. Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ
XX Sequence 26 AA;
XX
XX Query Match 100.0%; Score 73; DB 8; Length 26;
XX Best Local Similarity 100.0%; Pred. No. 4.9e-06;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 ISVQLASRYRRTSSK 16
XX |||||
XX Db 10 ISVQLASRYRRTSSK 25

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CC blood cells or leukocytes is increased. (I) are also useful for  
 CC maintaining cells capable of divisions in a quiescent state cells in a  
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)  
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a  
 CC patient by administering (I) to the patient. (I) are also useful for  
 CC treating or preventing inflammatory conditions, graft rejection,  
 CC bacterial infection, viral infection, vascular conditions (e.g.  
 CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-  
 CC reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell  
 CC mobilization, vaccine production and blood cell recovery following  
 CC chemotherapy. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 26 AA;

Query Match 100.0%; Score 73; DB 8; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQLASYYRRITSSK 16  
 |||||  
 Db 10 ISVQLASYYRRITSSK 25

RESULT 8  
 ADM71727  
 ID ADM71727 standard; peptide; 35 AA.  
 AC  
 XX ADM71727;  
 DT 17-JUN-2004 (first entry)  
 DE Chemokine analog, g11, SEQ ID 1360.  
 XX  
 KW Chemokine analog; Chemokine; interleukin-8; IL-8;  
 KW Interferon inducible Protein-10; IP-10; CXCL 10;  
 KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;  
 KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;  
 KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;  
 KW infectious disease; inflammatory condition; graft rejection;  
 KW bacterial infection; viral infection; vascular condition;  
 KW atherosclerosis; restenosis; systemic lupus erythematosus;  
 KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;  
 KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;  
 KW Immunosuppressive; Dermatological; Antiinflammatory.  
 XX  
 OS Synthetic.

Key Location/Qualifiers  
 Modified-site 1 /note= "RNH-Gln"  
 FT  
 FT Misc-difference 8 /note= "Any amino acid"  
 FT  
 FT Misc-difference 11 /note= "Any amino acid"  
 FT  
 FT Misc-difference 12 /note= "Any amino acid"  
 FT  
 FT Modified-site 35 /note= "Lys-(OH)-NH2"  
 FT  
 XX WO2004024088-A2.  
 PN  
 XX 25-MAR-2004.  
 PD  
 XX 11-SEP-2003; 2003WO-US028745.  
 PF  
 XX 13-SEP-2002; 2002US-00243795.  
 PR  
 XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 PA  
 XX Merzouk A, Wong D, Salari H;  
 PI  
 XX

DR WPI; 2004-329387/30.

XX Compound useful for treating cancer and cardiovascular disease, comprises  
 PT structure of chemokine analogs such as interleukin-8 and interferon  
 FT inducible protein-10.

XX Claim 1; SEQ ID NO 1360; 271pp; English.

XX The present invention relates to chemokine analogs (I, ADM70378-  
 CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible  
 CC Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-  
 CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,  
 CC Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309  
 CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28  
 CC analogs. (I) are useful for treating a disease or disorder by  
 CC administering (I) to a patient. The disease or disorder is chosen from  
 CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease  
 CC or infectious disease. The administration increases the hemocrit, assist  
 CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)  
 CC are also useful for modulating the activity of chemokine receptor, which  
 CC involves contacting the chemokine receptor with (I), for mobilizing  
 CC intracellular calcium in a patient, which involves administering (I) to a  
 CC patient in need of such treatment. (I) are also useful for protecting  
 CC haematopoietic cells in a patient undergoing treatment with cytotoxic  
 CC agent, by administering (I) to the patient, where the survival of white  
 CC blood cells or leukocytes is increased. (I) are also useful for  
 CC maintaining cells capable of divisions in a quiescent state cells in a  
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)  
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a  
 CC patient by administering (I) to the patient. (I) are also useful for  
 CC treating or preventing inflammatory conditions, graft rejection,  
 CC bacterial infection, viral infection, vascular conditions (e.g.  
 CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-  
 CC reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell  
 CC mobilization, vaccine production and blood cell recovery following  
 CC chemotherapy. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX

SQ Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQLASYYRRITSSK 16  
 |||||  
 Db 20 ISVQLASYYRRITSSK 35

RESULT 9  
 ADM71718  
 ID ADM71718 standard; peptide; 35 AA.

XX ADM71718;

DT 17-JUN-2004 (first entry)

XX Chemokine analog, g2, SEQ ID 1351.

XX Chemokine analog; Chemokine; interleukin-8; IL-8;  
 KW Interferon inducible Protein-10; IP-10; CXCL 10;  
 KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;  
 KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;  
 KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;  
 KW infectious disease; inflammatory condition; graft rejection;  
 KW bacterial infection; viral infection; vascular condition;  
 KW atherosclerosis; restenosis; systemic lupus erythematosus;  
 KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;  
 KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;  
 KW Immunosuppressive; Dermatological; Antiinflammatory.  
 XX  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "RNH-Gln"  
 FT Misc-difference 11  
 FT Misc-difference 12 /note= "Any amino acid"  
 FT Misc-difference 12 /note= "Any amino acid"  
 FT Modified-site 35 /note= "Lys- (OH) -NH2"  
 FT  
 XX WO2004024088-A2.  
 XX  
 XX 25-MAR-2004.  
 XX  
 XX 11-SEP-2003; 2003WO-US028745.  
 XX  
 XX 13-SEP-2002; 2002US-00243795.  
 XX  
 XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 XX  
 XX Merzouk A, Wong D, Salari H;  
 XX WPI; 2004-329387/30.  
 XX  
 XX Compound useful for treating cancer and cardiovascular disease, comprises  
 XX structure of chemokine analogs such as interleukin-8 and interferon  
 XX inducible protein-10.  
 XX  
 XX Claim 1; SEQ ID NO 1351; 271pp; English.  
 XX  
 XX The present invention relates to chemokine analogs (I, ADM70378-  
 XX ADM72006), including interleukin (IL)-8 analogs, interferon inducible  
 XX Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-  
 XX alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,  
 XX Normal T-cell Expressed, and Presumably Secreted or CCL5) analogs, I-309  
 XX analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28  
 XX analogs. (I) are useful for treating a disease or disorder by  
 XX administering (I) to a patient. The disease or disorder is chosen from  
 XX autoimmune diseases, cancer, chronic inflammation, cardiovascular disease  
 XX or infectious disease. The administration increases the hemocrit, assist  
 XX in mobilizing stem cells, in vaccine production or in gene therapy. (I)  
 XX are also useful for modulating the activity of chemokine receptor, which  
 XX involves contacting the chemokine receptor with (I), for mobilizing  
 XX intracellular calcium in a patient, which involves administering (I) to a  
 XX patient in need of such treatment. (I) are also useful for protecting  
 XX haematopoietic cells in a patient undergoing treatment with cytotoxic  
 XX agent, by administering (I) to the patient, where the survival of white  
 XX blood cells or leukocytes is increased. (I) are also useful for  
 XX maintaining cells capable of divisions in a quiescent state cells in a  
 XX  
 XX Query Match 100.0%; Score 73; DB 8; Length 35;  
 XX Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 ISVQRLASYRRITSSK 16  
 XX |||||||||||||  
 XX 20 ISVQRLASYRRITSSK 35

RESULT 10  
 ADM71720  
 ID ADM71720 standard; peptide; 35 AA.  
 XX  
 XX AC  
 XX ADM71720;  
 XX  
 XX 17-JUN-2004 (first entry)  
 XX  
 XX Chemokine analog, g4, SEQ ID 1353.  
 XX  
 XX Chemokine analog; Chemokine; interleukin-8; IL-8;  
 XX Interferon inducible Protein-10; IP-10; CXCL10;  
 XX Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;  
 XX I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;  
 XX autoimmune disease; cancer; chronic inflammation; cardiovascular disease;  
 XX infectious disease; inflammatory condition; graft rejection;  
 XX bacterial infection; viral infection; vascular condition;  
 XX atherosclerosis; restenosis; systemic lupus erythematosus;  
 XX ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;  
 XX Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;  
 XX Immunosuppressive; Dermatological; Antiinflammatory.  
 XX  
 XX Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "RNH-Xaa, where Xaa is any amino acid"  
 FT Misc-difference 11 /note= "Any amino acid"  
 FT Misc-difference 12 /note= "Any amino acid"  
 FT Modified-site 35 /note= "Lys- (OH) -NH2"  
 FT  
 XX WO2004024088-A2.  
 XX  
 XX 25-MAR-2004.  
 XX  
 XX 11-SEP-2003; 2003WO-US028745.  
 XX  
 XX 13-SEP-2002; 2002US-00243795.  
 XX  
 XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 XX  
 XX Merzouk A, Wong D, Salari H;  
 XX WPI; 2004-329387/30.  
 XX  
 XX Compound useful for treating cancer and cardiovascular disease, comprises  
 XX structure of chemokine analogs such as interleukin-8 and interferon  
 XX inducible protein-10.  
 XX  
 XX Claim 1; SEQ ID NO 1353; 271pp; English.  
 XX  
 XX The present invention relates to chemokine analogs (I, ADM70378-  
 XX ADM72006), including interleukin (IL)-8 analogs, interferon inducible  
 XX Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-  
 XX alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,  
 XX Normal T-cell Expressed, and Presumably Secreted or CCL5) analogs, I-309  
 XX analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28  
 XX analogs. (I) are useful for treating a disease or disorder by  
 XX administering (I) to a patient. The disease or disorder is chosen from  
 XX autoimmune diseases, cancer, chronic inflammation, cardiovascular disease  
 XX or infectious disease. The administration increases the hemocrit, assist  
 XX in mobilizing stem cells, in vaccine production or in gene therapy. (I)  
 XX are also useful for modulating the activity of chemokine receptor, which  
 XX involves contacting the chemokine receptor with (I), for mobilizing  
 XX intracellular calcium in a patient, which involves administering (I) to a  
 XX patient in need of such treatment. (I) are also useful for protecting  
 XX haematopoietic cells in a patient undergoing treatment with cytotoxic  
 XX agent, by administering (I) to the patient, where the survival of white  
 XX blood cells or leukocytes is increased. (I) are also useful for  
 XX maintaining cells capable of divisions in a quiescent state cells in a

CC patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;  
Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQLASYYRRTSSK 16  
Dy 20 ISVQLASYYRRTSSK 35

RESULT 11

ADM71736  
ID ADM71736 standard; peptide; 35 AA.

XX AC ADM71736;

XX 17-JUN-2004 (first entry)

XX Chemokine analog, g20, SEQ ID 1369.

XX Chemokine analog; Chemokine; interleukin-8; IL-8;

XX Interferon inducible Protein-10; IP-10; CXCL 10;

XX Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;

XX I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;

XX autoimmune disease; cancer; chronic inflammation; cardiovascular disease;

XX infectious disease; inflammatory condition; graft rejection;

XX bacterial infection; viral infection; vascular condition;

XX atherosclerosis; restenosis; systemic lupus erythematosus;

XX ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;

XX Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;

XX Immunosuppressive; Dermatological; Antiinflammatory.

XX Synthetic.

XX Key Location/Qualifiers

XX Modified-site 1 /note= "RHH-Gln"

XX Misc-difference 5 /note= "Any amino acid"

XX Misc-difference 11 /note= "Any amino acid"

XX Misc-difference 12 /note= "Any amino acid"

XX Modified-site 35 /note= "Lys- (OH) -NH2"

XX WO2004024088-A2.

XX 25-MAR-2004.

XX 11-SEP-2003; 2003WO-US028745.

XX 13-SEP-2002; 2002US-00243795.

XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.

XX Merzouk A, Wong D, Salari H;

XX WPI; 2004-329387/30.

PT Compound useful for treating cancer and cardiovascular disease, comprises  
PT structure of chemokine analogs such as interleukin-8 and interferon  
PT inducible protein-10.

PS Claim 1; SEQ ID NO 1369; 271pp; English.

XX The present invention relates to chemokine analogs (I, ADM70378-  
CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible  
CC Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-  
CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,  
CC Normal T-cell expressed, and presumably Secreted or CC15) analogs, I-309  
CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28  
CC analogs. (I) are useful for treating a disease or disorder by  
CC administering (I) to a patient. The disease or disorder is chosen from  
CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease  
CC or infectious disease. The administration increases the hemocrit, assist  
CC in mobilizing stem cells, in vaccine production or in gene therapy, which  
CC are also useful for modulating the activity of chemokine receptor, which  
CC involves contacting the chemokine receptor with (I), for mobilizing  
CC intracellular calcium in a patient, which involves administering (I) to a  
CC patient in need of such treatment. (I) are also useful for protecting  
CC haematopoietic cells in a patient undergoing treatment with cytotoxic  
CC agent, by administering (I) to the patient, where the survival of white  
CC blood cells or leukocytes is increased. (I) are also useful for  
CC maintaining cells capable of divisions in a quiescent state cells in a  
CC patient undergoing treatment with a cytotoxic agent, by administering (I)  
CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a  
CC patient by administering (I) to the patient. (I) are also useful for  
CC treating or preventing inflammatory conditions, graft rejection,  
CC bacterial infection, viral infection, systemic lupus erythematosus, and ischaemia-  
CC atherosclerosis, restenosis, tumourigenesis, and angiogenesis, stem cell  
CC mobilization, vaccine production and blood cell recovery following  
CC chemotherapy. Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;  
Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQLASYYRRTSSK 16  
Dy 20 ISVQLASYYRRTSSK 35

RESULT 12

ADM71741

ID ADM71741 standard; peptide; 35 AA.

XX AC ADM71741;

XX 17-JUN-2004 (first entry)

XX Chemokine analog, g25, SEQ ID 1374.

XX Chemokine analog; Chemokine; interleukin-8; IL-8;

XX Interferon inducible Protein-10; IP-10; CXCL 10;

XX Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;

XX I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;

XX autoimmune disease; cancer; chronic inflammation; cardiovascular disease;

XX infectious disease; inflammatory condition; graft rejection;

XX bacterial infection; viral infection; vascular condition;

XX atherosclerosis; restenosis; systemic lupus erythematosus;

XX ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;

XX Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;

XX Immunosuppressive; Dermatological; Antiinflammatory.

XX Synthetic.

XX Key Location/Qualifiers

XX Modified-site 1 /note= "RHH-Gln"

XX Misc-difference 5 /note= "Any amino acid"

XX Misc-difference 11 /note= "Any amino acid"

XX Misc-difference 12 /note= "Any amino acid"

XX Modified-site 35 /note= "Lys- (OH) -NH2"



FT Modified-site 1 /note= "RNH-Gln"

FT Misc-difference 10 /note= "Any amino acid"

FT Misc-difference 11 /note= "Any amino acid"

FT Misc-difference 12 /note= "Any amino acid"

FT Modified-site 35 /note= "Lys- (OH) -NH2"

XX WO2004024088-A2.

XX 25-MAR-2004.

XX 11-SEP-2003; 2003WO-US028745.

XX 13-SEP-2002; 2002US-00243795.

XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.

XX Merzouk A, Wong D, Salari H;

XX WPI; 2004-329387/30.

XX Compound useful for treating cancer and cardiovascular disease, comprises structure of chemokine analogs such as interleukin-8 and interferon inducible protein-10.

XX Claim 1; SEQ ID NO 1374; 271pp; English.

XX The present invention relates to chemokine analogs (I, ADM70378-ADM72006), including interleukin (IL)-8 analogs, interferon inducible protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation, Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309 analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28 analogs. (I) are useful for treating a disease or disorder by administering (I) to a patient. The disease or disorder is chosen from autoimmune diseases, cancer, chronic inflammation, cardiovascular disease or infectious diseases. The administration increases the hemocrit, assist in mobilizing stem cells, in vaccine production or in gene therapy. (I) are also useful for modulating the activity of chemokine receptor, which involves contacting the chemokine receptor with (I), for mobilizing intracellular calcium in a patient, which involves administering (I) to a patient in need of such treatment. (I) are also useful for protecting haematopoietic cells in a patient undergoing treatment with cytotoxic agent, by administering (I) to the patient, where the survival of white blood cells or leukocytes is increased. (I) are also useful for maintaining cells capable of divisions in a quiescent state cells in a patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, vascular conditions (e.g. atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;

Best Local Similarity 100.0%; Pred. No. 6.7e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ISVQLASRYRITSSK 16  
|||||

Db 20 ISVQLASRYRITSSK 35

RESULT 13

ADM71725

ID ADM71725 standard; peptide; 35 AA.

XX AC ADM71725;

XX 17-JUN-2004 (first entry)

XX Chemokine analog, g9, SEQ ID 1358.

XX Chemokine analog; Chemokine; Interleukin-8; IL-8;

XX Interferon inducible Protein-10; IP-10; CXCL10;

XX Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;

XX I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;

XX autoimmune disease; cancer; chronic inflammation; cardiovascular disease;

XX infectious disease; inflammatory condition; graft rejection;

XX bacterial infection; viral infection; vascular condition;

XX atherosclerosis; restenosis; systemic lupus erythematosus;

XX ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;

XX Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;

XX Immunosuppressive; Dermatological; Antiinflammatory.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "RNH-Gln"

FT Misc-difference 6 /note= "Any amino acid"

FT Misc-difference 11 /note= "Any amino acid"

FT Misc-difference 12 /note= "Any amino acid"

FT Modified-site 35 /note= "Lys- (OH) -NH2"

XX WO2004024088-A2.

XX 25-MAR-2004.

XX 11-SEP-2003; 2003WO-US028745.

XX 13-SEP-2002; 2002US-00243795.

XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.

XX Merzouk A, Wong D, Salari H;

XX WPI; 2004-329387/30.

XX Compound useful for treating cancer and cardiovascular disease, comprises structure of chemokine analogs such as interleukin-8 and interferon inducible protein-10.

XX Claim 1; SEQ ID NO 1358; 271pp; English.

XX The present invention relates to chemokine analogs (I, ADM70378-ADM72006), including interleukin (IL)-8 analogs, Interferon Inducible Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation, Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309 analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28 analogs. (I) are useful for treating a disease or disorder by administering (I) to a patient. The disease or disorder is chosen from autoimmune diseases, cancer, chronic inflammation, cardiovascular disease or infectious diseases. The administration increases the hemocrit, assist in mobilizing stem cells, in vaccine production or in gene therapy. (I) are also useful for modulating the activity of chemokine receptor, which involves contacting the chemokine receptor with (I), for mobilizing intracellular calcium in a patient, which involves administering (I) to a patient in need of such treatment. (I) are also useful for protecting haematopoietic cells in a patient undergoing treatment with cytotoxic agent, by administering (I) to the patient, where the survival of white blood cells or leukocytes is increased. (I) are also useful for maintaining cells capable of divisions in a quiescent state cells in a patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, vascular conditions (e.g. atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

CC blood cells or leukocytes is increased. (I) are also useful for  
 CC maintaining cells capable of divisions in a quiescent state cells in a  
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)  
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a  
 CC patient by administering (I) to the patient. (I) are also useful for  
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 CC reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell  
 CC mobilization, vaccine production and blood cell recovery following  
 CC chemotherapy. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX Sequence 35 AA;  
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 CC Db 20 ISVQRLASYRRITSSK 35  
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 CC DT 17-JUN-2004 (first entry)  
 CC DE Chemokine analog, g10, SEQ ID 1359.  
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 CC Interferon inducible Protein-10; IP-10; CXCL 10;  
 CC Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;  
 CC I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;  
 CC autoimmune disease; cancer; chronic inflammation; graft rejection;  
 CC infectious disease; inflammatory condition; vascular condition;  
 CC bacterial infection; viral infection; restenosis; systemic lupus erythematosus;  
 CC atherosclerosis; restenosis; sepsis; tumourigenesis; angiogenesis; Cytostatic;  
 CC ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;  
 CC Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;  
 CC Immunosuppressive; Dermatological; Antiinflammatory.  
 CC OS Synthetic.  
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 CC Key Location/Qualifiers  
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 CC FT  
 CC XX WO2004024088-A2.  
 CC PN  
 CC XX 25-MAR-2004.  
 CC PD  
 CC XX 11-SEP-2003; 2003WO-US028745.  
 CC PF  
 CC XX 13-SEP-2002; 2002US-00243795.  
 CC PR  
 CC XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 CC PA  
 CC XX Merzouk A, Wong D, Salari H;  
 CC PI  
 CC XX

DR WPI; 2004-329387/30.  
 XX Compound useful for treating cancer and cardiovascular disease, comprises  
 PT structure of chemokine analogs such as interleukin-8 and interferon  
 PT inducible protein-10.  
 XX  
 XX Claim 1; SEQ ID NO 1359; 271pp; English.  
 XX  
 CC The present invention relates to chemokine analogs (I, ADM70378-  
 CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible  
 CC Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-  
 CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,  
 CC Normal T-cell Expressed, and presumably Secreted or CCU5) analogs, I-309  
 CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28  
 CC analogs. (I) are useful for treating a disease or disorder by  
 CC administering (I) to a patient. The disease or disorder is chosen from  
 CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease  
 CC or infectious disease. The administration increases the hemocrit, assist  
 CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)  
 CC are also useful for modulating the activity of chemokine receptor, which  
 CC involves contacting the chemokine receptor with (I), for mobilizing  
 CC intracellular calcium in a patient, which involves administering (I) to a  
 CC patient in need of such treatment. (I) are also useful for protecting  
 CC haematopoietic cells in a patient undergoing treatment with cytotoxic  
 CC agent, by administering (I) to the patient, where the survival of white  
 CC blood cells or leukocytes is increased. (I) are also useful for  
 CC maintaining cells capable of divisions in a quiescent state cells in a  
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)  
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a  
 CC patient by administering (I) to the patient. (I) are also useful for  
 CC treating or preventing inflammatory conditions, graft rejection,  
 CC bacterial infection, viral infection, vascular conditions (e.g.  
 CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-  
 CC reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell  
 CC mobilization, vaccine production and blood cell recovery following  
 CC chemotherapy. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX Sequence 35 AA;  
 CC  
 CC Query Match 100.0%; Score 73; DB 8; Length 35;  
 CC Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
 CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 CC Db 20 ISVQRLASYRRITSSK 35  
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 CC RESULT 15  
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 CC ID ADM71719 standard; peptide; 35 AA.  
 CC AC ADM71719;  
 CC XX  
 CC DT 17-JUN-2004 (first entry)  
 CC DE Chemokine analog, g3, SEQ ID 1352.  
 CC XX  
 CC Chemokine analog; Chemokine; interleukin-8; IL-8;  
 CC Interferon inducible Protein-10; IP-10; CXCL 10;  
 CC Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;  
 CC I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;  
 CC autoimmune disease; cancer; chronic inflammation; graft rejection;  
 CC infectious disease; inflammatory condition; vascular condition;  
 CC bacterial infection; viral infection; restenosis; systemic lupus erythematosus;  
 CC atherosclerosis; restenosis; sepsis; tumourigenesis; angiogenesis; Cytostatic;  
 CC ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;  
 CC Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;  
 CC Immunosuppressive; Dermatological; Antiinflammatory.  
 CC OS Synthetic.



XX PH Key Location/Qualifiers  
 FT Modified-site 1 /note= "RNH-Gln"  
 FT Misc-difference 11  
 FT Misc-difference 12 /note= "Any amino acid"  
 FT Misc-difference 12 /note= "Any amino acid"  
 FT Modified-site 35  
 FT /note= "Lys- (OH)-NH2"  
 XX  
 XX WO2004024088-A2.  
 PN  
 XX  
 XX 25-MAR-2004.  
 PD  
 XX  
 XX 11-SEP-2003; 2003WO-US028745.  
 XX  
 XX 13-SEP-2002; 2002US-00243795.  
 XX  
 XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 PA  
 XX Merzouk A, Wong D, Salari H;  
 PI  
 XX WPI; 2004-329387/30.  
 DR  
 XX  
 XX Compound useful for treating cancer and cardiovascular disease, comprises  
 PT structure of chemokine analogs such as interleukin-8 and interferon  
 PT inducible protein-10.  
 XX  
 XX Claim 1; SEQ ID NO 1352; 271pp; English.  
 PS  
 XX  
 XX The present invention relates to chemokine analogs (I, ADM70378-  
 CC ADM72006), including interleukin (IL)-8 analogs, interferon inducible  
 CC protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-  
 CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,  
 CC Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309  
 CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28  
 CC analogs. (I) are useful for treating a disease or disorder by  
 CC administering (I) to a patient. The disease or disorder is chosen from  
 CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease  
 CC or infectious diseases. The administration increases the hemocrit, assist  
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 CC are also useful for modulating the activity of chemokine receptor, which  
 CC involves contacting the chemokine receptor with (I), for mobilizing  
 CC intracellular calcium in a patient, which involves administering (I) to a  
 CC patient in need of such treatment. (I) are also useful for protecting  
 CC haematopoietic cells in a patient undergoing treatment with cytotoxic  
 CC agent, by administering (I) to the patient, where the survival of white  
 CC blood cells or leukocytes is increased. (I) are also useful for  
 CC maintaining cells capable of divisions in a quiescent state cells in a  
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)  
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a  
 CC patient by administering (I) to the patient. (I) are also useful for  
 CC treating or preventing inflammatory conditions, graft rejection,  
 CC bacterial infection, viral infection, vascular conditions (e.g.  
 CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-  
 CC reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell  
 CC mobilization, vaccine production and blood cell recovery following  
 CC chemotherapy. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX Sequence 35 AA;  
 SQ  
 Query Match 100.0%; Score 73; DB 8; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ISVQRLASYYRITSSK 16  
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 Db 20 ISVQRLASYYRITSSK 35

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 DT 17-JUN-2004 (first entry)  
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 DE  
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 KW Interferon inducible Protein-10; IP-10; CXCL 10;  
 KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;  
 KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;  
 KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;  
 KW infectious disease; inflammatory condition; graft rejection;  
 KW bacterial infection; viral infection; vascular condition;  
 KW atherosclerosis; restenosis; systemic lupus erythematosus;  
 KW ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;  
 KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;  
 KW Immunosuppressive; Dermatological; Antiinflammatory.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "RNH-Gln"  
 FT Misc-difference 4 /note= "Any amino acid"  
 FT Misc-difference 11 /note= "Any amino acid"  
 FT Misc-difference 12 /note= "Any amino acid"  
 FT Modified-site 35 /note= "Lys- (OH)-NH2"  
 XX  
 PN WO2004024088-A2.  
 XX  
 XX 25-MAR-2004.  
 XX  
 XX 11-SEP-2003; 2003WO-US028745.  
 XX  
 XX 13-SEP-2002; 2002US-00243795.  
 XX  
 XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 PA  
 XX Merzouk A, Wong D, Salari H;  
 PI  
 XX WPI; 2004-329387/30.  
 DR  
 XX  
 XX Compound useful for treating cancer and cardiovascular disease, comprises  
 PT structure of chemokine analogs such as interleukin-8 and interferon  
 PT inducible protein-10.  
 XX  
 XX Claim 1; SEQ ID NO 1356; 271pp; English.  
 PS  
 XX  
 XX The present invention relates to chemokine analogs (I, ADM70378-  
 CC ADM72006), including interleukin (IL)-8 analogs, interferon inducible  
 CC protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-  
 CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,  
 CC Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309  
 CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28  
 CC analogs. (I) are useful for treating a disease or disorder by  
 CC administering (I) to a patient. The disease or disorder is chosen from  
 CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease  
 CC or infectious diseases. The administration increases the hemocrit, assist  
 CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)  
 CC are also useful for modulating the activity of chemokine receptor, which  
 CC involves contacting the chemokine receptor with (I), for mobilizing  
 CC intracellular calcium in a patient, which involves administering (I) to a  
 CC patient in need of such treatment. (I) are also useful for protecting  
 CC haematopoietic cells in a patient undergoing treatment with cytotoxic  
 CC agent, by administering (I) to the patient, where the survival of white  
 CC blood cells or leukocytes is increased. (I) are also useful for  
 CC maintaining cells capable of divisions in a quiescent state cells in a  
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)  
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a  
 CC patient by administering (I) to the patient. (I) are also useful for  
 CC treating or preventing inflammatory conditions, graft rejection,  
 CC bacterial infection, viral infection, vascular conditions (e.g.  
 CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-  
 CC reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell  
 CC mobilization, vaccine production and blood cell recovery following  
 CC chemotherapy. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
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 XX Sequence 35 AA;  
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CC blood cells or leukocytes is increased. (I) are also useful for  
 CC maintaining cells capable of divisions in a quiescent state cells in a  
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)  
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a  
 CC patient by administering (I) to the patient. (I) are also useful for  
 CC treating or preventing inflammatory conditions, graft rejection,  
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 CC reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell  
 CC mobilization, vaccine production and blood cell recovery following  
 CC chemotherapy. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
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 XX Sequence 35 AA;  
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 CC Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
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 CC DT 17-JUN-2004 (first entry)  
 CC DE Chemokine analog, g14, SEQ ID 1363.  
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 CC Chemokine analog; Interleukin-8; IL-8;  
 CC Interferon inducible Protein-10; IP-10; CXCL 10;  
 CC Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;  
 CC I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;  
 CC autoimmune disease; cancer; chronic inflammation; cardiovascular disease;  
 CC infectious disease; inflammation; graft rejection;  
 CC bacterial infection; viral infection; vascular condition;  
 CC atherosclerosis; restenosis; systemic lupus erythematosus;  
 CC ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;  
 CC Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;  
 CC Immunosuppressive; Dermatological; Antiinflammatory.  
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 CC Key Location/Qualifiers  
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 CC Misc-difference 11 /note= "Any amino acid"  
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 CC Misc-difference 12 /note= "Any amino acid"  
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 CC Modified-site 35 /note= "Lys- (OH) -NH2"  
 CC FT  
 CC XX  
 CC WO2004024088-A2.  
 CC XX  
 CC 25-MAR-2004.  
 CC PD  
 CC 11-SEP-2003; 2003WO-US028745.  
 CC XX  
 CC 13-SEP-2002; 2002US-00243795.  
 CC PF  
 CC (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 CC XX  
 CC Merzouk A, Wong D, Salari H;  
 CC FI  
 CC WPI; 2004-329387/30.  
 CC DR  
 CC XX

PT Compound useful for treating cancer and cardiovascular disease, comprises  
 PT structure of chemokine analogs such as interleukin-8 and interferon  
 XX inducible protein-10.  
 PS Claim 1; SEQ ID NO 1363; 271pp; English.  
 XX  
 CC The present invention relates to chemokine analogs (I, ADM70378-  
 CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible  
 CC Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-  
 CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,  
 CC Normal T-cell expressed, and presumably Secreted or CCU5) analogs, I-309  
 CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28  
 CC analogs. (I) are useful for treating a disease or disorder by  
 CC administering (I) to a patient. The disease or disorder is chosen from  
 CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease  
 CC or infectious disease. The administration increases the hemocrit, assist  
 CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)  
 CC are also useful for modulating the activity of chemokine receptor, which  
 CC involves contacting the chemokine receptor with (I), for mobilizing  
 CC intracellular calcium in a patient, which involves administering (I) to a  
 CC patient in need of such treatment. (I) are also useful for protecting  
 CC haematopoietic cells in a patient undergoing treatment with cytotoxic  
 CC agent, by administering (I) to the patient, where the survival of white  
 CC blood cells or leukocytes is increased. (I) are also useful for  
 CC maintaining cells capable of divisions in a quiescent state cells in a  
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)  
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a  
 CC patient by administering (I) to the patient. (I) are also useful for  
 CC treating or preventing inflammatory conditions, graft rejection,  
 CC bacterial infection, viral infection, vascular conditions (e.g.  
 CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-  
 CC reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell  
 CC mobilization, vaccine production and blood cell recovery following  
 CC chemotherapy. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX Sequence 35 AA;  
 CC  
 CC Query Match 100.0%; Score 73; DB 8; Length 35;  
 CC Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
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 CC DT 17-JUN-2004 (first entry)  
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 CC XX  
 CC Chemokine analog; Interleukin-8; IL-8;  
 CC Interferon inducible Protein-10; IP-10; CXCL 10;  
 CC Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;  
 CC I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;  
 CC autoimmune disease; cancer; chronic inflammation; cardiovascular disease;  
 CC infectious disease; inflammation; graft rejection;  
 CC bacterial infection; viral infection; vascular condition;  
 CC atherosclerosis; restenosis; systemic lupus erythematosus;  
 CC ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis;  
 CC Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;  
 CC Immunosuppressive; Dermatological; Antiinflammatory.  
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 XX Synthetic.  
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 CC FT  
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 CC XX  
 CC 25-MAR-2004.  
 CC PD  
 CC 11-SEP-2003; 2003WO-US028745.  
 CC XX  
 CC 13-SEP-2002; 2002US-00243795.  
 CC PF  
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 CC XX  
 CC Merzouk A, Wong D, Salari H;  
 CC FI  
 CC WPI; 2004-329387/30.  
 CC DR  
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FT Modified-site 1 /note= "RNH-Gln"  
 FT Misc-difference 3 /note= "Any amino acid"  
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 PN WO2004024088-A2.  
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 XX 25-MAR-2004.  
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 PF 11-SEP-2003; 2003WO-US028745.  
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 PR 13-SEP-2002; 2002US-00243795.  
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 XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 XX  
 PI Merzouk A, Wong D, Salari H;  
 XX  
 XX WPI; 2004-329387/30.  
 DR  
 XX  
 XX Compound useful for treating cancer and cardiovascular disease, comprises  
 PT structure of chemokine analogs such as interleukin-8 and interferon  
 PT inducible protein-10.  
 XX  
 XX Claim 1; SEQ ID NO 1355; 271pp; English.  
 PS  
 XX The present invention relates to chemokine analogs (I, ADM70378-  
 CC ADM72006), including interleukin (IL)-8 analogs, interferon inducible  
 CC Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-  
 CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,  
 CC Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309  
 CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28  
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 CC agent, by administering (I) to the patient, where the survival of white  
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 CC reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell  
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 XX  
 SQ Sequence 35 AA;  
 Query Match 100.0%; Score 73; DB 8; Length 35;  
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 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ISVQRLASYYRRITSSK 16  
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 Db 20 ISVQRLASYYRRITSSK 35

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 ID ADM71728 standard; peptide; 35 AA.  
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 DT 17-JUN-2004 (first entry)  
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 XX Chemokine analog; Chemokine; Interleukin-8; IL-8;  
 KW Interferon inducible Protein-10; IP-10; CXCL 10;  
 KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;  
 KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;  
 KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;  
 KW infectious disease; inflammatory condition; graft rejection;  
 KW bacterial infection; viral infection; vascular condition;  
 KW atherosclerosis; restenosis; systemic lupus erythematosus;  
 KW ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;  
 KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;  
 KW Immunosuppressive; Dermatological; Antiinflammatory.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "RNH-Gln"  
 FT Misc-difference 9 /note= "Any amino acid"  
 FT Misc-difference 11 /note= "Any amino acid"  
 FT Misc-difference 12 /note= "Any amino acid"  
 FT Modified-site 35 /note= "Lys-(OH)-NH2"  
 FT  
 PN WO2004024088-A2.  
 XX  
 PD 25-MAR-2004.  
 XX  
 XX 11-SEP-2003; 2003WO-US028745.  
 XX  
 PR 13-SEP-2002; 2002US-00243795.  
 XX  
 XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 XX  
 PI Merzouk A, Wong D, Salari H;  
 XX  
 XX WPI; 2004-329387/30.  
 DR  
 XX Compound useful for treating cancer and cardiovascular disease, comprises  
 PT structure of chemokine analogs such as interleukin-8 and interferon  
 PT inducible protein-10.  
 XX  
 XX Claim 1; SEQ ID NO 1361; 271pp; English.  
 PS  
 XX The present invention relates to chemokine analogs (I, ADM70378-  
 CC ADM72006), including interleukin (IL)-8 analogs, interferon inducible  
 CC Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-  
 CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,  
 CC Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309  
 CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28  
 CC analogs. (I) are useful for treating a disease or disorder by  
 CC administering (I) to a patient. The disease or disorder is chosen from  
 CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease  
 CC or infectious diseases. The administration increases the hemocrit, assist  
 CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)  
 CC are also useful for modulating the activity of chemokine receptor, which  
 CC involves contacting the chemokine receptor with (I), for mobilizing  
 CC intracellular calcium in a patient, which involves administering (I) to a  
 CC patient in need of such treatment. (I) are also useful for protecting  
 CC haematopoietic cells in a patient undergoing treatment with cytotoxic  
 CC agent, by administering (I) to the patient, where the survival of white  
 CC blood cells or leukocytes is increased. (I) are also useful for  
 CC maintaining cells capable of divisions in a quiescent state cells in a  
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)  
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a  
 CC patient by administering (I) to the patient. (I) are also useful for  
 CC treating or preventing inflammatory conditions, graft rejection,  
 CC bacterial infection, viral infection, vascular conditions (e.g.  
 CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-  
 CC reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell  
 CC mobilization, vaccine production and blood cell recovery following  
 CC chemotherapy. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 35 AA;  
 Query Match 100.0%; Score 73; DB 8; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ISVQRLASYYRRITSSK 16  
 |||||  
 Db 20 ISVQRLASYYRRITSSK 35

CC blood cells or leukocytes is increased. (I) are also useful for  
 CC maintaining cells capable of divisions in a quiescent state cells in a  
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)  
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a  
 CC patient by administering (I) to the patient. (I) are also useful for  
 CC treating or preventing inflammatory conditions, graft rejection,  
 CC bacterial infection, viral infection, vascular conditions (e.g.  
 CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-  
 CC reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell  
 CC mobilization, vaccine production and blood cell recovery following  
 CC chemotherapy. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
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 XX  
 SQ Sequence 35 AA;  
 Query Match 100.0%; Score 73; DB 8; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ISVQRLASYRRITSSK 16  
 |||||  
 Db 20 ISVQRLASYRRITSSK 35  
 RESULT 20  
 ADM71734  
 ID ADM71734 standard; peptide; 35 AA.  
 XX  
 AC ADM71734;  
 XX  
 DT 17-JUN-2004 (first entry)  
 DE  
 DE Chemokine analog, g18, SEQ ID 1367.  
 XX  
 KW Chemokine analog; Chemokine; interleukin-8; IL-8;  
 KW Interferon inducible Protein-10; IP-10; CXCL 10;  
 KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; RANTES; CCL5;  
 KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;  
 KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;  
 KW infectious disease; inflammatory condition; graft rejection;  
 KW bacterial infection; viral infection; vascular condition;  
 KW atherosclerosis; restenosis; systemic lupus erythematosus;  
 KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;  
 KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;  
 KW Immunosuppressive; Dermatological; Antiinflammatory.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "RNH-Gln"  
 FT Misc-difference 3  
 FT /note= "Any amino acid"  
 FT Misc-difference 11  
 FT /note= "Any amino acid"  
 FT Misc-difference 12  
 FT /note= "Any amino acid"  
 FT Modified-site 35  
 FT /note= "Lys- (OH)-NH2"  
 XX  
 XX WO2004024088-A2.  
 PN  
 XX  
 PD 25-MAR-2004.  
 XX  
 PD 11-SEP-2003; 2003WO-US028745.  
 PF  
 XX 13-SEP-2002; 2002US-00243795.  
 PR  
 XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 PA  
 XX Merzouk A, Wong D, Salari H;  
 PI  
 XX

DR WPI; 2004-329387/30.  
 XX Compound useful for treating cancer and cardiovascular disease, comprises  
 PT structure of chemokine analogs such as interleukin-8 and interferon  
 PT inducible protein-10.  
 XX  
 PS Claim 1; SEQ ID NO 1367; 271pp; English.  
 XX  
 CC The present invention relates to chemokine analogs (I, ADM70378-  
 CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible  
 CC Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-  
 CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,  
 CC Normal T-cell Expressed, and Presumably Secreted or CCL5) analogs, I-309  
 CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28  
 CC analogs. (I) are useful for treating a disease or disorder by  
 CC administering (I) to a patient. The disease or disorder is chosen from  
 CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease  
 CC or infectious disease. The administration increases the hemocrit, assist  
 CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)  
 CC are also useful for modulating the activity of chemokine receptor, which  
 CC involves contacting the chemokine receptor with (I), for mobilizing  
 CC intracellular calcium in a patient, which involves administering (I) to a  
 CC patient in need of such treatment. (I) are also useful for protecting  
 CC haematopoietic cells in a patient undergoing treatment with cytotoxic  
 CC agent, by administering (I) to the patient, where the survival of white  
 CC blood cells or leukocytes is increased. (I) are also useful for  
 CC maintaining cells capable of divisions in a quiescent state cells in a  
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)  
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a  
 CC patient by administering (I) to the patient. (I) are also useful for  
 CC treating or preventing inflammatory conditions, graft rejection,  
 CC bacterial infection, viral infection, vascular conditions (e.g.  
 CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-  
 CC reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell  
 CC mobilization, vaccine production and blood cell recovery following  
 CC chemotherapy. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 35 AA;  
 Query Match 100.0%; Score 73; DB 8; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ISVQRLASYRRITSSK 16  
 |||||  
 Db 20 ISVQRLASYRRITSSK 35  
 RESULT 21  
 ADM71735  
 ID ADM71735 standard; peptide; 35 AA.  
 XX  
 AC ADM71735;  
 XX  
 DT 17-JUN-2004 (first entry)  
 DE  
 DE Chemokine analog, g19, SEQ ID 1368.  
 XX  
 KW Chemokine analog; Chemokine; interleukin-8; IL-8;  
 KW Interferon inducible Protein-10; IP-10; CXCL 10;  
 KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; RANTES; CCL5;  
 KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;  
 KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;  
 KW infectious disease; inflammatory condition; graft rejection;  
 KW bacterial infection; viral infection; vascular condition;  
 KW atherosclerosis; restenosis; systemic lupus erythematosus;  
 KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;  
 KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;  
 KW Immunosuppressive; Dermatological; Antiinflammatory.  
 XX  
 OS Synthetic.

XX FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "RNH-Gln"  
 FT Misc-difference 4 /note= "Any amino acid"  
 FT Misc-difference 11 /note= "Any amino acid"  
 FT Misc-difference 12 /note= "Any amino acid"  
 FT Modified-site 35 /note= "Lys-(OH)-NH2"  
 FT WO2004024088-A2.  
 XX PD 25-MAR-2004.  
 XX PF 11-SEP-2003; 2003WO-US028745.  
 XX PR 13-SEP-2002; 2002US-00243795.  
 XX PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 XX PI Merzouk A, Wong D, Salari H;  
 XX WPI; 2004-329387/30.  
 XX Compound useful for treating cancer and cardiovascular disease, comprises  
 FT structure of chemokine analogs such as interleukin-8 and interferon  
 FT inducible protein-10.  
 XX Claim 1; SEQ ID NO 1368; 271pp; English.  
 XX The present invention relates to chemokine analogs (I, ADM70378-  
 CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible  
 CC Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-  
 CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,  
 CC Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309  
 CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28  
 CC analogs. (I) are useful for treating a disease or disorder by  
 CC administering (I) to a patient. The disease or disorder is chosen from  
 CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease  
 CC or infectious disease. The administration increases the hemocrit, assist  
 CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)  
 CC are also useful for modulating the activity of chemokine receptor, which  
 CC involves contacting the chemokine receptor with (I), for mobilizing  
 CC intracellular calcium in a patient, which involves administering (I) to a  
 CC patient in need of such treatment. (I) are also useful for protecting  
 CC haematopoietic cells in a patient undergoing treatment with cytotoxic  
 CC agent, by administering (I) to the patient, where the survival of white  
 CC blood cells or leukocytes is increased. (I) are also useful for  
 CC maintaining cells capable of divisions in a quiescent state cells in a  
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)  
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a  
 CC patient by administering (I) to the patient. (I) are also useful for  
 CC treating or preventing inflammatory conditions, Graft rejection,  
 CC bacterial infection, viral infection, vascular conditions (e.g.  
 CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-  
 CC reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell  
 CC mobilization, vaccine production and blood cell recovery following  
 CC chemotherapy. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pt\_sequences.  
 XX Sequence 35 AA;  
 XX Query Match 100.0%; Score 73; DB 8; Length 35;  
 XX Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ISVQRLASRYRITSSK 16  
 |||||  
 DB 20 ISVQRLASRYRITSSK 35

RESULT 22  
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 ID ADM71740 standard; peptide; 35 AA.  
 XX AC ADM71740;  
 XX DT 17-JUN-2004 (first entry)  
 XX DE Chemokine analog, g24, SEQ ID 1373.  
 XX KW Chemokine analog; Chemokine; interleukin-8; IL-8;  
 KW Interferon inducible Protein-10; IP-10; CXCL10;  
 KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; RANTES; CCL5;  
 KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;  
 KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;  
 KW infectious disease; inflammatory condition; graft rejection;  
 KW bacterial infection; viral infection; vascular condition;  
 KW atherosclerosis; restenosis; systemic lupus erythematosus;  
 KW ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;  
 KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;  
 KW Immunosuppressive; Dermatological; Antiinflammatory.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "RNH-Gln"  
 FT Misc-difference 9 /note= "Any amino acid"  
 FT Misc-difference 11 /note= "Any amino acid"  
 FT Misc-difference 12 /note= "Any amino acid"  
 FT Modified-site 35 /note= "Lys-(OH)-NH2"  
 FT WO2004024088-A2.  
 XX PD 25-MAR-2004.  
 XX PF 11-SEP-2003; 2003WO-US028745.  
 XX PR 13-SEP-2002; 2002US-00243795.  
 XX PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 XX PI Merzouk A, Wong D, Salari H;  
 XX WPI; 2004-329387/30.  
 XX Compound useful for treating cancer and cardiovascular disease, comprises  
 FT structure of chemokine analogs such as interleukin-8 and interferon  
 FT inducible protein-10.  
 XX Claim 1; SEQ ID NO 1373; 271pp; English.  
 XX The present invention relates to chemokine analogs (I, ADM70378-  
 CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible  
 CC Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-  
 CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,  
 CC Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309  
 CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28  
 CC analogs. (I) are useful for treating a disease or disorder by  
 CC administering (I) to a patient. The disease or disorder is chosen from  
 CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease  
 CC or infectious disease. The administration increases the hemocrit, assist  
 CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)  
 CC are also useful for modulating the activity of chemokine receptor, which  
 CC involves contacting the chemokine receptor with (I), for mobilizing  
 CC intracellular calcium in a patient, which involves administering (I) to a  
 CC patient in need of such treatment. (I) are also useful for protecting  
 CC haematopoietic cells in a patient undergoing treatment with cytotoxic  
 CC agent, by administering (I) to the patient, where the survival of white  
 CC blood cells or leukocytes is increased. (I) are also useful for  
 CC maintaining cells capable of divisions in a quiescent state cells in a  
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)  
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a  
 CC patient by administering (I) to the patient. (I) are also useful for  
 CC treating or preventing inflammatory conditions, Graft rejection,  
 CC bacterial infection, viral infection, vascular conditions (e.g.  
 CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-  
 CC reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell  
 CC mobilization, vaccine production and blood cell recovery following  
 CC chemotherapy. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pt\_sequences.  
 XX Sequence 35 AA;  
 XX Query Match 100.0%; Score 73; DB 8; Length 35;  
 XX Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ISVQRLASRYRITSSK 16  
 |||||  
 DB 20 ISVQRLASRYRITSSK 35

CC haematopoietic cells in a patient undergoing treatment with cytotoxic  
CC agent, by administering (I) to the patient, where the survival of white  
CC blood cells or leukocytes is increased. (I) are also useful for  
CC maintaining cells capable of divisions in a quiescent state cells in a  
CC patient undergoing treatment with a cytotoxic agent, by administering (I)  
CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a  
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CC reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell  
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CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 35 AA;  
  
Query Match 100.0%; Score 73; DB 8; Length 35;  
Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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|||||  
Db 20 ISVQRLASYRRITSSK 35  
  
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ID ADM71733 standard; peptide; 35 AA.  
XX  
XX  
AC ADM71733;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
XX Chemokine analog, g17, SEQ ID 1366.  
XX  
XX Chemokine analog; Chemokine; interleukin-8; IL-8;  
KW Interferon inducible Protein-10; IP-10; CXCL 10;  
KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; RANTES; CCL5;  
KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;  
KW autoimmunity disease; cancer; chronic inflammation; cardiovascular disease;  
KW infectious disease; inflammatory condition; graft rejection;  
KW bacterial infection; viral infection; vascular condition;  
KW atherosclerosis; restenosis; systemic lupus erythematosus;  
KW ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;  
KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;  
KW Immunosuppressive; Dermatological; Antiinflammatory.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Modified-site 1 /note= "RNH-Gln"  
FT  
FT Misc-difference 2 /note= "Any amino acid"  
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FT Misc-difference 11 /note= "Any amino acid"  
FT  
FT Misc-difference 12 /note= "Any amino acid"  
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FT Modified-site 35 /note= "Lys- (OH)-NH2"  
FT  
XX  
XX WO2004024088-A2.  
XX  
XX 25-MAR-2004.  
XX  
XX 11-SEP-2003; 2003WO-US028745.  
XX  
XX 13-SEP-2002; 2002US-00243795.  
XX  
XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.

PI Merzouk A, Wong D, Salari H;  
XX WPI; 2004-329387/30.  
XX  
XX Compound useful for treating cancer and cardiovascular disease, comprises  
FT structure of chemokine analogs such as interleukin-8 and interferon  
FT inducible protein-10.  
XX  
PS Claim 1; SEQ ID NO 1366; 271pp; English.  
XX  
XX The present invention relates to chemokine analogs (I, ADM70378-  
CC ADM72006), including interleukin (IL)-8 analogs, interferon inducible  
CC Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-  
CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,  
CC Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309  
CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28  
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CC administering (I) to a patient. The disease or disorder is chosen from  
CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease  
CC or infectious disease. The administration increases the hemocrit, assist  
CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)  
CC are also useful for modulating the activity of chemokine receptor, which  
CC involves contacting the chemokine receptor with (I), for mobilizing  
CC intracellular calcium in a patient, which involves administering (I) to a  
CC haematopoietic cells in a patient undergoing treatment with cytotoxic  
CC agent, by administering (I) to the patient, where the survival of white  
CC blood cells or leukocytes is increased. (I) are also useful for  
CC maintaining cells capable of divisions in a quiescent state cells in a  
CC patient undergoing treatment with a cytotoxic agent, by administering (I)  
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CC reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell  
CC mobilization, vaccine production and blood cell recovery following  
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CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 35 AA;  
  
Query Match 100.0%; Score 73; DB 8; Length 35;  
Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 ISVQRLASYRRITSSK 16  
|||||  
Db 20 ISVQRLASYRRITSSK 35  
  
RESULT 24  
ADM71780  
ID ADM71780 standard; peptide; 35 AA.  
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AC ADM71780;  
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DT 17-JUN-2004 (first entry)  
XX  
XX Chemokine analog, g64, SEQ ID 1413.  
XX  
XX Chemokine analog; Chemokine; interleukin-8; IL-8;  
KW Interferon inducible Protein-10; IP-10; CXCL 10;  
KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; RANTES; CCL5;  
KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;  
KW autoimmunity disease; cancer; chronic inflammation; cardiovascular disease;  
KW infectious disease; inflammatory condition; graft rejection;  
KW bacterial infection; viral infection; vascular condition;  
KW atherosclerosis; restenosis; systemic lupus erythematosus;  
KW ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;  
KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;  
KW Immunosuppressive; Dermatological; Antiinflammatory; cyclic.



XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site 1

XX FT Misc-difference 11 /note= "RNH-Gln"

XX FT Misc-difference 12 /note= "Any amino acid"

XX FT Misc-difference 13 /note= "Any amino acid"

XX FT Modified-site 13

XX FT Modified-site 19 /note= "The residue at this position forms a bond with Lys19 to form a cyclic peptide"

XX FT Modified-site 19

XX FT Modified-site 35 /note= "The residue at this position forms a bond with Glu3 to form a cyclic peptide"

XX FT Modified-site 35

XX FT /note= "Lys-(OH)-NH2"

XX PN WO2004024088-A2.

XX PD 25-MAR-2004.

XX PF 11-SEP-2003; 2003WO-US028745.

XX PR 13-SEP-2002; 2002US-00243795.

XX PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.

XX PI Merzouk A, Wong D, Salari H;

XX PX WPI; 2004-329387/30.

XX DR Compound useful for treating cancer and cardiovascular disease, comprises structure of chemokine analogs such as interleukin-8 and interferon inducible protein-10.

XX PS Claim 1; SEQ ID NO 1413; 271pp; English.

XX CC The present invention relates to chemokine analogs (I, ADM70378-ADM72006), including interleukin (IL)-8 analogs, Interferon inducible Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation, Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309 analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28 analogs. (I) are useful for treating a disease or disorder by administering (I) to a patient. The disease or disorder is chosen from autoimmune diseases, cancer, chronic inflammation, cardiovascular disease or infectious diseases. The administration increases the hemocrit, assist in mobilizing stem cells, in vaccine production or in gene therapy. (I) are also useful for modulating the activity of chemokine receptor, which involves contacting the chemokine receptor with (I), for mobilizing intracellular calcium in a patient, which involves administering (I) to a patient in need of such treatment. (I) are also useful for protecting haematopoietic cells in a patient undergoing treatment with cytotoxic agent, by administering (I) to the patient, where the survival of white blood cells or leukocytes is increased. (I) are also useful for maintaining cells capable of divisions in a quiescent state cells in a patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, vascular conditions (e.g. atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;

Best Local Similarity 100.0%; Pred. No. 6.7e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVORLASYYRRITSSK 16

DB 20 ISVORLASYYRRITSSK 35

RESULT 25

ADM71721

ID ADM71721 standard; peptide; 35 AA.

XX AC ADM71721;

XX DT 17-JUN-2004 (first entry)

XX DE Chemokine analog, g5, SEQ ID 1354.

XX KW Chemokine analog; Chemokine; interleukin-8; IL-8;

XX KW Interferon inducible Protein-10; IP-10; CXCL10;

XX KW Macrophage inflammatory Protein-1-alpha; MIP-1-alpha; RANTES; CCL5;

XX KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;

XX KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;

XX KW infectious disease; inflammatory condition; graft rejection;

XX KW bacterial infection; viral infection; vascular condition;

XX KW atherosclerosis; restenosis; systemic lupus erythematosus;

XX KW ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;

XX KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;

XX KW Immunosuppressive; Dermatological; Antiinflammatory.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site 1 /note= "RNH-Gln"

XX FT Misc-difference 2 /note= "Any amino acid"

XX FT Misc-difference 11 /note= "Any amino acid"

XX FT Misc-difference 12 /note= "Any amino acid"

XX FT Misc-difference 35 /note= "Lys-(OH)-NH2"

XX PN WO2004024088-A2.

XX PD 25-MAR-2004.

XX PF 11-SEP-2003; 2003WO-US028745.

XX PR 13-SEP-2002; 2002US-00243795.

XX PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.

XX PI Merzouk A, Wong D, Salari H;

XX PX WPI; 2004-329387/30.

XX DR Compound useful for treating cancer and cardiovascular disease, comprises structure of chemokine analogs such as interleukin-8 and interferon inducible protein-10.

XX PS Claim 1; SEQ ID NO 1354; 271pp; English.

XX CC The present invention relates to chemokine analogs (I, ADM70378-ADM72006), including interleukin (IL)-8 analogs, Interferon inducible Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation, Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309 analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28 analogs. (I) are useful for treating a disease or disorder by administering (I) to a patient. The disease or disorder is chosen from autoimmune diseases, cancer, chronic inflammation, cardiovascular disease

or infectious disease. The administration increases the hemocrit, assist in mobilizing stem cells, in vaccine production or in gene therapy. (I) are also useful for modulating the activity of chemokine receptor, which involves contacting the chemokine receptor with (I), for mobilizing intracellular calcium in a patient, which involves administering (I) to a patient in need of such treatment. (I) are also useful for protecting haematopoietic cells in a patient undergoing treatment with cytotoxic agent, by administering (I) to the patient, where the survival of white blood cells or leukocytes is increased. (I) are also useful for maintaining cells capable of divisions in a quiescent state cells in a patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, vascular conditions (e.g. atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;  
Best Local Similarity 100.0%; Pred. No. 6.7e-06; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 0;

QY 1 ISVQRLASYRRITSSK 16  
|||||  
DB 20 ISVQRLASYRRITSSK 35

## RESULT 26

ADM71724  
ID ADM71724 standard; peptide; 35 AA.

AC ADM71724;

XX 17-JUN-2004 (first entry)

DE Chemokine analog, 98, SEQ ID 1357.

XX Chemokine analog; Chemokine; interleukin-8; IL-8;  
KW Interferon inducible Protein-10; IP-10; CXCL 10;  
KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;  
KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;  
KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;  
KW infectious disease; inflammatory condition; graft rejection;  
KW bacterial infection; viral infection; vascular condition;  
KW atherosclerosis; restenosis; systemic lupus erythematosus;  
KW ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;  
KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;  
KW Immunosuppressive; Dermatological; Antiinflammatory.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "RNH-Gln"

FT Misc-difference 5 /note= "Any amino acid"

FT Misc-difference 11 /note= "Any amino acid"

FT Misc-difference 12 /note= "Any amino acid"

FT Modified-site 35 /note= "Lys- (OH) -NH2"

FT WO2004024088-A2.

XX 25-MAR-2004.

XX

PF 11-SEP-2003; 2003WO-US028745.

XX 13-SEP-2002; 2002US-00243795.

PR (CHEM-) CHEMOKINE THERAPEUTICS CORP.

PA Merzouk A, Wong D, Salari H;

XX WPI; 2004-329387/30.

XX Compound useful for treating cancer and cardiovascular disease, comprises

XX structure of chemokine analogs such as interleukin-8 and interferon

XX inducible protein-10.

XX Claim 1; SEQ ID NO 1357; 271pp; English.

XX The present invention relates to chemokine analogs (I, ADM70378-  
XX ADM72006), including interleukin (IL)-8 analogs, interferon inducible  
XX Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-  
XX alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,  
XX Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309  
XX analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28  
XX analogs. (I) are useful for treating a disease or disorder by  
XX administering (I) to a patient. The disease or disorder is chosen from  
XX autoimmune diseases, cancer, chronic inflammation, cardiovascular disease  
XX or infectious disease. The administration increases the hemocrit, assist  
XX in mobilizing stem cells, in vaccine production or in gene therapy. (I)  
XX are also useful for modulating the activity of chemokine receptor, which  
XX involves contacting the chemokine receptor with (I), for mobilizing  
XX intracellular calcium in a patient, which involves administering (I) to a  
XX patient in need of such treatment. (I) are also useful for protecting  
XX haematopoietic cells in a patient undergoing treatment with cytotoxic  
XX agent, by administering (I) to the patient, where the survival of white  
XX blood cells or leukocytes is increased. (I) are also useful for  
XX maintaining cells capable of divisions in a quiescent state cells in a  
XX patient undergoing treatment with a cytotoxic agent, by administering (I)  
XX to the patient, and for mobilizing leukocytes e.g. neutrophils in a  
XX patient by administering (I) to the patient. (I) are also useful for  
XX treating or preventing inflammatory conditions, graft rejection,  
XX bacterial infection, viral infection, vascular conditions (e.g.  
XX atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-  
XX reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell  
XX mobilization, vaccine production and blood cell recovery following  
XX chemotherapy. Note: The sequence data for this patent did not form part  
XX of the printed specification, but was obtained in electronic format  
XX directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;

Best Local Similarity 100.0%; Pred. No. 6.7e-06; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0;

QY 1 ISVQRLASYRRITSSK 16  
|||||  
DB 20 ISVQRLASYRRITSSK 35

## RESULT 27

ADM71731  
ID ADM71731 standard; peptide; 35 AA.

XX ADM71731;

XX 17-JUN-2004 (first entry)

XX Chemokine analog, g15, SEQ ID 1364.

XX Chemokine analog; Chemokine; interleukin-8; IL-8;

XX Interferon inducible Protein-10; IP-10; CXCL 10;

XX Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;

XX I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;

XX autoimmune disease; cancer; chronic inflammation; cardiovascular disease;

XX



infectious disease; inflammatory condition; graft rejection;  
bacterial infection; viral infection; vascular condition;  
atherosclerosis; restenosis; systemic lupus erythematosus;  
ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis;  
Antiartherosclerotic; Virucide; Antibacterial; Vasotropic;  
Immunosuppressive; Dermatological; Antiinflammatory.  
Synthetic.

Key Location/Qualifiers  
Modified-site 1 /note= "RNH-Gln"  
Misc-difference 11 /note= "Any amino acid"  
Misc-difference 12 /note= "Any amino acid"  
Modified-site 35 /note= "Lys- (OH) -NH2"

WO2004024088-A2.  
25-MAR-2004.  
11-SEP-2003; 2003WO-US028745.  
13-SEP-2002; 2002US-00243795.  
(CHEM-) CHEMOKINE THERAPEUTICS CORP.  
Merzouk A, Wong D, Salari H;  
WPI; 2004-329387/30.  
Compound useful for treating cancer and cardiovascular disease, comprises structure of chemokine analogs such as interleukin-8 and interferon inducible protein-10.  
Claim 1; SEQ ID NO 1364; 271pp; English.

The present invention relates to chemokine analogs (I, ADM70378-ADM72006), including interleukin (IL)-8 analogs, Interferon inducible Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation, Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309 analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28 analogs. (I) are useful for treating a disease or disorder by administering (I) to a patient. The disease or disorder is chosen from autoimmune diseases, cancer, chronic inflammation, cardiovascular disease or infectious disease. The administration increases the hemocrit, assist in mobilizing stem cells, in vaccine production or in gene therapy. (I) are also useful for modulating the activity of chemokine receptor, which involves contacting the chemokine receptor with (I), for mobilizing intracellular calcium in a patient, which involves administering (I) to a patient in need of such treatment. (I) are also useful for protecting haematopoietic cells in a patient undergoing treatment with cytotoxic agent, by administering (I) to the patient, where the survival of white blood cells or leukocytes is increased. (I) are also useful for maintaining cells capable of divisions in a quiescent state cells in a patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, vascular conditions (e.g. atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 35 AA;  
Query Match 100.0%; Score 73; DB 8; Length 35;

Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ISVQRLASYRRITSSK 16  
| | | | | | | | | | | | | | | |  
Db 20 ISVQRLASYRRITSSK 35

RESULT 28  
ADM71739  
ID ADM71739 standard; peptide; 35 AA.  
XX  
AC ADM71739;  
XX  
DI 17-JUN-2004 (first entry)  
XX  
DE Chemokine analog, g23, SEQ ID 1372.  
XX  
KW Chemokine analog; Chemokine; interleukin-8; IL-8;  
KW Interferon inducible Protein-10; IP-10; CXCL10;  
KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;  
KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;  
KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;  
KW infectious disease; inflammatory condition; graft rejection;  
KW bacterial infection; viral infection; vascular condition;  
KW atherosclerosis; restenosis; systemic lupus erythematosus;  
KW ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;  
KW Antiartherosclerotic; Virucide; Antibacterial; Vasotropic;  
KW Immunosuppressive; Dermatological; Antiinflammatory.  
XX  
OS Synthetic.

Key Location/Qualifiers  
Modified-site 1 /note= "RNH-Gln"  
Misc-difference 8 /note= "Any amino acid"  
Misc-difference 11 /note= "Any amino acid"  
Misc-difference 12 /note= "Any amino acid"  
Modified-site 35 /note= "Lys- (OH) -NH2"  
WO2004024088-A2.  
25-MAR-2004.  
11-SEP-2003; 2003WO-US028745.  
13-SEP-2002; 2002US-00243795.  
(CHEM-) CHEMOKINE THERAPEUTICS CORP.  
Merzouk A, Wong D, Salari H;  
WPI; 2004-329387/30.  
Compound useful for treating cancer and cardiovascular disease, comprises structure of chemokine analogs such as interleukin-8 and interferon inducible protein-10.  
Claim 1; SEQ ID NO 1364; 271pp; English.

The present invention relates to chemokine analogs (I, ADM70378-ADM72006), including interleukin (IL)-8 analogs, Interferon inducible Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation, Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309 analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28 analogs. (I) are useful for treating a disease or disorder by administering (I) to a patient. The disease or disorder is chosen from autoimmune diseases, cancer, chronic inflammation, cardiovascular disease or infectious disease. The administration increases the hemocrit, assist in mobilizing stem cells, in vaccine production or in gene therapy. (I) are also useful for modulating the activity of chemokine receptor, which involves contacting the chemokine receptor with (I), for mobilizing intracellular calcium in a patient, which involves administering (I) to a patient in need of such treatment. (I) are also useful for protecting haematopoietic cells in a patient undergoing treatment with cytotoxic agent, by administering (I) to the patient, where the survival of white blood cells or leukocytes is increased. (I) are also useful for maintaining cells capable of divisions in a quiescent state cells in a patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, vascular conditions (e.g. atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 35 AA;  
Query Match 100.0%; Score 73; DB 8; Length 35;

or infectious disease. The administration increases the hemocrit, assist in mobilizing stem cells, in vaccine production or in gene therapy. (I) are also useful for modulating the activity of chemokine receptor, which involves contacting the chemokine receptor with (I), for mobilizing intracellular calcium in a patient, which involves administering (I) to a patient in need of such treatment. (I) are also useful for protecting haematopoietic cells in a patient undergoing treatment with cytotoxic agent, by administering (I) to the patient, where the survival of white blood cells or leukocytes is increased. (I) are also useful for maintaining cells capable of divisions in a quiescent state cells in a patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, vascular conditions (e.g. atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX  
SQ Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;  
Best Local Similarity 100.0%; Pred. No. 6.7e-06; Length 35;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
|||||  
Db 20 ISVQRLASYRRITSSK 35

RESULT 29  
ADM71729  
ID ADM71729 standard; peptide; 35 AA.

XX  
AC ADM71729;

XX  
DT 17-JUN-2004 (first entry)

XX  
DE Chemokine analog, g13, SEQ ID 1362.

XX  
KW Chemokine analog; Chemokine; interleukin-8; IL-8;

KW Interferon inducible Protein-10; IP-10; CXCL 10;

KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; RANTES; CCL5;

KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;

KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;

KW infectious disease; inflammatory condition; graft rejection;

KW bacterial infection; viral infection; vascular condition;

KW atherosclerosis; restenosis; systemic lupus erythematosus;

KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis;

KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;

KW Immunosuppressive; Dermatological; Antiinflammatory.

XX  
OS Synthetic.

XX  
FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "RNH-Gln"

FT Misc-difference 10

FT /note= "Any amino acid"

FT Misc-difference 11

FT /note= "Any amino acid"

FT Misc-difference 12

FT /note= "Any amino acid"

FT Modified-site 35

FT /note= "Lys-(OH)-NH2"

XX  
WO2004024088-A2.

XX  
XX 25-MAR-2004.

XX  
XX

PF 11-SEP-2003; 2003MO-US028745.

XX  
PR 13-SEP-2002; 2002US-00243795.

XX  
PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.

XX  
PI Merzouk A, Wong D, Salari H;

XX  
XX WPI; 2004-329387/30.

DR  
XX Compound useful for treating cancer and cardiovascular disease, comprises structure of chemokine analogs such as interleukin-8 and interferon inducible protein-10.

PT  
XX Claim 1; SEQ ID NO 1362; 271pp; English.

PS  
XX The present invention relates to chemokine analogs (I, ADM70378-ADM72006), including interleukin (IL)-8 analogs, interferon inducible Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation, Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309 analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28 analogs. (I) are useful for treating a disease or disorder by administering (I) to a patient. The disease or disorder is chosen from autoimmune diseases, cancer, chronic inflammation, cardiovascular disease or infectious disease. The administration increases the hemocrit, assist in mobilizing stem cells, in vaccine production or in gene therapy. (I) are also useful for modulating the activity of chemokine receptor, which involves contacting the chemokine receptor with (I), for mobilizing intracellular calcium in a patient, which involves administering (I) to a patient in need of such treatment. (I) are also useful for protecting haematopoietic cells in a patient undergoing treatment with cytotoxic agent, by administering (I) to the patient, where the survival of white blood cells or leukocytes is increased. (I) are also useful for maintaining cells capable of divisions in a quiescent state cells in a patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, vascular conditions (e.g. atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX  
SQ Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;

Best Local Similarity 100.0%; Pred. No. 6.7e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
|||||  
Db 20 ISVQRLASYRRITSSK 35

RESULT 30

ADM71732

ID ADM71732 standard; peptide; 35 AA.

XX  
AC ADM71732;

XX  
DT 17-JUN-2004 (first entry)

XX  
DE Chemokine analog, g16, SEQ ID 1365.

XX  
KW Chemokine analog; Chemokine; interleukin-8; IL-8;

KW Interferon inducible Protein-10; IP-10; CXCL 10;

KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; RANTES; CCL5;

KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;

KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;

XX

KW	infectious disease; inflammatory condition; graft rejection;
KW	bacterial infection; viral infection; vascular condition;
KW	atherosclerosis; restenosis; systemic lupus erythematosus;
KW	ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis;
KW	Antiarterioleclerotic; Virucide; Antibacterial; Vasostrict;
KW	Immunosuppressive; Dermatological; Antiinflammatory.
XX	
OS	Synthetic.
XX	
Key	Location/Qualifiers
XX	
FT	Modified-site 1 /note= "RNH-Xaa, where Xaa is any amino acid"
FT	
FT	Misc-difference 11 /note= "Any amino acid"
FT	
FT	Misc-difference 12 /note= "Any amino acid"
FT	
FT	Modified-site 35 /note= "Lys-(OH)-NH2"
FT	
XX	
PN	WO2004024088-A2.
XX	
XX	25-MAR-2004.
XX	
PF	11-SEP-2003; 2003WO-US028745.
XX	
PR	13-SEP-2002; 2002US-00243795.
XX	
PA	(CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX	
PI	Merzouk A, Wong D, Salari H;
XX	
DR	WPI; 2004-329387/30.
XX	
PT	Compound useful for treating cancer and cardiovascular disease, comprises
PT	structure of chemokine analogs such as interleukin-8 and interferon
PT	inducible protein-10.
XX	
PS	Claim 1; SEQ ID NO 1365; 271pp; English.
XX	
CC	The present invention relates to chemokine analogs (I, ADM70378-
CC	ADM72006), including interleukin (IL)-8 analogs, Interferon inducible
CC	Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-
CC	alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,
CC	Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309
CC	analog, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28
CC	analog. (I) are useful for treating a disease or disorder by
CC	administering (I) to a patient. The disease or disorder is chosen from
CC	autoimmune diseases, cancer, chronic inflammation, cardiovascular diseases
CC	or infectious disease. The administration increases the hemocrit, assist
CC	in mobilizing stem cells, in vaccine production or in gene therapy. (I)
CC	are also useful for modulating the activity of chemokine receptor, which
CC	involves contacting the chemokine receptor with (I), for mobilizing
CC	intracellular calcium in a patient, which involves administering (I) to a
CC	patient in need of such treatment. (I) are also useful for protecting
CC	haematopoietic cells in a patient undergoing treatment with cytotoxic
CC	agent, by administering (I) to the patient, where the survival of white
CC	blood cells or leukocytes is increased. (I) are also useful for
CC	maintaining cells capable of divisions in a quiescent state cells in a
CC	patient undergoing treatment with a cytotoxic agent, by administering (I) to
CC	the patient, and for mobilizing leukocytes e.g. neutrophils in a
CC	patient by administering (I) to the patient. (I) are also useful for
CC	treating or preventing inflammatory conditions, graft rejection,
CC	bacterial infection, viral infection, vascular conditions (e.g.
CC	atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia
CC	reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell
CC	mobilization, vaccine production and blood cell recovery following
CC	chemotherapy. Note: The sequence data for this patent did not form part
CC	of the printed specification, but was obtained in electronic format
CC	directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX	
XX	Sequence 35 AA;

Best Local Similarity	100.0%;	Pred. No. 6.7e-06;				
Matches	16;	Conservative	0; Mismatches	0; Indels	0; Gaps	0;
Qy	1	ISVQLASVRRITSSK	16			
Db	20	ISVQLASVRRITSSK	35			
RESULT 31						
ADM71737						
ID	ADM71737	standard; peptide; 35 AA.				
AC	ADM71737;					
XX						
DT	17-JUN-2004	(first entry)				
XX						
DE	Chemokine analog, g21, SEQ ID 1370.					
XX						
KW	Chemokine analog; Chemokine; interleukin-8; IL-8;					
KW	Interferon inducible Protein-10; IP-10; CXCL 10;					
KW	Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;					
KW	I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;					
KW	autoimmune disease; cancer; chronic inflammation; cardiovascular disease;					
KW	infectious disease; inflammatory condition; graft rejection;					
KW	bacterial infection; viral infection; vascular condition;					
KW	atherosclerosis; restenosis; systemic lupus erythematosus;					
KW	ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;					
KW	Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;					
KW	Immunosuppressive; Dermatological; Antiinflammatory.					
OS	Synthetic.					
XX						
Key	Location/Qualifiers					
Modified-site	1 /note= "RNH-Gln"					
FT						
Misc-difference	6 /note= "Any amino acid"					
FT						
Misc-difference	11 /note= "Any amino acid"					
FT						
Misc-difference	12 /note= "Any amino acid"					
FT						
Modified-site	35 /note= "Lys-(OH)-NH2"					
FT						
XX						
PN	WO2004024088-A2.					
XX						
PD	25-MAR-2004.					
XX						
PF	11-SEP-2003; 2003WO-US028745.					
XX						
PR	13-SEP-2002; 2002US-00243795.					
XX						
PA	(CHEM-) CHEMOKINE THERAPEUTICS CORP.					
XX						
PI	Merzouk A, Wong D, Salari H;					
XX						
DR	WPI; 2004-329387/30.					
XX						
PT	Compound useful for treating cancer and cardiovascular disease, comprises					
PT	structure of chemokine analogs such as interleukin-8 and interferon					
PT	inducible protein-10.					
XX						
PS	Claim 1; SEQ ID NO 1370; 271pp; English.					
XX						
CC	The present invention relates to chemokine analogs (I, ADM70378-					
CC	ADM72006), including interleukin (IL)-8 analogs, Interferon inducible					
CC	Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-					
CC	alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,					
CC	Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309					
CC	analog, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28					
CC	analog. (I) are useful for treating a disease or disorder by					
CC	administering (I) to a patient. The disease or disorder is chosen from					
CC	autoimmune diseases, cancer, chronic inflammation, cardiovascular disease					

or infectious disease. The administration increases the hemocrit, assist in mobilizing stem cells, in vaccine production or in gene therapy. (I) are also useful for modulating the activity of chemokine receptor, which involves contacting the chemokine receptor with (I), for mobilizing intracellular calcium in a patient, which involves administering (I) to a patient in need of such treatment. (I) are also useful for protecting haematopoietic cells in a patient undergoing treatment with cytotoxic agent, by administering (I) to the patient, where the survival of white blood cells or leukocytes is increased. (I) are also useful for maintaining cells capable of divisions in a quiescent state cells in a patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, vascular conditions (e.g. atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;  
Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
|||||  
Db 20 ISVQRLASYRRITSSK 35

RESULT 32

ADM71738  
ID ADM71738 standard; peptide; 35 AA.

XX AC ADM71738;

XX DT 17-JUN-2004 (first entry)

XX DE Chemokine analog, g22, SEQ ID 1371.

XX KW Chemokine analog; Chemokine; interleukin-8; IL-8;

XX KW Interferon inducible Protein-10; IP-10; CXCL 10;

XX KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; RANTES; CCL5;

XX KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;

XX KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;

XX KW infectious disease; inflammatory condition; graft rejection;

XX KW bacterial infection; viral infection; vascular condition;

XX KW atherosclerosis; restenosis; systemic lupus erythematosus;

XX KW ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis;

XX KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;

XX KW Immunosuppressive; Dermatological; Antiinflammatory.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site 1

XX FT /note= "RNH-Gln"

XX FT Misc-difference 7

XX FT /note= "Any amino acid"

XX FT Misc-difference 11

XX FT /note= "Any amino acid"

XX FT Misc-difference 12

XX FT /note= "Any amino acid"

XX FT Modified-site 35

XX FT /note= "Lys-(OH)-NH2"

XX FT WO2004024088-A2.

XX FN 25-MAR-2004.

XX PD

XX XX

PF 11-SEP-2003; 2003WO-US028745.

XX PR 13-SEP-2002; 2002US-00243795.

XX PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.

XX PI Merzouk A, Wong D, Salari H;

XX PI WPI; 2004-329387/30.

XX DR Claim 1; SEQ ID NO 1371; 271pp; English.

XX PT The present invention relates to chemokine analogs (I, ADM70378-ADM72006), including interleukin (IL)-8 analogs, interferon inducible Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation, Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309 analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28 analogs. (I) are useful for treating a disease or disorder by administering (I) to a patient. The disease or disorder is chosen from autoimmune diseases, cancer, chronic inflammation, cardiovascular disease or infectious disease. The administration increases the hemocrit, assist in mobilizing stem cells, in vaccine production or in gene therapy. (I) are also useful for modulating the activity of chemokine receptor, which involves contacting the chemokine receptor with (I), for mobilizing intracellular calcium in a patient, which involves administering (I) to a patient in need of such treatment. (I) are also useful for protecting haematopoietic cells in a patient undergoing treatment with cytotoxic agent, by administering (I) to the patient, where the survival of white blood cells or leukocytes is increased. (I) are also useful for maintaining cells capable of divisions in a quiescent state cells in a patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, vascular conditions (e.g. atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;  
Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
|||||  
Db 20 ISVQRLASYRRITSSK 35

RESULT 33

ADM71745

ID ADM71745 standard; peptide; 41 AA.

XX AC ADM71745;

XX DT 17-JUN-2004 (first entry)

XX DE Chemokine analog, g29, SEQ ID 1378.

XX KW Chemokine analog; Chemokine; interleukin-8; IL-8;

XX KW Interferon inducible Protein-10; IP-10; CXCL 10;

XX KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; RANTES; CCL5;

XX KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;

XX KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;

CC	directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 41 AA;
	Query Match 100.0%; Score 73; DB 8; Length 41;
	Best Local Similarity 100.0%; Pred. No. 7.9e-06;
	Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 ISVQRLASYRRITSSK 16 
Dd	8 ISVQRLASYRRITSSK 23 
RESULT 34	
ADM71783	ID ADM71783 standard; peptide; 41 AA.
XX	
AC	ADM71783;
XX	
DT	17-JUN-2004 (first entry)
XX	
DE	Chemokine analog, g67, SEQ ID 1416.
XX	
KW	Chemokine analog; Chemokine; interleukin-8; IL-8;
KW	Interferon inducible Protein-10; IP-10; CXCL 10;
KW	Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; RANTES; CCL5;
KW	I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
KW	autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
KW	infectious disease; inflammatory condition; graft rejection;
KW	bacterial infection; viral infection; vascular condition;
KW	atherosclerosis; restenosis; systemic lupus erythematosus;
KW	ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis;
KW	Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
KW	Immunosuppressive; Dermatological; Antiinflammatory; cyclic.
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 1
FT	/note= "RNH-Tyr"
FT	Modified-site 23..28
FT	/note= "Lys-[linker]-Lys, where linker is a bifunctional group covalently attached to the N-terminal and C-terminal portions of the analog having the structure: H2N -ZA-COOH, wherein Za is selected from the group consisting of: (1) alkyl, alkenyl, aralkyl, alkynyl, (2) -(CH2)n- wherein n is an integer n=19 to 14, (3) any combination of four natural amino acids or non-natural amino acids and (4) -(Gly)4- (SEQ ID 1640)."
FT	Modified-site 35
FT	/note= "The residue at this position forms a bond with Lys39 to form a cyclic peptide"
FT	Modified-site 39
FT	/note= "The residue at this position forms a bond with Asp35 to form a cyclic peptide"
FT	Modified-site 41
FT	/note= "Thr-(OH)-NH2"
XX	
DN	WO2004024088-A2.
PD	
XX	25-MAR-2004.
XX	
Pf	11-SEP-2003; 2003WO-US028745.
XX	
PR	13-SEP-2002; 2002US-00243795.
XX	
PA	(CHEM-) CHEMOKINE THERAPEUTICS CORP.
PI	Merzouk A, Wong D, Salari H;
XX	
DR	WIPI; 2004-329387/30.
PT	Compound useful for treating cancer and cardiovascular disease, comprises

PT structure of chemokine analogs such as interleukin-8 and interferon  
 PT inducible protein-10.  
 XX  
 PS Claim 1; SEQ ID NO 1416; 271pp; English.  
 XX  
 CC The present invention relates to chemokine analogs (I, ADM70378-  
 CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible  
 CC Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-  
 CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,  
 CC Normal T-cell Expressed, and presumably Secreted or CCU5) analogs, I-309  
 CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28  
 CC analogs. (I) are useful for treating a disease or disorder by  
 CC administering (I) to a patient. The disease or disorder is chosen from  
 CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease  
 CC or infectious disease. The administration increases the hemocrit, assist  
 CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)  
 CC are also useful for modulating the activity of chemokine receptor, which  
 CC involves contacting the chemokine receptor with (I), for mobilizing  
 CC intracellular calcium in a patient, which involves administering (I) to a  
 CC patient in need of such treatment. (I) are also useful for protecting  
 CC haematopoietic cells in a patient undergoing treatment with cytotoxic  
 CC agent, by administering (I) to the patient, where the survival of white  
 CC blood cells or leukocytes is increased. (I) are also useful for  
 CC maintaining cells capable of divisions in a quiescent state cells in a  
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)  
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a  
 CC patient by administering (I) to the patient. (I) are also useful for  
 CC treating or preventing inflammatory conditions, graft rejection,  
 CC bacterial infection, viral infection, systemic lupus erythematosus, and ischaemia-  
 CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-  
 CC reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell  
 CC mobilization, vaccine production and blood cell recovery following  
 CC chemotherapy. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 41 AA;

Query Match 100.0%; Score 73; DB 8; Length 41;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16  
 |||||  
 Db 8 ISVQRLASYRRITSSK 23

RESULT 35  
 AEB70238  
 ID AEB70238 standard; protein; 65 AA.

XX AEB70238;

XX 20-OCT-2005 (first entry)

DE Small inducible cytokine A2 precursor variant S71513\_P2.

XX gynecological; gene therapy; diagnosis; selectable marker; endometriosis;  
 KW gynecological; genitourinary disease; gynecology and obstetrics;  
 KW S71513\_P2; small inducible cytokine A2 precursor.

XX Homo sapiens.

XX WO2005072049-A2.

XX 11-AUG-2005.

XX 27-JAN-2005; 2005WO-IB001188.

XX 27-JAN-2004; 2004US-0539128P.

PR 27-JAN-2004; 2004US-0539129P.

PR 22-OCT-2004; 2004US-0621004P.

PR 17-NOV-2004; 2004US-0628145P.

PR 17-NOV-2004; 2004US-0628178P.  
 PR 17-NOV-2004; 2004US-0628230P.  
 PR 27-JAN-2005; 55US-00621004.  
 XX  
 PA (COMP-) COMPUGEN USA INC.

XX Cohen Y, Pollock S, Novik A, Diber A;  
 PI WPI; 2005-555591/56.  
 XX N-PSDB; AEB70230.

PT New mammalian nucleic acid and polypeptide sequences useful for  
 PT screening, diagnosing or treating endometriosis, or in monitoring disease  
 PT progression or efficacy of treatment for endometriosis.

XX Claim 3; SEQ ID NO 9; 804pp; English.

XX The invention describes a nucleic acid sequence comprising any of the 7  
 CC nucleotide sequences having 29-1404 bp fully defined in the specification  
 CC (SEQ ID NOS: 1-7). Also described are: an amino acid sequence comprising  
 CC 65 amino acids fully defined in the specification (SEQ ID NO: 9); an  
 CC isolated chimeric polypeptide encoding for S71513\_P2, comprising a first  
 CC amino acid sequence being at least 90% homologous to Met-Lys-Val-Ser-Ala-  
 CC Ala-Leu-Leu-Cys-Leu-Leu-Ile-Ala-Thr-Phe-Ile-Pro-Gln-Gly-Leu-Arg-  
 CC Gln-Pro-Asp-Ala-Ile-Asn-Ala-Pro-Val-Thr-Cys-Tyr-Asn-Phe-Thr-Asn-Arg-  
 CC Lys-Ile-Ser-Val-Gln-Arg-Leu-Ala-Ser-Tyr-Arg-Arg-Ile-Thr-Ser-Ser-Lys-Cys-  
 CC Pro-Lys-Glu-Ala-Val corresponding to amino acids 1-64 of SY02 HUMAN,  
 CC which also corresponds to amino acids 1-64 of S71513\_P2, and a second  
 CC amino acid sequence comprising a polypeptide having the sequence M  
 CC corresponding to amino acid 65 of S71513\_P2, where the first amino acid  
 CC sequence and second amino acid sequence are contiguous and in a  
 CC sequential order; an antibody capable of specifically binding to an  
 CC epitope of the amino acid sequence mentioned above; a kit for detecting  
 CC endometriosis, comprising a kit detecting overexpression of the splice  
 CC variant or a kit comprising the above antibody; methods for detecting,  
 CC diagnosing or screening for endometriosis; a biomarker capable of  
 CC detecting endometriosis, comprising the above nucleic acid or amino acid  
 CC sequences, or their fragments; a method for monitoring disease  
 CC progression and/or treatment efficacy and/or relapse of endometriosis;  
 CC and a method of selecting a therapy for endometriosis. The composition  
 CC and methods are useful for screening, diagnosing or treating  
 CC endometriosis. These may also be used in monitoring disease progression  
 CC and the efficacy of treatment for endometriosis. This is the amino acid  
 CC sequence of S71513\_P2, a variant of the protein small inducible cytokine  
 CC A2 precursor (also known as SY02 HUMAN, CCL2, MCP-1, monocyte  
 CC chemoattractant protein-1, MCA, monocyte secretory protein JE or HC11), a  
 CC candidate marker for endometriosis.

XX Sequence 65 AA;

Query Match 100.0%; Score 73; DB 9; Length 65;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16  
 |||||  
 Db 43 ISVQRLASYRRITSSK 58

RESULT 36  
 AAW13598  
 ID AAW13598 standard; peptide; 66 AA.

XX AAW13598;

XX 07-NOV-1997 (first entry)

DE Monocyte chemoattractant protein analogue MCP-1 (10-76).

XX Truncated monocyte chemoattractant protein-1; inhibitor;  
 KW receptor binding; anti inflammatory; basophil; lymphocyte; allergy;  
 KW chronic inflammatory disease; arthritis; arteriosclerosis; lung disease.

```

OS Homo sapiens.
PN CA2152141-A.
XX
XX 20-DEC-1996.
XX
XX 19-JUN-1995; 95CA-02152141.
XX
XX 19-JUN-1995; 95CA-02152141.
XX
XX (LEWIS I.
XX Lewis I, Gong J;
XX WPI; 1997-165844/16.
XX
XX N-terminally truncated monocyte chemoattractant protein-1 (MCP-1) -
XX lacks MCP-1 activity and inhibits receptor binding, useful as anti-
XX inflammatory agent.
XX
XX Disclosure; Page 5; 27pp; English.
XX
XX The present sequence represents an analogue, MCP-1 (10-76), of monocyte
XX chemoattractant protein-1 (MCP-1). The analogue, which lacks the N-
XX terminal amino acids 1-9 of MCP-1, acts as an antagonist of MCP-1 as it
XX lacks MCP-1 biological activity and inhibits binding to a MCP-1 receptor.
XX The analogue is useful as an anti-inflammatory agent to block the effects
XX of MCP-1 which is an inflammatory mediator causing migration of monocytes
XX and other cells e.g. basophils and lymphocytes into inflammation sites.
XX MCP-1 has been implicated in allergic and chronic inflammatory diseases
XX e.g. arthritis, arteriosclerosis and several lung diseases. The analogue
XX competes more effectively with MCP-1 for binding MCP-1 receptors than
XX prior art mutant versions of MCP-1 e.g. preferably providing 50%
XX inhibition of binding at a 25:1 ratio or less, compared with 75:1 for
XX prior art mutant 7ND
XX
XX Sequence 66 AA;
XX
XX Query Match 100.0%; Score 73; DB 2; Length 66;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-05;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 ISVQRLASYRRITSSK 16
Db 10 ISVQRLASYRRITSSK 25
XX
RESULT 37
AAW13599
ID AAW13599 standard; peptide; 67 AA.
XX
XX AAW13599;
XX
XX 07-NOV-1997 (first entry)
XX
XX Monocyte chemoattractant protein analogue MCP-1 (11-76).
XX
XX Truncated monocyte chemoattractant protein-1; inhibitor;
XX receptor binding; anti inflammatory; basophil; lymphocyte; allergy;
XX chronic inflammatory disease; arthritis; arteriosclerosis; lung disease.
XX
XX Homo sapiens.
XX
XX CA2152141-A.
XX
XX 20-DEC-1996.
XX
XX 19-JUN-1995; 95CA-02152141.
XX
XX 19-JUN-1995; 95CA-02152141.
XX
XX (LEWIS I.
XX Lewis I, Gong J;
XX WPI; 1997-165844/16.
XX
XX N-terminally truncated monocyte chemoattractant protein-1 (MCP-1) -
XX lacks MCP-1 activity and inhibits receptor binding, useful as anti-
XX inflammatory agent.
XX
XX Claim 7; Page 5; 27pp; English.
XX
XX The present sequence represents an analogue, MCP-1 (9-76), of monocyte
XX chemoattractant protein-1 (MCP-1). The analogue, which lacks the N-

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PI Lewis I, Gong J;
XX WPI; 1997-165844/16.
XX
XX N-terminally truncated monocyte chemoattractant protein-1 (MCP-1) -
XX lacks MCP-1 activity and inhibits receptor binding, useful as anti-
XX inflammatory agent.
XX
XX Disclosure; Page 5; 27pp; English.
XX
XX The present sequence represents an analogue, MCP-1 (11-76), of monocyte
XX chemoattractant protein-1 (MCP-1). The analogue, which lacks the N-
XX terminal amino acids 1-10 of MCP-1, acts as an antagonist of MCP-1 as it
XX lacks MCP-1 biological activity and inhibits binding to a MCP-1 receptor.
XX The analogue is useful as an anti-inflammatory agent to block the effects
XX of MCP-1 which is an inflammatory mediator causing migration of monocytes
XX and other cells e.g. basophils and lymphocytes into inflammation sites.
XX MCP-1 has been implicated in allergic and chronic inflammatory diseases
XX e.g. arthritis, arteriosclerosis and several lung diseases. The analogue
XX competes more effectively with MCP-1 for binding MCP-1 receptors than
XX prior art mutant versions of MCP-1 e.g. preferably providing 50%
XX inhibition of binding at a 25:1 ratio or less, compared with 75:1 for
XX prior art mutant 7ND
XX
XX Sequence 67 AA;
XX
XX Query Match 100.0%; Score 73; DB 2; Length 67;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-05;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 ISVQRLASYRRITSSK 16
Db 11 ISVQRLASYRRITSSK 26
XX
RESULT 38
AAW13597
ID AAW13597 standard; peptide; 68 AA.
XX
XX AAW13597;
XX
XX 07-NOV-1997 (first entry)
XX
XX Monocyte chemoattractant protein analogue MCP-1 (9-76).
XX
XX Truncated monocyte chemoattractant protein-1; inhibitor;
XX receptor binding; anti inflammatory; basophil; lymphocyte; allergy;
XX chronic inflammatory disease; arthritis; arteriosclerosis; lung disease.
XX
XX Homo sapiens.
XX
XX CA2152141-A.
XX
XX 20-DEC-1996.
XX
XX 19-JUN-1995; 95CA-02152141.
XX
XX 19-JUN-1995; 95CA-02152141.
XX
XX (LEWIS I.
XX Lewis I, Gong J;
XX WPI; 1997-165844/16.
XX
XX N-terminally truncated monocyte chemoattractant protein-1 (MCP-1) -
XX lacks MCP-1 activity and inhibits receptor binding, useful as anti-
XX inflammatory agent.
XX
XX Claim 7; Page 5; 27pp; English.
XX
XX The present sequence represents an analogue, MCP-1 (9-76), of monocyte
XX chemoattractant protein-1 (MCP-1). The analogue, which lacks the N-

```



CC terminal amino acids 1-8 of MCP-1, acts as an antagonist of MCP-1 as it  
 CC lacks MCP-1 biological activity and inhibits binding to a MCP-1 receptor.  
 CC The analogue is useful as an anti-inflammatory agent to block the effects  
 CC of MCP-1 which is an inflammatory mediator causing migration of monocytes  
 CC and other cells e.g. basophils and lymphocytes into inflammation sites.  
 CC MCP-1 has been implicated in allergic and chronic inflammatory diseases  
 CC e.g. arthritis, arteriosclerosis and several lung diseases. The analogue  
 CC competes more effectively with MCP-1 for binding MCP-1 receptors than  
 CC prior art mutant versions of MCP-1 e.g. preferably providing 50%  
 CC inhibition of binding at a 25:1 ratio or less, compared with 75:1 for  
 CC prior art mutant 7ND  
 CC  
 SQ Sequence 68 AA;

Query Match 100.0%; Score 73; DB 2; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16  
 |||||  
 Db 12 ISVQRLASYRRITSSK 27

RESULT 39  
 AAW95037  
 ID AAW95037 standard; protein; 68 AA.

AC AAW95037;

DT 13-MAY-1999 (first entry)

DE MCP-1 analogue [V97]MCP1(9-76) (residues 9-76).

XX Monocyte chemoattractant protein-1; MCP-1; analogue; inflammatory;  
 KW rheumatoid arthritis; glomerular nephritis; lung fibrosis; restenosis;  
 KW alveolitis; asthma; atherosclerosis; psoriasis; hypersensitivity; skin;  
 KW inflammatory bowel disease; multiple sclerosis; brain tumour; stroke;  
 KW reperfusion injury; ischemia; myocardial infarction; medicament.

OS Homo sapiens.  
 OS Synthetic.

PH Key Location/Qualifiers

FT Misc-difference 1 /label= V97  
 FT /note= "wild-type Val is replaced with Thr"

XX WO9905279-A1.

XX 04-FEB-1999.

XX 21-JUL-1998; 98WO-GB002179.

XX 25-JUL-1997; 97GB-00015659.

XX 25-JUL-1997; 97GB-00015661.

XX 25-JUL-1997; 97GB-00015663.

XX (ZENE ) ZENECA LTD.

XX Barratt DG, Needham MRC;

XX WPI; 1999-142934/12.

XX N-PSDB; AAX21543.

XX New analogues of Monocyte Chemoattractant Protein-1 (MCP-1) - useful to  
 FT treat inflammatory diseases.

XX Claim 1; Page 42-43; 49pp; English.

XX The invention relates to novel analogues ([V9A]MCP1(9-76), [V9G]MCP1 (9-  
 CC 76) and [V97]MCP1(9-76)) of monocyte chemoattractant protein-1 (MCP-1)  
 CC having substitution of an Ala, Gly or Thr for the natural Val at position  
 CC 9 of full-length MCP-1. Host cells containing a vector comprising the

CC nucleic acids encoding the analogues are used for recombinant expression  
 CC of the proteins. MCP-1 is implicated in inflammatory diseases including  
 CC rheumatoid arthritis, glomerular nephritis, lung fibrosis, restenosis,  
 CC alveolitis, and asthma and in atherosclerosis, psoriasis, delayed-type  
 CC hypersensitivity reactions of the skin, inflammatory bowel disease, ful to  
 CC multiple sclerosis, and brain tumour. An MCP-1 inhibitor may be useful to  
 CC treat stroke, reperfusion injury, ischemia, myocardial infarction, and  
 CC transplant rejection. The analogues can be used as medicaments. The  
 CC present sequence represents a MCP-1 analogue [V97]MCP1(9-76) where the  
 CC wild-type valine is replaced with threonine

XX  
 SQ Sequence 68 AA;

Query Match 100.0%; Score 73; DB 2; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16  
 |||||  
 Db 12 ISVQRLASYRRITSSK 27

RESULT 40

AAW95035

ID AAW95035 standard; protein; 68 AA.

AC AAW95035;

DT 13-MAY-1999 (first entry)

DE MCP-1 analogue [V9A]MCP1(9-76) (residues 9-76).

XX Monocyte chemoattractant protein-1; MCP-1; analogue; inflammatory;  
 KW rheumatoid arthritis; glomerular nephritis; lung fibrosis; restenosis;  
 KW alveolitis; asthma; atherosclerosis; psoriasis; hypersensitivity; skin;  
 KW inflammatory bowel disease; multiple sclerosis; brain tumour; stroke;  
 KW reperfusion injury; ischemia; myocardial infarction; medicament.

OS Homo sapiens.  
 OS Synthetic.

PH Key Location/Qualifiers

FT Misc-difference 1 /label= V9A  
 FT /note= "wild-type Val is replaced with Ala"

XX WO9905279-A1.

XX 04-FEB-1999.

XX 21-JUL-1998; 98WO-GB002179.

XX 25-JUL-1997; 97GB-00015659.

XX 25-JUL-1997; 97GB-00015661.

XX 25-JUL-1997; 97GB-00015663.

XX (ZENE ) ZENECA LTD.

XX Barratt DG, Needham MRC;

XX WPI; 1999-142934/12.

XX N-PSDB; AAX21525.

XX New analogues of Monocyte Chemoattractant Protein-1 (MCP-1) - useful to  
 FT treat inflammatory diseases.

XX Claim 1; Page 37; 49pp; English.

XX The invention relates to novel analogues ([V9A]MCP1(9-76), [V9G]MCP1 (9-  
 CC 76) and [V97]MCP1(9-76)) of monocyte chemoattractant protein-1 (MCP-1)  
 CC having substitution of an Ala, Gly or Thr for the natural Val at position  
 CC 9 of full-length MCP-1. Host cells containing a vector comprising the  
 CC nucleic acids encoding the analogues are used for recombinant expression



CC of the proteins. MCP-1 is implicated in inflammatory diseases including  
 CC rheumatoid arthritis, glomerular nephritides, lung fibrosis, restenosis,  
 CC alveolitis, and asthma, and in atherosclerosis, psoriasis, delayed-type  
 CC hypersensitivity reactions of the skin, inflammatory bowel disease,  
 CC multiple sclerosis, and brain tumour. An MCP-1 inhibitor may be useful to  
 CC treat stroke, reperfusion injury, ischemia, myocardial infarction, and  
 CC transplant rejection. The analogues can be used as medicaments. The  
 CC present sequence represents a MCP-1 analogue [V9A]MCP1(9-76) where the  
 CC wild-type valine is substituted with alanine  
 XX  
 SQ Sequence 68 AA;

Query Match 100.0%; Score 73; DB 2; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
 |||||  
 Db 12 ISVQRLASYRRITSSK 27  
 |||||

RESULT 41  
 AAW95036  
 ID AAW95036 standard; protein; 68 AA.  
 XX  
 AC AAW95036;  
 XX  
 DT 13-MAY-1999 (first entry)  
 XX  
 DE MCP-1 analogue [V9G]MCP1(9-76) (residues 9-76).  
 XX  
 KW Monocyte chemoattractant protein-1; MCP-1; analogue; inflammatory;  
 KW rheumatoid arthritis; glomerular nephritides; lung fibrosis; restenosis;  
 KW alveolitis; asthma; atherosclerosis; psoriasis; hypersensitivity; skin;  
 KW inflammatory bowel disease; multiple sclerosis; brain tumour; stroke;  
 KW reperfusion injury; ischemia; myocardial infarction; medicament.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1 /label= V9G  
 FT /note= "wild-type Val is replaced with Gly"  
 XX  
 PN WO9905279-A1.  
 XX  
 PD 04-FEB-1999.  
 XX  
 XX 21-JUL-1998; 98WO-GB002179.  
 XX  
 PR 25-JUL-1997; 97GB-00015659.  
 PR 25-JUL-1997; 97GB-00015661.  
 PR 25-JUL-1997; 97GB-00015663.  
 XX  
 PA (ZENE ) ZENECA LTD.  
 XX  
 XX Barratt DG, Needham MRC;  
 PI  
 XX WPI; 1999-142934/12.  
 DR N-PSDB; AAX21541.  
 XX  
 XX New analogues of Monocyte Chemoattractant Protein-1 (MCP-1) - useful to  
 PT treat inflammatory diseases.  
 PT  
 XX Claim 1; Page 41-42; 49pp; English.  
 PS  
 XX The invention relates to novel analogues ([V9A]MCP1(9-76), [V9G]MCP1 (9-  
 CC 76) and [V9T]MCP1(9-76)) of monocyte chemoattractant protein-1 (MCP-1)  
 CC having substitution of an Ala, Gly or Thr for the natural Val at position  
 CC 9 of full-length MCP-1. Host cells containing a vector comprising the  
 CC nucleic acids encoding the analogues are used for recombinant expression  
 CC of the proteins. MCP-1 is implicated in inflammatory diseases including

CC rheumatoid arthritis, glomerular nephritides, lung fibrosis, restenosis,  
 CC alveolitis, and asthma, and in atherosclerosis, psoriasis, delayed-type  
 CC hypersensitivity reactions of the skin, inflammatory bowel disease,  
 CC multiple sclerosis, and brain tumour. An MCP-1 inhibitor may be useful to  
 CC treat stroke, reperfusion injury, ischemia, myocardial infarction, and  
 CC transplant rejection. The analogues can be used as medicaments. The  
 CC present sequence represents a MCP-1 analogue [V9G]MCP1(9-76) where the  
 CC wild-type valine is substituted with glycine  
 XX  
 SQ Sequence 68 AA;

Query Match 100.0%; Score 73; DB 2; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
 |||||  
 Db 12 ISVQRLASYRRITSSK 27  
 |||||

RESULT 42  
 ADN36565  
 ID ADN36565 standard; protein; 68 AA.  
 XX  
 AC ADN36565;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Chemokine receptor inhibitor-related protein R2 (MCP-1 (9-76)) #12.2.  
 XX  
 KW Chemokine receptor inhibitor; chimeric protein; HIV infection;  
 KW tumour metastasis; organ transplant rejection; autoimmune disease;  
 KW anti-HIV; cytostatic; immunosuppressive; R2; MCP-1.  
 XX  
 OS Unidentified.  
 XX  
 PN CN1435433-A.  
 XX  
 PD 13-AUG-2003.  
 XX  
 XX 30-AUG-2002; 2002CN-00129301.  
 XX  
 PR 30-AUG-2002; 2002CN-00129301.  
 XX  
 PA (GONG/) GONG X.  
 XX  
 PI Gong J;  
 XX  
 DR WPI; 2004-000227/01.  
 DR N-PSDB; ADN36586.  
 XX  
 XX Long-acting broad-spectrum chemotactic factor receptor inhibiting matter.  
 PT  
 PS Claim 16; Page 27; 43pp; Chinese.  
 XX  
 CC The invention relates to chimeric proteins for inhibition of chemokine  
 CC receptors. The invention also relates to nucleic acids encoding the  
 CC chimeric proteins, and a process for preparing and testing the chimeric  
 CC proteins. The chimeric proteins provide long-acting, broad spectrum  
 CC inhibition of chemokine receptors with high selectivity. They can be used  
 CC to prevent or treat HIV infection, tumour metastasis, organ transplant  
 CC rejection and autoimmune diseases. The present sequence represents a  
 CC protein sequence which may be incorporated into a chimeric protein of the  
 CC invention.  
 XX  
 SQ Sequence 68 AA;

Query Match 100.0%; Score 73; DB 8; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
 |||||

```

Db      12 ISVORLASVRRITSSK 27

RESULT 43
ADSV5933
ID      ADS75933 standard; protein; 68 AA.
XX
XX      ADS75933;
XX
XX      16-DEC-2004 (first entry)
XX
XX      Monocyte chemoattractant protein 1 protein fragment.
DE
XX      cytostatic; prostate cancer; monocyte chemoattractant protein-1; MCP-1.
XX
XX      Homo sapiens.
OS
XX      WO2004080273-A2.
XX
XX      23-SEP-2004.
XX
XX      14-MAR-2004; 2004WO-IL000240.
XX
XX      12-MAR-2003; 2003US-0453514P.
PR
XX      12-MAR-2003; 2003US-0453515P.
PR
XX      28-NOV-2003; 2003US-0525135P.
PR
XX      05-JAN-2004; 2004US-0534111P.
XX
XX      (RAPP-) RAPPAPORT FAMILY INST RES IN MEDICAL SCI.
PA
XX      Karin N;
XX
XX      WPI; 2004-690440/67.
DR
XX      N-PSDB; ADS75932.
XX
XX      Treating prostate cancer, involves administering agent capable of
PT      reducing activity and/or expression of monocyte chemoattractant protein-1
PT      or its effector to subject, thus treating prostate cancer in subject.
XX
XX      Disclosure; SEQ ID NO 12; 78pp; English.
XX
XX      The invention relates to a method of treating (M1) prostate cancer, by
XX      administering an agent capable of reducing activity and/or expression of
XX      monocyte chemoattractant protein-1 (MCP-1) or its effector to a subject,
XX      thus treating the prostate cancer in the subject. (M1) is useful for
XX      treating prostate cancer. An antibody (I) to MCP-1 is useful for
XX      manufacturing a medicament for the treatment of prostate cancer. This
XX      sequence corresponds to a fragment of the MCP-1 protein.
XX
XX      Sequence 68 AA;

Query Match      100.0%; Score 73; DB 8; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVORLASVRRITSSK 16
        |||||
Db      12 ISVORLASVRRITSSK 27

RESULT 44
AAR87678
ID      AAR87678 standard; protein; 69 AA.
XX
XX      AAR87678;
AC
XX      21-FEB-1996 (first entry)
XX
XX      des (2-8) MCP-1.
DE
XX      monocyte chemoattractant protein; MCP-1; mutant; restenosis; angioplasty.
XX
XX      Homo sapiens.
OS

XX      Key      Location/Qualifiers
XX      Modified-site 2..3
XX      /note= "amino acids 2-8 of the native protein have been
XX      deleted between these residues"
XX      Disulfide-bond 4..29
XX      Disulfide-bond 5..45
XX      WO9513295-A1.
XX
XX      18-MAY-1995.
XX
XX      07-NOV-1994; 94WO-US012874.
XX
XX      12-NOV-1993; 93US-00152301.
XX
XX      (DAND ) DANA FARBER CANCER INST INC.
XX
XX      Rollins B, Zhang YJ;
XX      WPI; 1995-215051/28.
XX
XX      Human monocyte chemo-attractant protein-1 (MCP-1) derive. - are capable
XX      of inhibiting the monocyte chemo-attractant activity of endogenous MCP-1
XX      and can be used to treat restenosis.
XX
XX      Claim 4; Page 11; 22pp; English.
XX
XX      Monocyte chemoattractant protein-1 (MCP-1) derivatives are mutated such
XX      that they inhibit the monocyte chemoattractant activity of endogenous MCP
XX      -1, provided that the derivative has not been modified by the
XX      substitution of 28-Tyr by Leu and/or 30-Arg by Val. Preferred mutations
XX      are: (1) substitution of 28 Tyr by aspartate; (2) substitution of 24 Arg
XX      by Phe; (3) substitution of 3-Asp by Ala; and/or (4) deletion of amino
XX      acids 2-8. The present sequence is a specifically claimed human MCP-1
XX      derivative based on the parent protein disclosed in Rollins, Molecular
XX      and Cellular Biology, Vol. 9, No. 11, pp. 4687-4695, Nov. 1989. The
XX      peptides can be used to prevent restenosis, e.g. in patients undergoing
XX      coronary artery angioplasty
XX
XX      Sequence 69 AA;

Query Match      100.0%; Score 73; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVORLASVRRITSSK 16
        |||||
Db      13 ISVORLASVRRITSSK 28

RESULT 45
AAW13596
ID      AAW13596 standard; peptide; 69 AA.
XX
XX      AAW13596;
AC
XX      07-NOV-1997 (first entry)
XX
XX      Monocyte chemoattractant protein analogue MCP-1 (8-76).
XX
XX      Truncated monocyte chemoattractant protein-1; inhibitor;
XX      receptor binding; anti inflammatory; basophil; lymphocyte; allergy;
XX      chronic inflammatory disease; arthritis; arteriosclerosis; lung disease.
XX
XX      Homo sapiens.
OS
XX      CA2152141-A.
XX
XX      20-DEC-1996.
XX
XX      19-JUN-1995; 95CA-02152141.
XX
XX

```

PR 19-JUN-1995; 95CA-02152141.  
XX (LEWIS) LEWIS I.  
XX Lewis I, Gong J;  
XX WPI; 1997-165844/16.  
XX N-terminally truncated monocyte chemoattractant protein-1 (MCP-1) -  
PT lacks MCP-1 activity and inhibits receptor binding, useful as anti-  
PT inflammatory agent.  
XX Claim 5; Page 5; 27pp; English.  
XX The present sequence represents an analogue, MCP-1 (8-76), of monocyte  
CC chemoattractant protein-1 (MCP-1). The analogue, which lacks the N-  
CC terminal amino acids 1-7 of MCP-1, acts as an antagonist of MCP-1 as it  
CC lacks MCP-1 biological activity and inhibits binding to a MCP-1 receptor.  
CC The analogue is useful as an anti-inflammatory agent to block the effects  
CC of MCP-1 which is an inflammatory mediator causing migration of monocytes  
CC and other cells e.g. basophils and lymphocytes into inflammation sites.  
CC MCP-1 has been implicated in allergic and chronic inflammatory diseases  
CC e.g. arthritis, arteriosclerosis and several lung diseases. The analogue  
CC competes more effectively with MCP-1 for binding MCP-1 receptors than  
CC prior art mutant versions of MCP-1 e.g. preferably providing 50%  
CC inhibition of binding at a 25:1 ratio or less, compared with 75:1 for  
CC prior art mutant 7ND  
XX Sequence 69 AA;  
SQ

Query Match 100.0%; Score 73; DB 2; Length 69;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ISVQRLASYRRITSSK 16  
| | | | | | | | | | | | | | | |  
Db 13 ISVQRLASYRRITSSK 28

RESULT 46  
AAM53049  
ID AAM53049 standard; protein; 69 AA.  
XX AAM53049;  
XX 26-MAR-2002 (first entry)  
XX Human mutant monocyte chemoattractant protein-1, 7ND-MCP-1.  
XX Human; monocyte chemoattractant protein-1; MCP-1; C-C chemokine family;  
KW pulmonary hypertension; primary; hypotensive; mutant; mutein.  
XX Homo sapiens.  
OS Synthetic.  
XX Key Location/Qualifiers  
FH Misc-difference 2.3  
FT /note= "There is an insertion of the sequence PDAINAP  
FT between these two residues in the wild-type human MCP-1  
FT (AAM53048)"  
XX WO200189582-A1.  
XX 29-NOV-2001.  
XX 25-MAY-2001; 2001WO-JP004381.  
XX 26-MAY-2000; 2000JP-00161145.  
XX (TAKE ) TAKEDA CHEM IND LTD.  
PA (EGAS/) EGASHIRA K.  
XX Egashira K, Yonemitsu Y, Sueishi K, Ikeda Y, Inada Y;

XX WPI; 2002-083059/11.  
DR N-PSDB; ABA02498.  
XX Preventives and remedies for pulmonary hypertension containing mutant of  
PT MCP-1 antagonistic inhibitory type or its salt, encoded DNA or  
PT neutralization antibody.  
XX Claim 2; Page 32; 39pp; Japanese.  
XX The invention relates to preventives and remedies for pulmonary  
CC hypertension, comprising an antagonistic inhibitory mutant of monocyte  
CC chemoattractant protein-1 (MCP-1). DNA encoding the mutant MCP-1, or a  
CC neutralising antibody against MCP-1. MCP-1 is a member of the C-C  
CC chemokine family. The preventives and remedies have hypotensive activity  
CC and can be used in the prevention and treatment of pulmonary hypertension  
CC particularly pulmonary primary hypertension. The present sequence  
CC represents a specifically claimed MCP-1 mutant, 7ND-MCP-1  
XX Sequence 69 AA;  
SQ

Query Match 100.0%; Score 73; DB 5; Length 69;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ISVQRLASYRRITSSK 16  
| | | | | | | | | | | | | | | |  
Db 13 ISVQRLASYRRITSSK 28

RESULT 47  
ADD14999  
ID ADD14999 standard; protein; 69 AA.  
XX ADD14999;  
XX 15-JAN-2004 (first entry)  
XX Truncated monocyte chemoattractant protein-1 (MCP-1) seq id 4.  
XX antiinflammatory; MCP-1 Antagonist; biocompatibility; medical device;  
KW monocyte chemoattractant protein 1; MCP-1; MCP-1 antagonist;  
KW chronic inflammation; fibrous encapsulation; human.  
XX Homo sapiens.  
OS Key Location/Qualifiers  
FH Misc-difference 1  
FT /note= "Encoded by CCA"  
XX US2003129214-A1.  
XX 10-JUL-2003.  
XX 09-JAN-2003; 2003US-00339778.  
XX 10-JAN-2002; 2002US-0347560P.  
XX (UNIW ) UNIV WASHINGTON.  
XX Bornstein P, Kyriakides T;  
PI WPI; 2003-787133/74.  
DR N-PSDB; ADD14996.  
XX Enhancing biocompatibility of a medical device implanted in a portion of  
PT a living body by contacting the portion of the body that is in contact  
PT with the implanted device with monocyte chemoattractant protein 1 (MCP-1)  
PT antagonist.  
XX Claim 19; SEQ ID NO 4; 18pp; English.  
PS The invention describes a method of enhancing (M1) the biocompatibility  
CC

CC of a medical device implanted within a portion of a living body  
 CC comprising contacting a portion of the living body in contact with the  
 CC device with a monocyte chemoattractant protein 1 (MCP-1) antagonist to  
 CC inhibit chronic inflammation induced by the presence of the medical  
 CC device or fibrous encapsulation of the medical device. The method is  
 CC useful for enhancing the biocompatibility of a medical device implanted  
 CC in a portion of a living body by inhibiting chronic inflammation or  
 CC formation of fibrous capsules around the device. This is the amino acid  
 CC sequence of a truncated version of human monocyte chemoattractant protein  
 CC -1 (MCP-1).  
 XX  
 XX

SQ Sequence 69 AA;

Query Match 100.0%; Score 73; DB 7; Length 69;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
 |||||  
 Db 13 ISVQRLASYRRITSSK 28

RESULT 48

ADN36567  
 ID ADN36567 standard; protein; 69 AA.

XX AC ADN36567;

XX DT 17-JUN-2004 (first entry)

XX DE Chemokine receptor inhibitor-related protein R2-4 (MCP-1 (8-76)) #13.2.

XX KW Chemokine receptor inhibitor; chimeric protein; HIV infection;  
 KW tumour metastasis; organ transplant rejection; autoimmune disease;  
 KW anti-HIV; cytostatic; immunosuppressive; R2; MCP-1.

XX OS Unidentified.

XX PN CNI435433-A.

XX PD 13-AUG-2003.

XX PF 30-AUG-2002; 2002CN-00129301.

XX PR 30-AUG-2002; 2002CN-00129301.

XX PA (GONG/) GONG X.

XX PI Gong J;

XX DR WPI; 2004-000227/01.

XX DR N-PSDB; ADN36585.

XX PT Long-acting broad-spectrum chemotactic factor receptor inhibiting matter.

XX PS Claim 16; Page 27; 43pp; Chinese.

XX CC The invention relates to chimeric proteins for inhibition of chemokine  
 CC receptors. The invention also relates to nucleic acids encoding the  
 CC chimeric proteins, and a process for preparing and testing the chimeric  
 CC proteins. The chimeric proteins provide long-acting, broad spectrum  
 CC inhibition of chemokine receptors with high selectivity. They can be used  
 CC to prevent or treat HIV infection, tumour metastasis, organ transplant  
 CC rejection and autoimmune diseases. The present sequence represents a  
 CC protein sequence which may be incorporated into a chimeric protein of the  
 CC invention.  
 XX

SQ Sequence 69 AA;

Query Match 100.0%; Score 73; DB 8; Length 69;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
 |||||  
 Db 13 ISVQRLASYRRITSSK 28

RESULT 49

ADT99562  
 ID ADT99562 standard; protein; 69 AA.

XX AC ADT99562;

XX DT 27-JAN-2005 (first entry)

XX DE Monocyte chemotactic factor-1 antagonist protein sequence - SEQ ID 2.

XX KW kidney ischaemia reperfusion injury;  
 KW monocyte chemotactic factor-1 inhibition; MCP-1 inhibition;  
 KW ischaemia reperfusion trauma; kidney transplantation; kidney surgery;  
 KW renal injury; renal infarction; renal-artery constriction;  
 KW renal arteriosclerosis; nephrosclerosis; renal haemorrhage; burn;  
 KW thermal burn; shock.

XX OS Homo sapiens.

XX PN JP2004307427-A.

XX PD 04-NOV-2004.

XX PF 10-APR-2003; 2003JP-00106080.

XX PR 10-APR-2003; 2003JP-00106080.

XX PA (EGAS/) EGASHIRA K.

XX PA (ANJE-) ANJESU MG KK.

XX DR WPI; 2004-778670/77.

XX DR N-PSDB; ADT99561.

XX PT Treatment, improvement and preventive agent of kidney ischemia  
 PT reperfusion trauma, useful for treating kidney ischemia reperfusion  
 PT trauma, comprises monocyte chemotactic factor-1 functional inhibitor as  
 PT active ingredient.

XX PS Claim 9; SEQ ID NO 2; 15pp; Japanese.

XX CC The invention comprises an agent for the treatment or prevention of  
 CC kidney ischaemia reperfusion injury, the agent of the invention comprises  
 CC a monocyte chemotactic factor-1 (MCP-1) functional inhibitor (MCP-1  
 CC antagonist) as an active ingredient. The agent of the invention is useful  
 CC for treating or preventing kidney ischaemia reperfusion trauma, caused  
 CC by: kidney transplantation, kidney surgery, renal injury, renal  
 CC infarction, renal-artery constriction, renal arteriosclerosis,  
 CC nephrosclerosis, renal haemorrhage, burn, thermal burn, or a shock. The  
 CC present amino acid sequence represents the MCP-1 antagonist of the  
 CC invention.  
 XX

SQ Sequence 69 AA;

Query Match 100.0%; Score 73; DB 8; Length 69;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
 |||||  
 Db 13 ISVQRLASYRRITSSK 28

RESULT 50

ADR90677  
 ID ADR90677 standard; protein; 74 AA.

XX AC ADR90677;

```

XX 02-DEC-2004 (first entry)
DT Human monocyte chemotactic protein 1 partial protein.
DE
DE dipeptidyl peptidase cleavage; antidiabetic; anorectic; antiinflammatory;
KW antiarteriosclerotic; tranquiliser; anticonvulsant; hypnotic;
KW gene therapy; metabolic disease; diabetes; obesity; inflammation;
KW atherosclerosis; nervous system disorder; anxiety; seizures;
KW sleep disorder; monocyte chemotactic protein 1; MCP-1; human.
XX
OS Homo sapiens.
XX
XX WO2004078777-A2.
XX
XX 16-SEP-2004.
XX
XX 04-MAR-2004; 2004WO-US006462.
XX
XX 04-MAR-2003; 2003US-00378094.
XX 28-AUG-2003; 2003WO-US026818.
XX
XX (BIOR-) BIOREXIS PHARM CORP.
XX
XX Sadeghi H, Prior CP, Ballance DJ;
XX WPI; 2004-653689/63.
XX
XX New modified polypeptides that are resistant to dipeptidyl peptidase
XX cleavage, useful for treating metabolic diseases (e.g. diabetes or
XX obesity), inflammation, atherosclerosis or nervous system disorders (e.g.
XX anxiety).
XX
XX Disclosure; SEQ ID NO 58; 125pp; English.
XX
XX This invention relates to a novel polypeptide molecule modified to
XX contain at least one additional amino acid at the N-terminal end that
XX substantially protects the polypeptide molecule from dipeptidyl peptidase
XX cleavage, where the modified polypeptide substantially retains
XX polypeptide activity. The invention may be useful for the production of
XX compounds with an antidiabetic, anorectic, antiinflammatory,
XX antiarteriosclerotic, tranquiliser, anticonvulsant or hypnotic activity.
XX In addition, the invention may be useful for gene therapy. The compounds
XX may be useful for treating metabolic diseases (for example diabetes or
XX obesity), inflammation, atherosclerosis and nervous system disorders,
XX such as anxiety, seizures and sleep disorders. The present sequence is
XX that of a polypeptide derived from a human protein which is related to
XX the invention.
XX
XX Sequence 74 AA;
XX
XX Query Match 100.0%; Score 73; DB 8; Length 74;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-05;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 ISVQRLASYRRITSSK 16
XX |||||
XX Db 20 ISVQRLASYRRITSSK 35

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Search completed: February 6, 2006, 14:25:10  
Job time : 229 secs

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OM protein - protein search, using sw model

Run on: February 6, 2006, 14:25:28 ; Search time 42 Seconds

(without alignments)  
36.654 Million cell updates/sec

Title: US-10-644-277-149\_COPY\_20\_35

Perfect score: 73

Sequence: 1 ISVQLASRYRITSSK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

1: PIR\_80.\*

2: PIR1.\*

3: PIR2.\*

4: PIR3.\*

5: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	73	100.0	99	2 A60299	monocyte chemoatrr
2	64	87.7	72	2 A55984	monocyte chemoatrr
3	64	87.7	99	2 JC21136	monocyte chemoatrr
4	61	83.6	99	1 A392396	monocyte chemoatrr
5	61	83.6	99	2 JC22336	monocyte chemoatrr
6	56	76.7	97	2 JC4912	eotaxin precursor
7	56	76.7	125	2 I46857	monocyte chemoatrr
8	52	71.2	96	2 JC2478	eotaxin precursor
9	52	71.2	96	2 I48099	eotaxin precursor
10	49	67.1	148	1 A30209	PDGF-inducible JB
11	47	64.4	109	2 A54678	monocyte chemoatrr
12	46	63.0	148	1 S07723	immediate-early se
13	45	61.6	97	2 A48093	monocyte cytokine
14	44	60.3	99	2 JC5295	monocyte chemoatrr
15	42	57.5	60	2 S62188	hypothetical prote
16	41	56.2	120	2 I48147	monocyte chemoatrr
17	41	56.2	339	2 F83026	conserved hypothet
18	41	56.2	1199	1 S76549	transcription-repa
19	39	53.4	398	2 T38233	probable cystathio
20	39	53.4	893	2 F72253	hypothetical prote
21	38	52.1	99	2 JC2417	monocyte chemoatrr
22	38	52.1	242	2 A82754	lipoprotein XF0855
23	38	52.1	311	2 JC5200	chemoreceptor Tb33
24	37.5	51.4	59	2 D37314	regulatory protein
25	37.5	51.4	146	2 A37774	lcrR protein - Yer
26	37.5	51.4	146	2 T43592	low calcium respon
27	37	50.7	194	2 T19339	hypothetical prote
28	37	50.7	374	2 T02021	hypothetical prote
29	37	50.7	378	2 C62112	flagellin FlaE VC2

30	37	50.7	379	2 G82107	flagellin core pro
31	37	50.7	474	2 S52444	flagellin - legion
32	37	50.7	498	1 FLEC	flagellin - Escher
33	37	50.7	550	2 S44980	flagellin - Shigel
34	37	50.7	565	2 I41061	flagellin - Escher
35	37	50.7	579	2 S61131	probable membrane
36	37	50.7	584	2 C48658	flagellin - Escher
37	37	50.7	585	2 F85809	hypothetical prote
38	37	50.7	585	2 F90961	flagellin (importe
39	37	50.7	595	2 B48658	flagellin - Escher
40	37	50.7	595	2 A48658	probable large ATP
41	37	50.7	840	2 T36175	hypothetical prote
42	37	50.7	1175	2 D85089	hypothetical prote
43	37	50.7	1198	2 E86402	hypothetical prote
44	37	50.7	1285	2 H85041	hypothetical prote
45	37	50.7	1305	2 H96559	hypothetical prote
46	37	50.7	1312	2 D85066	hypothetical prote
47	37	50.7	1314	2 T47331	hypothetical prote
48	37	50.7	1472	2 A84470	hypothetical prote
49	37	50.7	1756	2 T02599	hypothetical prote
50	36	49.3	113	2 B41657	probable immunity
51	36	49.3	113	2 S52207	meac protein - Leu
52	36	49.3	156	2 T07174	tuberculosis-relat
53	36	49.3	217	2 H84852	probable RING zinc
54	36	49.3	223	2 C86233	Golgi SNARE 11 pro
55	36	49.3	269	1 A27067	careinin - chick
56	36	49.3	290	2 C71416	probable ABC trans
57	36	49.3	345	2 F71261	probable lipase -
58	36	49.3	394	2 A37853	flagellin, 40K - P
59	36	49.3	455	2 B83260	conserved hypothet
60	36	49.3	530	2 D87255	apolipoprotein N-a
61	36	49.3	815	2 A71700	phenylalanine-tRNA
62	36	49.3	844	2 C86339	hypothetical prote
63	36	49.3	844	2 F97772	protein F2D10.12
64	36	49.3	1113	2 T47381	hypothetical prote
65	36	49.3	1148	1 G64855	transcription/rep
66	36	49.3	1148	2 A10644	transcription-repa
67	36	49.3	1148	2 H85674	hypothetical prote
68	36	49.3	1148	2 D90815	transcription-repa
69	36	49.3	1413	2 G84790	probable ABC trans
70	36	49.3	1742	2 T17120	cellulase (EC 3.2.
71	36	49.3	4302	2 A38971	polycystic kidney
72	35	48.6	319	2 B82381	transcription regu
73	35	47.9	137	2 B83659	hypothetical prote
74	35	47.9	163	2 F85046	hypothetical prote
75	35	47.9	205	2 S34833	stylar protein (al
76	35	47.9	209	2 AF2354	imidazoleglycerol-
77	35	47.9	256	2 G84061	ferrichrome ABC tr
78	35	47.9	281	2 C83802	nicotinate-nucleot
79	35	47.9	287	2 S28040	flagellin - lister
80	35	47.9	287	2 AB1161	flagellin protein
81	35	47.9	287	2 AB1520	flagellin protein
82	35	47.9	300	2 F83621	hypothetical prote
83	35	47.9	311	2 AH0867	transcription acti
84	35	47.9	347	1 A44245	alcohol dehydrogen
85	35	47.9	367	2 JC2560	flagellin flic-2 -
86	35	47.9	438	2 B82077	outer membrane pro
87	35	47.9	463	1 DMCH	desmin - chicken
88	35	47.9	469	1 DMHU	desmin - human
89	35	47.9	469	2 A24783	desmin - golden ha
90	35	47.9	469	2 A54104	desmin - mouse
91	35	47.9	469	2 152469	desmin - rat
92	35	47.9	473	2 T39028	citrate synthase p
93	35	47.9	548	2 H97820	60K chaperonin (im
94	35	47.9	598	2 T42070	protein serine/thr
95	35	47.9	682	2 E83782	alpha-glucuronidas
96	35	47.9	736	2 JC7518	subtilisin-like se
97	35	47.9	808	2 A96791	hypothetical prote
98	35	47.9	816	2 S54518	probable membrane
99	35	47.9	846	2 T38840	hypothetical trp-a
100	35	47.9	1490	2 T47840	multi resistance p
101	34.5	47.3	431	2 E69211	UDP-N-acetyl-D-man
102	34.5	47.3	470	2 T32137	hypothetical prote

103	34	46.6	68	2	AF0976	hypothetical prote	176	33	45.2	98	2	S14883	hypothetical prote
104	34	46.6	105	2	E69058	hypothetical prote	177	33	45.2	103	2	T23242	hypothetical prote
105	34	46.6	132	2	S70314	transcription repr	178	33	45.2	128	2	C53380	polyribonucleotide
106	34	46.6	208	2	I64209	ribosomal protein	179	33	45.2	155	2	B72503	hypothetical prote
107	34	46.6	246	2	H82419	conserved hypothet	180	33	45.2	216	2	T47329	hypothetical prote
108	34	46.6	271	1	A60253	calretinin - human	181	33	45.2	235	2	AB1975	hypothetical prote
109	34	46.6	279	2	JH0655	macrotetrolide res	182	33	45.2	236	2	H84612	hypothetical prote
110	34	46.6	284	2	B83557	probable transcrip	183	33	45.2	245	2	A95164	acyl-ACP thioester
111	34	46.6	296	1	QRECPD	ferrichrome-iron t	184	33	45.2	245	2	H98029	hypothetical prote
112	34	46.6	296	2	D90648	ferrichrome-iron t	185	33	45.2	247	2	D83671	amino acid ABC tra
113	34	46.6	296	2	D85499	ferrichrome-iron t	186	33	45.2	283	2	T31275	2-hydroxyymuconate-
114	34	46.6	313	2	JC5754	flagellin - Xenorh	187	33	45.2	283	2	S34851	hypothetical 31.9K
115	34	46.6	320	2	AE2598	mutT/nudix family	188	33	45.2	283	2	T36996	probable noncompos
116	34	46.6	320	2	B97370	NADH pyrophosphata	189	33	45.2	286	1	JC5419	2-hydroxyymuconate-
117	34	46.6	351	2	JU0036	flagellin - Serrat	190	33	45.2	287	2	JB0094	syntxin 11 - huma
118	34	46.6	358	2	S78460	flagellin fleA, 36	191	33	45.2	291	2	T21475	hypothetical prote
119	34	46.6	364	2	J78461	flagellin fleB, 37	192	33	45.2	305	2	AC1513	oxidoreductase hom
120	34	46.6	365	2	JC2559	flagellin fleC-1 -	193	33	45.2	317	2	T30232	methyltransferase
121	34	46.6	369	2	AG0224	thermoregulated mo	194	33	45.2	338	2	T34364	hypothetical prote
122	34	46.6	378	2	S69767	flagellin fleC, 39	195	33	45.2	346	2	B75111	glycerol 1-phospha
123	34	46.6	379	2	JG6021	flagellin A - Vibr	196	33	45.2	351	2	H71432	probable glucosylt
124	34	46.6	391	2	A40594	major flagellin pr	197	33	45.2	362	2	A70547	probable menE - My
125	34	46.6	401	2	T50548	GTP cyclonhydrolase	198	33	45.2	364	2	T05401	hypothetical prote
126	34	46.6	403	2	T38078	hypothetical prote	199	33	45.2	372	2	T08273	conserved hypothet
127	34	46.6	406	2	S76451	hypothetical prote	200	33	45.2	378	2	T20236	hypothetical prote
128	34	46.6	467	2	T41053	triglyceride lipas	201	33	45.2	387	2	F85066	hypothetical prote
129	34	46.6	476	2	T35769	probable transemb	202	33	45.2	399	2	AC1601	platelet glycoprot
130	34	46.6	486	2	E84438	hypothetical prote	203	33	45.2	411	1	I55604	hypothetical prote
131	34	46.6	488	2	E83507	flagellin type B P	204	33	45.2	411	2	T19728	hypothetical prote
132	34	46.6	489	2	S09637	flagellin - Salmon	205	33	45.2	430	2	D86514	CR132 hypothetical
133	34	46.6	490	2	A24262	phase-1 i flagelli	206	33	45.2	430	2	G72108	ct132 hypothetical
134	34	46.6	493	2	S07375	flagellin H-1 - Sa	207	33	45.2	430	2	G81562	hypothetical prote
135	34	46.6	494	2	S07276	flagellin H-1A - S	208	33	45.2	442	2	B75634	hypothetical prote
136	34	46.6	504	2	S16121	flagellin - Salmon	209	33	45.2	457	2	T50402	probable mitochond
137	34	46.6	504	2	S33193	phase-1 flagellin	210	33	45.2	471	1	A35867	cytochrome P450 71
138	34	46.6	504	2	S33190	phase-1 flagellin	211	33	45.2	480	2	B71313	probable V-type AT
139	34	46.6	504	2	S33191	phase-1 flagellin	212	33	45.2	502	2	T52256	cytochrome P-450I
140	34	46.6	504	2	S33194	phase-1 flagellin	213	33	45.2	506	2	T33770	hypothetical prote
141	34	46.6	504	2	S33186	phase-1 flagellin	214	33	45.2	512	2	I80311	sepc protein - Bsc
142	34	46.6	504	2	S33189	phase-1 flagellin	215	33	45.2	550	2	A71668	60 kd chaperonin (
143	34	46.6	504	2	S33188	phase-1 flagellin	216	33	45.2	624	2	T21072	hypothetical prote
144	34	46.6	504	2	S33187	phase-1 flagellin	217	33	45.2	627	2	S48968	NDP80 protein - ye
145	34	46.6	505	2	S09638	flagellin - Salmon	218	33	45.2	743	2	S67635	PM75 protein - yea
146	34	46.6	506	2	AH0750	flagellin [impor	219	33	45.2	784	2	PN0009	neurofilament trip
147	34	46.6	507	2	S33185	phase-1 flagellin	220	33	45.2	823	2	T35280	probable integr
148	34	46.6	507	2	S33192	phase-1 flagellin	221	33	45.2	843	2	H82362	adenylate cyclase
149	34	46.6	508	2	A53465	phase-1 flagellin	222	33	45.2	965	2	T21073	hypothetical prote
150	34	46.6	524	2	S44982	flagellin - Shigel	223	33	45.2	1075	2	T48805	hypothetical prote
151	34	46.6	577	2	A61372	hemolysin, extrac	224	33	45.2	1148	2	AD0198	transcription-repa
152	34	46.6	578	2	S26577	beta-hemolysin - A	225	33	45.2	1171	2	G97174	pyruvate:ferredoxi
153	34	46.6	586	2	G71656	single-stranded-dn	226	33	45.2	1237	2	T46609	calcium-activated
154	34	46.6	618	2	S06446	cytolysin-related	227	33	45.2	1420	2	T02644	ABC-type transport
155	34	46.6	620	2	JH0821	95K golgi antigen	228	33	45.2	1451	2	B86286	F91.15 protein -
156	34	46.6	637	2	T50951	hypothetical prote	229	33	45.2	1673	2	T50806	complement compone
157	34	46.6	666	2	B56639	1,4-alpha-glucan b	230	33	45.2	2022	2	T48818	Glucan 1,4-alpha-g
158	34	46.6	721	2	S31824	gene Mx protein -	231	32	43.8	57	2	C84977	carbon storage reg
159	34	46.6	721	2	S31820	gene Mx protein -	232	32	43.8	61	1	B40608	glycogen biosynthe
160	34	46.6	721	2	A37472	interferon-inducib	233	32	43.8	61	2	AD0401	carbon storage reg
161	34	46.6	731	2	I60729	ornithine decarbox	234	32	43.8	61	2	AE0843	carbon storage reg
162	34	46.6	783	1	WMBEHQ	UL5 protein - huma	235	32	43.8	61	2	D85917	glycogen biosynthe
163	34	46.6	882	1	WMBEUS	gene UL5 protein -	236	32	43.8	61	2	A91073	glycogen biosynthe
164	34	46.6	903	2	G82516	hypothetical prote	237	32	43.8	63	1	H64095	carbon storage reg
165	34	46.6	986	2	T10754	cis-Golgi matrix p	238	32	43.8	67	2	T44077	hypothetical prote
166	34	46.6	1290	2	S76853	hypothetical prote	239	32	43.8	76	2	AG2612	hypothetical prote
167	34	46.6	1389	2	T47796	ABC transporter-li	240	32	43.8	92	2	B82603	hypothetical prote
168	34	46.6	3011	1	GNWVCH	genome polyprotein	241	32	43.8	112	2	T17556	hypothetical prote
169	34	46.6	3011	1	S40770	genome polyprotein	242	32	43.8	126	2	T23246	hypothetical prote
170	34	46.6	3194	2	D71917	toxin-like outer m	243	32	43.8	130	2	C69061	hypothetical prote
171	33.5	45.9	383	2	A58871	probable glucosylt	244	32	43.8	136	2	AB2542	transcription repr
172	33.5	45.9	1065	2	G72330	hypothetical prote	245	32	43.8	175	2	T23245	hypothetical prote
173	33.5	45.9	1208	2	T00362	hypothetical prote	246	32	43.8	179	2	A87654	hypothetical prote
174	33	45.2	75	2	S12191	hypothetical prote	247	32	43.8	183	2	F71127	hypothetical prote
175	33	45.2	93	2	S76897	hypothetical prote	248	32	43.8	194	2	G95941	probable small hea



249	32	43.8	196	2	JC4257	beta A4-crystallin	322	32	43.8	686	2	S43562	KOBE5.3 protein -
250	32	43.8	200	1	A71127	hypothetical prote	323	32	43.8	687	2	A34879	maturase-related p
251	32	43.8	202	2	T13124	repressor protein	324	32	43.8	688	2	S53605	hypothetical prote
252	32	43.8	207	2	AC2069	acyl carrier prote	325	32	43.8	728	2	E83228	hypothetical 91.8K
253	32	43.8	213	2	G30176	conserved hypotet	326	32	43.8	752	2	H98161	GGDEF family prote
254	32	43.8	233	2	D81398	hypothetical prote	327	32	43.8	779	2	AH3125	chitinase (EC 3.2.
255	32	43.8	238	2	S75534	hydrogenase chain	328	32	43.8	799	2	PC4106	chitinase (EC 3.2.
256	32	43.8	239	2	AC2643	flagellar L-ring p	329	32	43.8	820	2	A40633	DNA-directed DNA p
257	32	43.8	239	2	G97425	flagellar L-ring p	330	32	43.8	831	2	S26675	protein F33E2.2 [i
258	32	43.8	240	2	S01299	OX-45 membrane gly	331	32	43.8	848	2	B87950	hypothetical prote
259	32	43.8	245	2	T43174	hypothetical prote	332	32	43.8	853	2	S74279	hypothetical prote
260	32	43.8	248	2	F69198	conserved hypotet	333	32	43.8	855	2	T20082	hypothetical prote
261	32	43.8	249	1	B70693	probable echa16 pr	334	32	43.8	891	2	T40417	DNA polymerase I (
262	32	43.8	255	1	Q8ECW3	membrane-bound iro	335	32	43.8	908	2	C70158	hypothetical prote
263	32	43.8	256	2	AS2019	hypothetical prote	336	32	43.8	920	2	T40771	hypothetical prote
264	32	43.8	262	2	A70348	hypothetical prote	337	32	43.8	953	2	S75285	mechyl-accepting c
265	32	43.8	273	2	AH2222	ABC nitrate transp	338	32	43.8	957	2	S66755	probable membrane
266	32	43.8	284	2	D70513	probable hisg atp	339	32	43.8	990	2	T43445	hypothetical prote
267	32	43.8	291	2	T00855	hypothetical prote	340	32	43.8	1039	2	E90308	hypothetical prote
268	32	43.8	293	2	C70160	ribosomal protein	341	32	43.8	1039	2	T25591	isoleucine-tRNA li
269	32	43.8	294	2	E70692	hypothetical prote	342	32	43.8	1070	2	T42339	glutamate synthase
270	32	43.8	299	2	E90777	replication protei	343	32	43.8	1137	2	T02097	probable potassium
271	32	43.8	304	2	S42400	gene O protein - p	344	32	43.8	1139	2	A10379	transcription/rep
272	32	43.8	304	2	B23431	hypothetical prote	345	32	43.8	1146	1	I64112	transcription/rep
273	32	43.8	309	2	D90520	conserved hypotet	346	32	43.8	1185	2	AG2457	probable RNA-direc
274	32	43.8	317	2	S75694	hypothetical prote	347	32	43.8	1309	2	T00078	ABC transport prot
275	32	43.8	320	2	S46824	ribose-phosphate d	348	32	43.8	1336	2	T18288	Rhs-family protein
276	32	43.8	322	2	F88029	protein F46F5.5 [i	349	32	43.8	1354	2	AG0538	hypothetical prote
277	32	43.8	332	2	D83519	probable transcrip	350	32	43.8	1421	2	T34225	MRP-like ABC trans
278	32	43.8	337	2	A85920	ascBF operon repre	351	32	43.8	1515	2	T52081	ferredoxin-depnde
279	32	43.8	337	2	B91075	ascBF operon repre	352	32	43.8	1629	2	C84839	1,4-beta-glucanase
280	32	43.8	343	2	A86241	hypothetical prote	353	32	43.8	1711	2	T31337	hypothetical prote
281	32	43.8	361	2	T25196	hypothetical prote	354	32	43.8	1892	2	C97804	probable non-ribos
282	32	43.8	370	2	D75503	hypothetical prote	355	32	43.8	2124	2	H83357	unconventional myo
283	32	43.8	371	2	A13507	glycerol trinitrat	356	32	43.8	3530	2	A59266	DNA-directed DNA p
284	32	43.8	377	2	F82107	flagellin FlaC VC2	357	31.5	43.2	76	2	AD0217	hypothetical prote
285	32	43.8	400	2	H91163	probable DNA proce	358	31.5	43.2	240	2	T19349	hypothetical prote
286	32	43.8	402	2	D84840	hypothetical prote	359	31.5	43.2	302	2	T19348	alcohol dehydrogen
287	32	43.8	403	2	S71356	glucocorticoid-att	360	31.5	43.2	347	1	S51120	two-component syet
288	32	43.8	404	2	T19480	hypothetical prote	361	31.5	43.2	386	2	F82721	glutamyl-tRNA synt
289	32	43.8	428	2	A10034	probable transmemb	362	31.5	43.2	502	2	T45422	cyclic beta 1-2 gl
290	32	43.8	431	2	A86014	probable DNA proce	363	31.5	43.2	2831	2	T31419	cellobiose-phospho
291	32	43.8	444	2	H75544	hypothetical prote	364	31.5	43.2	2867	2	AG3481	hypothetical prote
292	32	43.8	452	2	C97382	probable glutamine	365	31	42.5	36	2	S70806	hypothetical prote
293	32	43.8	458	2	A43554	desmin - African c	366	31	42.5	41	2	AH1876	hypothetical prote
294	32	43.8	460	2	AB2600	P60 extracellular	367	31	42.5	54	2	F82545	hypothetical prote
295	32	43.8	465	2	AG1506	cannabinoid recept	368	31	42.5	64	2	S01103	hypothetical prote
296	32	43.8	472	2	S17595	cannabinoid recept	369	31	42.5	73	2	T31698	hypothetical prote
297	32	43.8	473	2	A33117	P60 extracellular	370	31	42.5	75	2	E90974	probable cell divi
298	32	43.8	482	2	AG1147	protein P60 precur	371	31	42.5	76	2	B64660	hypothetical prote
299	32	43.8	484	2	A41487	type II site-speci	372	31	42.5	77	2	C84332	hypothetical prote
300	32	43.8	489	2	AG1166	CDCl protein - yea	373	31	42.5	93	2	S08613	transcription regu
301	32	43.8	491	2	S49779	hypothetical prote	374	31	42.5	93	2	A26135	hypothetical prote
302	32	43.8	503	2	T29868	multidrug resistan	375	31	42.5	97	2	C75089	ribosomal protein
303	32	43.8	519	2	B71726	beta-mannosidase p	376	31	42.5	113	2	C70810	transcription repr
304	32	43.8	520	2	G75141	hypothetical prote	377	31	42.5	132	2	H97806	hypothetical prote
305	32	43.8	532	2	T04748	H+-transporting tw	378	31	42.5	135	2	H72471	hypothetical prote
306	32	43.8	545	1	PWBYA	hydrogenase (EC 1.	379	31	42.5	135	2	AG3590	transcription regu
307	32	43.8	567	1	C55516	probable large sub	380	31	42.5	137	2	B69747	hypothetical prote
308	32	43.8	567	2	G85958	hydrogenase-2 larg	381	31	42.5	138	2	PC1208	envelope protein -
309	32	43.8	567	2	G91113	conserved hypotet	382	31	42.5	146	2	B39414	pyruvate (flavodox
310	32	43.8	572	2	F90564	hypothetical prote	383	31	42.5	154	2	S72939	conserved hypotet
311	32	43.8	602	2	AH2485	hemagglutinin - ph	384	31	42.5	154	2	F69520	conserved hypotet
312	32	43.8	607	1	HNN2PD	hemagglutinin - ph	385	31	42.5	157	2	C70080	hypothetical prote
313	32	43.8	607	1	J01535	segment polarity p	386	31	42.5	159	2	D71033	hypothetical prote
314	32	43.8	623	2	A49840	hypothetical prote	387	31	42.5	160	2	D98089	probable membrane
315	32	43.8	645	2	T27186	probable membrane	388	31	42.5	165	2	T49872	hypothetical prote
316	32	43.8	652	2	S52683	hypothetical prote	389	31	42.5	167	2	T35320	probable membrane
317	32	43.8	660	2	H87325	maturase-related p	390	31	42.5	170	2	S66125	hypothetical prote
318	32	43.8	673	2	S51604	maturase-related p	391	31	42.5	170	2	B83664	beta-crystallin A3
319	32	43.8	674	2	T07017	maturase homolog -	392	31	42.5	177	2	S10088	hypothetical prote
320	32	43.8	675	2	JC5898	beta-galactoside a	393	31	42.5	181	2	A70673	hypothetical prote
321	32	43.8	678	2	B38489	maturase-related p	394	31	42.5	185	2	D72118	conserved hypotet

395	31	42.5	185	2	E86504	hypothetical prote	468	31	42.5	374	2	E64489	hypothetical prote
396	31	42.5	185	2	G96791	probable RING zinc	469	31	42.5	377	2	B82112	flagellin FlaD VC2
397	31	42.5	190	2	S41476	calretinin - mouse	470	31	42.5	379	2	AF2409	mannosyl transfera
398	31	42.5	198	1	CYMSB	beta-crystallin -	471	31	42.5	382	2	E81195	phospholipase A1,
399	31	42.5	198	2	S55512	beta-AI-2 crystall	472	31	42.5	384	2	E69050	GlcNAc-phosphatidy
400	31	42.5	198	2	S55513	beta-AI-1 crystall	473	31	42.5	384	2	S66758	probable membrane
401	31	42.5	198	2	S01608	beta-crystallin A1	474	31	42.5	386	2	AF2687	conserved hypotnet
402	31	42.5	204	2	T44257	thiamine-phosphate	475	31	42.5	387	2	H82176	carboxymorspermid
403	31	42.5	205	2	C26135	keratin, 50K type	476	31	42.5	391	2	B97469	probable membrane
404	31	42.5	205	2	T33826	hypothetical prote	477	31	42.5	395	2	F82852	conserved hypotnet
405	31	42.5	206	2	G85085	hypothetical prote	478	31	42.5	406	2	T03111	hypothetical prote
406	31	42.5	207	2	T02514	hypothetical prote	479	31	42.5	406	2	H71139	hypothetical prote
407	31	42.5	209	2	D96755	hypothetical prote	480	31	42.5	409	2	H81831	probable phospholip
408	31	42.5	212	2	G82103	phosphoribosylglyc	481	31	42.5	411	2	E75381	conserved hypotnet
409	31	42.5	215	2	T45857	beta-crystallin -	482	31	42.5	413	1	S03631	homeotic protein S
410	31	42.5	215	2	S55514	beta-A3-2 crystall	483	31	42.5	415	2	B70981	hypothetical prote
411	31	42.5	215	2	S55515	beta-A3-1 crystall	484	31	42.5	416	2	S52827	hypothetical prote
412	31	42.5	216	2	T38474	olfactory receptor	485	31	42.5	420	2	T41236	conserved hypotnet
413	31	42.5	216	2	T38470	olfactory receptor	486	31	42.5	421	2	E83108	probable type II s
414	31	42.5	218	2	S51751	dihydrodipicolinat	487	31	42.5	423	2	C72376	hypothetical prote
415	31	42.5	218	2	JC2487	GMP-binding protei	488	31	42.5	424	2	S37780	keratin 20, type I
416	31	42.5	218	2	AC0380	probable tetR-fami	489	31	42.5	429	2	A40452	keratin 21, type I
417	31	42.5	218	2	T10353	hypothetical prote	490	31	42.5	432	2	S30433	keratin 17, type I
418	31	42.5	225	2	T38478	olfactory receptor	491	31	42.5	442	2	T20638	hypothetical prote
419	31	42.5	229	2	B70158	conserved hypotnet	492	31	42.5	445	2	E84714	probable protein k
420	31	42.5	235	2	S32747	genome polyprotein	493	31	42.5	454	2	G81828	probable periplasm
421	31	42.5	235	2	F72522	hypothetical prote	494	31	42.5	454	2	A86345	FlaF4.13 protein -
422	31	42.5	243	2	S19148	thiolglucosidase (B	495	31	42.5	457	2	S38296	gamma-aminobutyric
423	31	42.5	244	2	A11414	merr-family transc	496	31	42.5	466	2	T47789	hypothetical prote
424	31	42.5	244	2	AH1790	transcription init	497	31	42.5	468	2	T20475	hypothetical prote
425	31	42.5	255	1	C37165	hypothetical prote	498	31	42.5	472	1	KRHUE	keratin 14, type I
426	31	42.5	255	2	G95260	hypothetical prote	499	31	42.5	473	4	A33652	keratin 16, type I
427	31	42.5	255	2	D98126	conserved hypotnet	500	31	42.5	473	4	A33652	probable keratin 1
428	31	42.5	259	2	S76295	hypothetical prote	501	31	42.5	475	2	B81047	secretion protein,
429	31	42.5	264	2	E95410	probable ABC trans	502	31	42.5	484	2	S73490	glutamate-tRNA lig
430	31	42.5	271	1	S25006	calretinin - rat	503	31	42.5	484	2	AG2889	modulation protein
431	31	42.5	279	2	T51515	syntaxin homolog F	504	31	42.5	494	2	S23315	hypothetical prote
432	31	42.5	282	2	H82394	pirin-related prot	505	31	42.5	496	2	S51668	tyrosine kinase -
433	31	42.5	286	2	F87075	membrane transport	506	31	42.5	502	2	S38139	LAS1 protein - yea
434	31	42.5	291	2	F87676	ATP synthase Fl, g	507	31	42.5	502	2	T22045	hypothetical prote
435	31	42.5	295	2	S50729	sporulation protei	508	31	42.5	506	2	S13720	coat protein - ara
436	31	42.5	296	2	AB0527	ferrichrome-bindin	509	31	42.5	508	2	AF0314	probable aldehyde
437	31	42.5	297	2	G83216	probable transcrip	510	31	42.5	512	2	A53092	reduced folate car
438	31	42.5	297	2	A41898	positive regulator	511	31	42.5	513	2	JC2304	gluconate kinase (
439	31	42.5	310	2	AD0243	hypothetical prote	512	31	42.5	513	2	D97665	nodT protein homol
440	31	42.5	311	2	B64332	hypothetical prote	513	31	42.5	516	2	F71529	probable exodoxvri
441	31	42.5	314	2	S20572	hypothetical prote	514	31	42.5	518	2	A53207	probable folate tr
442	31	42.5	314	2	AF0540	olfactory receptor	515	31	42.5	528	2	T31905	hypothetical prote
443	31	42.5	315	2	A47269	LysR-family transc	516	31	42.5	532	2	A35149	ipah protein - Shi
444	31	42.5	317	2	S72851	hypothetical prote	517	31	42.5	533	2	B86325	T29M8.4 protein -
445	31	42.5	318	2	C69192	stomatatin-like prot	518	31	42.5	534	2	T24141	hypothetical prote
446	31	42.5	321	2	T41036	ribose-phosphate p	519	31	42.5	544	2	S65231	trNA-pseudouridine
447	31	42.5	322	2	C70905	hypothetical prote	520	31	42.5	556	1	A55483	transcription init
448	31	42.5	324	2	A69934	thioedoxin reduct	521	31	42.5	564	2	T40883	WD repeat protein
449	31	42.5	324	2	S43835	regulatory protein	522	31	42.5	567	2	A40899	gag polyprotein -
450	31	42.5	324	2	AF0270	cys regulon transc	523	31	42.5	574	2	B35149	ipah protein - Shi
451	31	42.5	324	2	F84719	probable glyoxalas	524	31	42.5	579	2	C97601	hypothetical prote
452	31	42.5	327	2	T32583	hypothetical prote	525	31	42.5	580	2	F84471	hypothetical prote
453	31	42.5	336	2	A47306	cysteine proteinas	526	31	42.5	588	2	AI3543	60K inner membrane
454	31	42.5	337	2	F65051	asc operon repress	527	31	42.5	595	2	T06111	adenosylhomocyste
455	31	42.5	339	2	AF0300	probable oxidoredu	528	31	42.5	597	2	T08681	hypothetical prote
456	31	42.5	339	2	JC7712	transcription coac	529	31	42.5	603	2	T08955	hypothetical prote
457	31	42.5	341	2	A11439	transcription regu	530	31	42.5	619	2	B71559	probable metallopr
458	31	42.5	341	2	AG1803	transcription regu	531	31	42.5	629	2	AD1838	Na+/H+ antiporter
459	31	42.5	345	2	E69484	conserved hypotnet	532	31	42.5	637	2	AH1160	hypothetical prote
460	31	42.5	347	2	S44846	K06H7.6 protein -	533	31	42.5	637	2	AH1519	hypothetical prote
461	31	42.5	350	2	A82798	hypothetical prote	534	31	42.5	667	2	G90883	probable collagena
462	31	42.5	351	2	D71955	hypothetical prote	535	31	42.5	667	2	H85734	probable collagena
463	31	42.5	359	2	B26135	keratin, 52K type	536	31	42.5	667	2	F64895	hypothetical prote
464	31	42.5	360	2	E89086	cell division prot	537	31	42.5	668	2	A42890	transcription fact
465	31	42.5	362	2	S27530	sporulation protei	538	31	42.5	671	2	D38490	maturen-related p
466	31	42.5	364	2	G96666	hypothetical prote	539	31	42.5	675	2	D65083	urease-lipoprotein
467	31	42.5	369	2	S76784	hypothetical prote	540	31	42.5	731	2	A98109	ornithine decarbox

541	31	42.5	731	2	D85954	ornithine decarbox	614	30	41.1	115	2	S45370	nonspecific lipid
542	31	42.5	737	2	P00219	RNA-2 polyprotein	615	30	41.1	121	2	T48832	hypothetical prote
543	31	42.5	784	2	D86564	myosin-like protei	616	30	41.1	122	2	F82812	hypothetical prote
544	31	42.5	787	2	A83207	conserved hypothet	617	30	41.1	125	2	C83691	hypothetical prote
545	31	42.5	791	2	B90566	conserved hypothet	618	30	41.1	130	2	S17961	BLT4 protein - bar
546	31	42.5	800	2	S29344	protein kinase KIN	619	30	41.1	132	2	D81096	hypothetical prote
547	31	42.5	815	2	I57487	Na+/H+-exchanging	620	30	41.1	134	2	T50998	hypothetical prote
548	31	42.5	816	2	S16328	Na+/H+-exchanging	621	30	41.1	138	2	AC1102	polyribonucleotide
549	31	42.5	818	2	A48858	Na+/H+-exchanging	622	30	41.1	142	2	AC1102	polyribonucleotide
550	31	42.5	820	2	T46412	ubiquitin-protein	623	30	41.1	142	2	AC1484	hypothetical prote
551	31	42.5	820	2	A40204	Na+/H+-exchanging	624	30	41.1	153	2	G85438	hypothetical prote
552	31	42.5	822	2	S30198	Na+/H+-exchanging	625	30	41.1	155	2	T51842	conserved hypothet
553	31	42.5	831	2	JX0359	DNA-directed DNA p	626	30	41.1	156	2	H82354	conserved hypothet
554	31	42.5	832	2	A33530	DNA-directed DNA p	627	30	41.1	157	2	A81660	probable membrane
555	31	42.5	899	2	F88391	protein R06B10.4 (	628	30	41.1	159	2	S61040	probable membrane
556	31	42.5	927	2	B82075	sensor histidine k	629	30	41.1	168	1	C1F6G2	gamma-crystallin I
557	31	42.5	932	2	E91286	probable ATP-depen	630	30	41.1	169	2	T01783	gamma-2-crystallin
558	31	42.5	952	2	A86128	probable ATP-depen	631	30	41.1	174	2	T01980	dnaj protein homol
559	31	42.5	980	2	AH1844	hypothetical prote	632	30	41.1	174	2	T45335	hypothetical prote
560	31	42.5	988	2	S37078	chloride channel p	633	30	41.1	175	2	JN0681	gamma2-crystallin
561	31	42.5	1063	2	A33830	cation efflux syst	634	30	41.1	176	2	G70599	hypothetical prote
562	31	42.5	1063	2	JC4700	cadmium, zinc, cob	635	30	41.1	178	2	T42179	hypothetical prote
563	31	42.5	1077	2	D71660	hypothetical prote	636	30	41.1	188	2	S75574	transposase sl1080
564	31	42.5	1092	2	S77546	cobN protein - Syn	637	30	41.1	190	2	C86724	hypothetical prote
565	31	42.5	1112	2	S46313	phytochrome E - Ar	638	30	41.1	195	2	S38667	ribonuclease (EC 3
566	31	42.5	1152	2	T31911	hypothetical prote	639	30	41.1	196	2	S06613	chorion protein s1
567	31	42.5	1153	2	A97179	ATP-dependent exon	640	30	41.1	197	2	F83846	spore maturation p
568	31	42.5	1166	2	T13958	syngAP-b1 protein	641	30	41.1	197	2	T24133	hypothetical prote
569	31	42.5	1171	2	T28701	probable polyketid	642	30	41.1	200	2	A84994	hypothetical prote
570	31	42.5	1177	1	D71416	probable PD85-like	643	30	41.1	201	2	AB0759	precorrin-6Y C5,15
571	31	42.5	1203	2	A39607	DNA-directed RNA p	644	30	41.1	205	2	S29308	hypothetical prote
572	31	42.5	1215	2	S50428	probable Cad+-tran	645	30	41.1	205	2	F83013	probable transcrip
573	31	42.5	1225	2	A49464	chromosome segrega	646	30	41.1	206	2	G87251	hypothetical prote
574	31	42.5	1249	2	T14270	Ras-GTPase activat	647	30	41.1	207	2	B27626	hypothetical prote
575	31	42.5	1287	2	AF2031	two-component hybr	648	30	41.1	211	1	JC2368	ribosomal protein
576	31	42.5	1293	2	T14259	ras GTPase-activat	649	30	41.1	211	2	S23753	ribosomal protein
577	31	42.5	1353	2	JC4279	adenylate cyclase	650	30	41.1	211	2	T49686	glial cell line-de
578	31	42.5	1388	2	T00063	hypothetical prote	651	30	41.1	211	2	A37499	glial cell line-de
579	31	42.5	1408	2	S57049	hypothetical prote	652	30	41.1	215	2	JC1231	hypothetical prote
580	31	42.5	1508	2	T27828	hypothetical prote	653	30	41.1	218	2	S35289	beta-crystallin A3
581	31	42.5	1519	2	T27829	hypothetical prote	654	30	41.1	225	2	T24226	competence negativ
582	31	42.5	1649	2	T39938	hypothetical prote	655	30	41.1	226	2	C82209	hypothetical prote
583	31	42.5	1676	2	E71410	probable centromer	656	30	41.1	230	1	B69876	conserved hypothet
584	31	42.5	1876	2	S50235	1,3-beta-glucan sy	657	30	41.1	230	1	C75552	hypothetical prote
585	31	42.5	1895	2	S50240	1,3-beta-glucan sy	658	30	41.1	232	2	T44456	arginine/ornithine
586	31	42.5	1943	2	B64596	toxin-like outer m	659	30	41.1	232	2	B90318	transporter (proto
587	31	42.5	2039	2	S64540	probable calcium c	660	30	41.1	235	2	A22962	carbonate dehydrat
588	31	42.5	2048	2	C94609	hypothetical prote	661	30	41.1	235	2	T41184	hypothetical prote
589	31	42.5	2562	2	T14266	Xin protein - chic	662	30	41.1	238	2	AD2138	hypothetical prote
590	31	42.5	2588	2	T14342	NSD1 protein - mou	663	30	41.1	243	2	G71507	hypothetical prote
591	31	42.5	4687	1	A39638	plectin - rat	664	30	41.1	253	2	AF0916	uridine phosphoryl
592	30.5	41.8	124	2	A81844	hypothetical prote	665	30	41.1	253	2	T46830	uridine phosphoryl
593	30.5	41.8	159	2	D87585	transcription regu	666	30	41.1	258	2	T08843	14-3-3 protein hom
594	30.5	41.8	251	2	T44757	hypothetical prote	667	30	41.1	258	2	T33409	hypothetical prote
595	30.5	41.8	308	1	Q8ECUH	leucine transport	668	30	41.1	259	2	S57283	14-3-3 brain prote
596	30.5	41.8	308	2	AG0992	high-affinity bran	669	30	41.1	260	1	JH0768	site-specific DNA-
597	30.5	41.8	308	2	H91166	leucine transport	670	30	41.1	260	1	CRHO1D	transcription regu
598	30.5	41.8	308	2	H86012	leucine transport	671	30	41.1	261	2	AB3569	conserved hypothet
599	30.5	41.8	308	2	JH0668	high-affinity bran	672	30	41.1	266	2	AB0665	FPHD protein limpo
600	30.5	41.8	308	2	G75137	sun protein (fmu p	673	30	41.1	271	2	AB2898	transcription anti
601	30.5	41.8	461	2	T00621	hypothetical prote	674	30	41.1	276	2	S39702	uridine phosphoryl
602	30.5	41.8	714	2	F81962	probable iron-regu	675	30	41.1	279	2	JC4327	hypothetical prote
603	30.5	41.8	34	1	TVTUV2	protamine Y2 - blu	676	30	41.1	280	2	T22357	NAD-dependent form
604	30	41.1	34	1	TVTUV2	protamine Y2 - blu	677	30	41.1	281	2	D97673	flagellin family p
605	30	41.1	34	1	TVTUV2	protamine Z2 - str	678	30	41.1	283	2	B97167	sortase, probable
606	30	41.1	34	2	JX0204	protamine Z1 - str	679	30	41.1	283	2	C95054	hypothetical prote
607	30	41.1	34	2	JX0203	protamine 1 - Japa	680	30	41.1	284	2	E70506	hypothetical prote
608	30	41.1	39	1	S28546	protamine 2 - Japa	681	30	41.1	285	2	A82458	S-adenosylmethioni
609	30	41.1	40	1	S14717	hypothetical prote	682	30	41.1	285	2	A97255	outer membrane lip
610	30	41.1	52	2	G84477	carbon storage reg	683	30	41.1	286	2	G86664	hypothetical prote
611	30	41.1	65	2	E82308	hypothetical prote	684	30	41.1	287	2	T25064	DNA-binding WRKY-1
612	30	41.1	90	2	D57418	conserved hypothet	685	30	41.1	289	2	T49154	glycyl-tRNA synth
613	30	41.1	101	2	A82636		686	30	41.1	296	2	AC1257	

687	30	41.1	296	2	AG1619	glycyl-tRNA synthetase	760	30	41.1	401	2	G96972	hypothetical protein
688	30	41.1	296	2	T27300	hypothetical protein	761	30	41.1	401	2	AG1238	hypothetical protein
689	30	41.1	300	2	T00274	hypothetical protein	762	30	41.1	403	1	WMLJ92	bel-2 protein - si
690	30	41.1	303	2	G85062	hypothetical protein	763	30	41.1	411	2	D87014	conserved hypothetical protein
691	30	41.1	311	1	G85062	regulatory protein	764	30	41.1	412	2	B85433	salt-inducible like
692	30	41.1	311	2	C85936	positive regulator	765	30	41.1	418	2	C84565	hypothetical protein
693	30	41.1	311	2	H91090	positive regulator	766	30	41.1	419	2	T23666	hypothetical protein
694	30	41.1	311	2	T40896	hypothetical protein	767	30	41.1	421	2	E69467	hypothetical protein
695	30	41.1	312	2	C71806	hypothetical protein	768	30	41.1	422	2	S18741	bel-2 protein - si
696	30	41.1	312	2	C64712	toxR-activated gene	769	30	41.1	428	2	F85485	flavoprotein, elec
697	30	41.1	313	2	S59448	hypothetical protein	770	30	41.1	428	2	E90634	flavoprotein [limp
698	30	41.1	313	2	F86295	T24D18.18 protein	771	30	41.1	428	2	C64725	fixC protein - Esc
699	30	41.1	314	2	C70579	probable cell divi	772	30	41.1	428	2	T52620	membrane-associate
700	30	41.1	315	2	A99192	nirv precursor (AF	773	30	41.1	433	2	AD0161	serine transporter
701	30	41.1	315	2	A13094	nitrite reductase,	774	30	41.1	433	2	G70345	hypothetical protein
702	30	41.1	316	1	S72959	probable integrase	775	30	41.1	434	2	D86530	N utilization prot
703	30	41.1	316	2	G87079	integrase/recombin	776	30	41.1	434	2	E72093	N utilization subs
704	30	41.1	317	2	T36926	dihydrodipicolinat	777	30	41.1	434	2	H81709	N utilization subs
705	30	41.1	317	2	AD3153	deoxyribose-phosph	778	30	41.1	440	2	A82369	thiamin-phosphate
706	30	41.1	320	2	B86544	NADH (ubiquinone)	779	30	41.1	442	2	AD2113	hypothetical protein
707	30	41.1	320	2	F72078	probable sodium-tr	780	30	41.1	450	2	S46117	probable regulator
708	30	41.1	322	2	T21478	hypothetical protein	781	30	41.1	451	2	T23265	hypothetical protein
709	30	41.1	324	2	F86788	transcription regu	782	30	41.1	453	2	F88042	protein F56D12.1
710	30	41.1	324	2	S50958	hypothetical protein	783	30	41.1	457	2	S52206	meas protein - Leu
711	30	41.1	325	2	S18575	svrM protein - Rhi	784	30	41.1	465	2	B83449	conserved hypothetical
712	30	41.1	326	2	A44505	svrM protein - Rhi	785	30	41.1	468	2	I52418	cytochrome P450 -
713	30	41.1	326	2	F95319	SyrM transcription	786	30	41.1	468	2	G87513	beta-glucosidase
714	30	41.1	327	2	T15594	hypothetical protein	787	30	41.1	470	2	F86526	Mg++ transporter
715	30	41.1	327	2	T38261	hypothetical protein	788	30	41.1	470	2	H72097	Mg++ transporter
716	30	41.1	328	2	T39111	chromatin-associat	789	30	41.1	473	2	T22830	hypothetical protein
717	30	41.1	329	2	T47419	hypothetical protein	790	30	41.1	475	2	F85430	serine C-palmitoyl
718	30	41.1	333	2	AH0272	conserved hypotet	791	30	41.1	477	2	D82179	probable multidrug
719	30	41.1	334	2	B98812	hypothetical protein	792	30	41.1	478	2	H90445	hypothetical protein
720	30	41.1	335	2	T22565	hypothetical protein	793	30	41.1	485	2	D91182	probable outer mem
721	30	41.1	336	2	D69074	polyferredoxin 4x2	794	30	41.1	485	2	H86028	probable fimbrial
722	30	41.1	337	2	S29814	glyceraldehyde-3-p	795	30	41.1	487	2	J44248	bet protein - simi
723	30	41.1	341	2	AB3002	conserved hypotet	796	30	41.1	488	2	JC2241	prostaglandin E re
724	30	41.1	341	2	F98281	hypothetical protein	797	30	41.1	491	2	T25662	interferon-induced
725	30	41.1	343	2	T09299	O-methyltransferas	798	30	41.1	495	1	HHC8BA	chaperonin groEL -
726	30	41.1	345	2	G98134	CGI-26 protein [im	799	30	41.1	495	2	T16900	cytochrome P450 mo
727	30	41.1	345	2	S09858	hypothetical protein	800	30	41.1	497	2	T16900	hypothetical protein
728	30	41.1	345	2	A24587	membrane antigen t	801	30	41.1	499	2	S52422	chitinase (EC 3.2.
729	30	41.1	346	2	D93340	hypothetical protein	802	30	41.1	499	2	S04856	chitinase (EC 3.2.
730	30	41.1	348	2	B64552	conserved hypotet	803	30	41.1	501	2	T31754	hypothetical protein
731	30	41.1	348	2	A83250	O-antigen chain le	804	30	41.1	504	2	I56542	calmodulin-binding
732	30	41.1	349	2	S74433	polyferredoxin 4x2	805	30	41.1	510	2	E71695	hypothetical protein
733	30	41.1	352	2	H86454	CDS protein F9L11.	806	30	41.1	512	2	T00869	probable cytochrom
734	30	41.1	352	2	T09707	isoflavone-O-methy	807	30	41.1	513	2	A46638	conserved hypotet
735	30	41.1	352	2	T09254	isoflavone-7-O-met	808	30	41.1	527	2	T18232	cationic amino aci
736	30	41.1	352	2	T23684	hypothetical protein	809	30	41.1	531	2	E69471	neurofilament trip
737	30	41.1	353	2	H70636	probable ribA prot	810	30	41.1	532	1	OPPGM	protein F3F19.5 li
738	30	41.1	353	2	A22033	hypothetical protein	811	30	41.1	547	2	C86264	probable triacylg l
739	30	41.1	358	2	G95892	probable Transposa	812	30	41.1	548	2	S37969	GTP cyclohydrolase
740	30	41.1	359	2	A43532	B-cell surface ant	813	30	41.1	552	2	T06410	hypothetical protein
741	30	41.1	363	2	S18765	Sd protein - fruit	814	30	41.1	555	2	S63137	hypothetical protein
742	30	41.1	367	2	E90547	hypothetical protein	815	30	41.1	556	2	E82182	enterobactin synth
743	30	41.1	372	2	H97277	glycoyltransferas	816	30	41.1	575	2	T24681	hypothetical protein
744	30	41.1	372	2	S69574	hypothetical protein	817	30	41.1	585	2	AC3388	arginine-tRNA liga
745	30	41.1	374	2	T00561	nodulin-like prote	818	30	41.1	585	2	T24362	hypothetical protein
746	30	41.1	375	1	H69688	response regulator	819	30	41.1	588	2	S23312	retrovirus-related
747	30	41.1	378	2	S76193	hypothetical protein	820	30	41.1	588	2	B95406	probable beta-fruc
748	30	41.1	379	2	C75294	zinc metallohydrol	821	30	41.1	592	2	T07616	hypothetical protein
749	30	41.1	380	2	T11299	ubiquinol-cytochro	822	30	41.1	608	2	S09790	abc1 protein homol
750	30	41.1	380	2	B41545	pregnancy-specific	823	30	41.1	610	2	S71110	oligodeopeptidase
751	30	41.1	383	2	AG3304	pleiotropic regula	824	30	41.1	611	1	S62811	hypothetical protein
752	30	41.1	386	2	A72313	hypothetical protein	825	30	41.1	611	2	T04510	nifS-like protein
753	30	41.1	387	2	C82336	conserved hypotet	826	30	41.1	611	2	T44909	hypothetical protein
754	30	41.1	391	2	G82320	probable oxygen-in	827	30	41.1	619	2	AC0816	hypothetical protein
755	30	41.1	393	2	A81146	histidyl-tRNA synt	828	30	41.1	620	2	T16657	hypothetical protein
756	30	41.1	394	2	AG0883	D-mannosate hydrol	829	30	41.1	638	2	H83905	hypothetical protein
757	30	41.1	395	2	T09895	hypothetical protein	830	30	41.1	644	2	S55395	neurofilament prot
758	30	41.1	396	2	T18854	hypothetical protein	831	30	41.1	644	2	A72164	A4L protein - vari
759	30	41.1	398	2	A96764	cell division prot	832	30	41.1	644	2	D36848	major core protein

833	30	41.1	644	2	T28545	hypothetical prote	906	30	41.1	1084	2	S23319	hypothetical prote
834	30	41.1	651	2	P95045	transcription regu	907	30	41.1	1085	2	C96797	unknown protein [i
835	30	41.1	651	2	E97916	conserved hypotet	908	30	41.1	1091	2	T34107	hypothetical prote
836	30	41.1	651	2	A72384	conserved hypotet	909	30	41.1	1102	2	T17367	potassium channel
837	30	41.1	656	2	H69379	chemotaxis histidi	910	30	41.1	1116	2	S41915	DNA-directed RNA p
838	30	41.1	657	1	A64079	2',3'-cyclic-nucle	911	30	41.1	1155	2	G87477	transcription-repa
839	30	41.1	657	2	D71351	probable primosoma	912	30	41.1	1193	2	D82856	transcription-repa
840	30	41.1	658	2	A86828	transketolase (EC	913	30	41.1	1203	2	I55466	N-methyl-D-asparta
841	30	41.1	664	2	F83376	conserved hypotet	914	30	41.1	1208	2	B82091	exodeoxyribonuclea
842	30	41.1	666	2	D82386	methyl-accepting c	915	30	41.1	1210	2	H88451	protein ZC155.3 [i
843	30	41.1	666	2	F71310	probable periplasm	916	30	41.1	1220	2	S48387	SLM1 protein - yea
844	30	41.1	667	2	T23010	hypothetical prote	917	30	41.1	1225	2	T09057	probable protein-h
845	30	41.1	668	2	T34317	protein-tyrosine-p	918	30	41.1	1245	2	T42920	hypothetical prote
846	30	41.1	672	2	E70717	hypothetical prote	919	30	41.1	1253	2	F86436	hypothetical prote
847	30	41.1	678	2	H96552	hypothetical prote	920	30	41.1	1288	2	T09908	hypothetical prote
848	30	41.1	690	2	F97164	flagellar biosynth	921	30	41.1	1291	1	S05465	retrovirus-related
849	30	41.1	692	2	E48376	orf5 3' to phbc -	922	30	41.1	1293	2	S42402	xeroderma pigmento
850	30	41.1	695	2	T40717	hypothetical prote	923	30	41.1	1327	2	T41647	probable pre-mrna
851	30	41.1	712	2	T12452	hypothetical prote	924	30	41.1	1511	2	S60932	probable membrane
852	30	41.1	719	2	S63392	probable membrane	925	30	41.1	1582	2	E70876	probable polyketid
853	30	41.1	723	2	S46744	Fif1 protein homol	926	30	41.1	1638	2	T25352	hypothetical prote
854	30	41.1	725	2	T52158	hypothetical prote	927	30	41.1	1780	2	T20695	hypothetical prote
855	30	41.1	747	1	VPXR4S	outer layer protei	928	30	41.1	1787	2	F84528	probable retroelom
856	30	41.1	765	2	H84247	adaptive-response	929	30	41.1	2004	2	AC0314	probable membrane
857	30	41.1	775	1	VPXRT2	outer layer protei	930	30	41.1	2115	2	S38480	nonstructural prot
858	30	41.1	776	1	A5395	outer layer protei	931	30	41.1	2185	1	S60200	acetyl-CoA carboxy
859	30	41.1	776	1	VPXRB3	outer layer protei	932	30	41.1	2205	1	MNVRN	nonstructural poly
860	30	41.1	776	1	VPXRT1	outer layer protei	933	30	41.1	2512	1	XYCHFA	enoyl-lacyl-carrie
861	30	41.1	776	1	A82787	TonB-dependent rec	934	30	41.1	2523	2	T18477	hypothetical prote
862	30	41.1	776	2	S24410	hypothetical outer	935	30	41.1	3169	2	T00296	toxin B - Escheric
863	30	41.1	777	2	A2410	serine/threonine k	936	30	41.1	3951	1	VP1HB1	F1 protein - avian
864	30	41.1	779	2	AF1094	ATP dependent heli	937	30	41.1	4447	2	A96679	polyketide synthas
865	30	41.1	794	2	T52441	hypothetical prote	938	30	41.1	4563	1	LPHUB	apolipoprotein B-1
866	30	41.1	795	2	T07709	hypothetical prote	939	29.5	40.4	99	1	DNBP11	DNA-binding protei
867	30	41.1	798	2	S40052	glycogen phosphory	940	29.5	40.4	167	2	D81951	hypothetical prote
868	30	41.1	800	2	D86712	glycogen phosphory	941	29.5	40.4	173	2	B81920	probable regulator
869	30	41.1	812	2	C97105	glycogen phosphory	942	29.5	40.4	186	2	D81154	hypothetical prote
870	30	41.1	812	2	A81621	conserved hypotet	943	29.5	40.4	190	2	D81183	Neak-related prote
871	30	41.1	817	2	T49642	hypothetical prote	944	29.5	40.4	266	2	G84757	hypothetical prote
872	30	41.1	819	2	T29486	hypothetical prote	945	29.5	40.4	385	2	A83466	probable RND efflu
873	30	41.1	831	2	F72044	ct620 hypothetical	946	29.5	40.4	713	2	A56268	Fe-regulated prote
874	30	41.1	831	2	C86581	CT620 hypothetical	947	29.5	40.4	771	2	T21633	hypothetical prote
875	30	41.1	833	2	H81700	DNA gyrase, chain	948	29.5	40.4	1473	2	A20872	ovostatin precursor
876	30	41.1	837	2	T00618	hypothetical prote	949	29	39.7	15	2	G35141	T-cell receptor de
877	30	41.1	843	1	JDVLJ1	DNA-directed DNA p	950	29	39.7	57	2	S74994	ribosomal protein
878	30	41.1	843	2	T16906	hypothetical prote	951	29	39.7	57	2	S61291	tyrosyl-tRNA synth
879	30	41.1	845	2	A45669	neurofilament trip	952	29	39.7	73	2	T30357	hypothetical prote
880	30	41.1	849	2	S00030	neurofilament trip	953	29	39.7	97	2	A71054	ribosomal protein
881	30	41.1	858	2	S15762	neurofilament trip	954	29	39.7	99	2	B90211	hypothetical prote
882	30	41.1	873	2	T50171	hypothetical prote	955	29	39.7	99	2	T43600	probable transposa
883	30	41.1	879	2	T50388	hypothetical prote	956	29	39.7	106	2	S43069	hypothetical prote
884	30	41.1	891	2	A46203	matng type A-alpha	957	29	39.7	109	2	S77925	exoskeletal protei
885	30	41.1	897	2	G89923	hypothetical prote	958	29	39.7	110	2	B64889	ydbL protein precu
886	30	41.1	898	2	A69092	alanine-tRNA ligas	959	29	39.7	112	2	T48738	hypothetical prote
887	30	41.1	902	1	S37199	nitrate reductase	960	29	39.7	114	2	A82983	conserved hypotet
888	30	41.1	916	2	A27864	neurofilament trip	961	29	39.7	116	2	T01231	hypothetical prote
889	30	41.1	924	1	S13913	hexokinase (EC 2.7	962	29	39.7	116	2	A83693	transcription regu
890	30	41.1	941	2	F71332	probable chromosom	963	29	39.7	118	2	G70306	ribosomal protein
891	30	41.1	943	2	E84429	probable receptor-	964	29	39.7	119	2	H64341	hypothetical prote
892	30	41.1	944	2	S26710	spindle pole body	965	29	39.7	130	1	WMWGN2	14k protein - narc
893	30	41.1	969	2	A70912	probable leus prot	966	29	39.7	132	2	S40257	hypothetical prote
894	30	41.1	971	2	E96794	hypothetical prote	967	29	39.7	139	2	S36325	T-cell receptor de
895	30	41.1	980	2	S71090	peroxisome biogene	968	29	39.7	144	2	E82039	conserved hypotet
896	30	41.1	984	2	A55137	hyaluronate lyase	969	29	39.7	144	2	T46334	hypothetical prote
897	30	41.1	988	2	T51054	related to alpha-a	970	29	39.7	148	2	T31141	transcription regu
898	30	41.1	998	2	G83022	probable two-compo	971	29	39.7	150	2	S36544	E6 protein - human
899	30	41.1	1028	2	T16475	hypothetical prote	972	29	39.7	157	2	H71502	probable (ARPA o
900	30	41.1	1036	2	G83329	probable RND efflu	973	29	39.7	159	2	AF1111	B. subtilis fyda p
901	30	41.1	1037	2	T50518	ABC transporter-li	974	29	39.7	162	2	D82983	leucine-responsive
902	30	41.1	1052	2	T00067	hypothetical prote	975	29	39.7	162	2	T32261	hypothetical prote
903	30	41.1	1054	2	B75384	transcription-repa	976	29	39.7	163	2	B84081	dihydrofolate redu
904	30	41.1	1075	2	T49879	hypothetical prote	977	29	39.7	165	2	S60655	dihydrofolate redu
905	30	41.1	1083	1	WZBE6	gene 6 protein - h	978	29	39.7	178	2	B72556	hypothetical prote



monocyte chemotactic protein 7b-MCP-1b - bovine (fragments)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 09-May-1997  
A:Accession: A55984  
R:Probst, P.; Wuyts, A.; Lenaerts, J.P.; Van Damme, J.  
Biochemistry 33, 13406-13412, 1994  
A:Title: Purification, sequence analysis, and biological characterization of a second bovine monocyte chemotactic protein 7b-MCP-1b  
A:Reference number: A55984; MUID:95034774; PMID:7947749  
A:Accession: A55984  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-72 <PRO>  
A:Cross-references: UNIPARC:UPI000017674C  
C:Superfamily: macrophage inflammatory protein

Query Match 87.7%; Score 64; DB 2; Length 72;  
Best Local Similarity 81.2%; Pred. No. 8.1e-05;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16  
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DB 18 ISMQRLMSYRRVTSSK 33

RESULT 3  
JC2136  
monocyte chemoattractant protein-1 precursor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 09-Jul-2004  
A:Accession: JC2136; S57498  
R:Hosang, K.; Knöke, I.; Klaudiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.  
Biochem. Biophys. Res. Commun. 199, 962-968, 1994  
A:Title: Porcine luteal cells express monocyte chemoattractant protein-1 (MCP-1): Analysis of the role of MCP-1 in the regulation of luteal cell function  
A:Reference number: JC2136; MUID:94183284; PMID:7510962  
A:Accession: JC2136  
A:Molecule type: mRNA  
A:Residues: 1-99 <HOS>  
A:Cross-references: UNIPROT:P42831; UNIPARC:UPI00001362C7; GB:Z48479; NID:9683716; PIDN: submitted to the EMBL Data Library, July 1994  
R:Zach, O.  
A:Reference number: S57497  
A:Accession: S57498  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-99 <ZAC>  
A:Cross-references: UNIPARC:UPI00001362C7; EMBL:X79416; NID:9872312; PIDN:CAA55945.1; PIDN:CAA55945.1; PIDN:CAA55945.1  
C:Superfamily: macrophage inflammatory protein  
C:Keywords: glycoprotein  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-99/Product: monocyte chemoattractant protein-1 #status predicted <MAT>  
F:94/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.7%; Score 64; DB 2; Length 99;  
Best Local Similarity 81.2%; Pred. No. 0.00011;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16  
||:|||||:|||||  
DB 43 ISMQRLMSYRRVTSSK 58

RESULT 4  
A39296  
monocyte chemoattractant protein 1 precursor - bovine  
N:Alternate names: monocyte chemotactic factor 1; seminal plasma protein P6  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A39296; B39296  
R:Wempe, F.; Henschen, A.; Scheit, K.H.  
DNA Cell Biol. 10, 671-679, 1991  
A:Title: Gene expression and cDNA cloning identified a major basic protein constituent of bovine seminal plasma  
A:Reference number: A39296; MUID:92096117; PMID:1721821  
A:Accession: A39296

Query Match 87.7%; Score 64; DB 2; Length 99;  
Best Local Similarity 81.2%; Pred. No. 0.00011;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16  
||:|||||:|||||  
DB 43 ISMQRLMSYRRVTSSK 58

RESULT 5  
JC2336  
monocyte chemoattractant protein-1 - bovine  
C:Species: Bos primigenius indicus (zebu cattle)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 03-May-1996  
C:Accession: JC2336  
R:Wempe, F.; Kuhlmann, J.K.; Scheit, K.H.  
Biochem. Biophys. Res. Commun. 202, 1272-1279, 1994  
A:Title: Characterization of the bovine monocyte chemoattractant protein-1 gene.  
A:Reference number: JC2336; MUID:94338337; PMID:8060303  
A:Accession: JC2336  
A:Molecule type: protein  
A:Residues: 1-99 <WEM>  
A:Cross-references: UNIPARC:UPI000012EDA7  
C:Genetics: MCP-1  
A:Gene: MCP-1  
A:Introns: 26/1; 65/2  
C:Superfamily: macrophage inflammatory protein

Query Match 83.6%; Score 61; DB 2; Length 99;  
Best Local Similarity 75.0%; Pred. No. 0.00041;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16  
||:|||||:|||||  
DB 43 ISMQRLMSYRRVTSSK 58

RESULT 6  
JC4912  
eotaxin precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
C:Accession: JC4912  
R:Bartels, J.; Schlueter, C.; Richter, E.; Noso, N.; Kulke, R.; Christophers, E.; Schroefer, R.; Bartels, J.; Schlueter, C.; Richter, E.; Noso, N.; Kulke, R.; Christophers, E.; Schroefer, R.  
Biochem. Biophys. Res. Commun. 225, 1045-1051, 1996  
A:Title: Human dermal fibroblasts express eotaxin: Molecular cloning, mRNA expression, and functional analysis  
A:Reference number: JC4912; MUID:96374440; PMID:8780731  
A:Accession: JC4912  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-97 <BAR>  
A:Cross-references: UNIPROT:P51671; UNIPARC:UPI000016A67B; EMBL:Z755668; NID:91531982; PIDN:Z755668; NID:91531982; PIDN:Z755668  
C:Experimental source: dermal fibroblast  
C:Comment: This protein has eosinophil specific chemotactic activity.  
C:Superfamily: macrophage inflammatory protein  
C:Keywords: fibroblast  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-97/Product: eotaxin #status predicted <MAT>



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Query Match      76.7%; Score 56; DB 2; Length 97;
Best Local Similarity 75.0%; Pred. No. 0.0035;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
   :||| ||||| |||
Db 41 IPLQRLSEYRITSSK 56

RESULT 7
146857
monocyte chemoattractant protein-1 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C:Accession: I46857
R:Yoshimura, T.; Iuhki, N.
J. Immunol. 146, 3483-3488, 1991
A:Title: Neutrophil attractant/activation protein-1 and monocyte chemoattractant protein
A:Reference number: I46857; MUID:91225489; PMID:2026877
A:Accession: I46857
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-125 <YOS>
A:Cross-references: UNIPROT:P28292; UNIPARC:UPI00001362C8; GB:M57440; NID:g165469; PIDN:
C:Superfamily: macrophage inflammatory protein

Query Match      76.7%; Score 56; DB 2; Length 125;
Best Local Similarity 75.0%; Pred. No. 0.0046;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
   :||| ||||| |||
Db 43 ISVRLMSYRINSTK 58

RESULT 8
JC2478
eotaxin precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 16-Jul-1999
C:Accession: JC2478
R:Jose, P.J.; Adcock, I.M.; Griffiths-Johnson, D.A.; Berkman, N.; Wells, T.N.C.; Williams
Biochem. Biophys. Res. Commun. 205, 788-794, 1994
A:Title: Eotaxin: Cloning of an eosinophil chemoattractant cytokine and increased mRNA e
A:Reference number: JC2478; MUID:95091818; PMID:7999113
A:Accession: JC2478
A:Molecule type: mRNA
A:Residues: 1-96 <JOS>
A:Cross-references: UNIPARC:UPI000017074E; EMBL:X77603; NID:G602551; PIDN:CAA54698.1; PI
C:Comment: This protein is identified as a potent eosinophil chemoattractant.
C:Superfamily: macrophage inflammatory protein
C:Keywords: glycoprotein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-96/Product: eotaxin #status predicted <MAT>
F:93/Binding site: carbohydrate (Thr) (covalent) #status predicted

Query Match      71.2%; Score 52; DB 2; Length 96;
Best Local Similarity 75.0%; Pred. No. 0.019;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
   :||| ||||| |||
Db 40 ISFQRLSKYKITSSK 55

RESULT 9
I48099
eotaxin precursor - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48099
R:Rothenberg, M.E.; Luster, A.D.; Lilly, C.M.; Drazen, J.M.; Leder, P.
J. Exp. Med. 181, 1211-1216, 1995
```

```
A:Title: Constitutive and allergen-induced expression of eotaxin mRNA in the guinea pig
A:Reference number: I48099; MUID:95173589; PMID:7869037
A:Accession: I48099
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-96 <RES>
A:Cross-references: UNIPROT:P80325; UNIPARC:UPI000012A065; EMBL:U18941; NID:G687655; PID:
C:Superfamily: macrophage inflammatory protein

Query Match      71.2%; Score 52; DB 2; Length 96;
Best Local Similarity 75.0%; Pred. No. 0.019;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
   :||| ||||| |||
Db 40 ISFQRLSKYKITSSK 55

RESULT 10
A30209
PDGP-inducible JE glycoprotein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A30209; A44771; A30861
R:Rollins, B.J.; Morrison, E.D.; Stiles, C.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 3738-3742, 1988
A:Title: Cloning and expression of JE, a gene inducible by platelet-derived growth facto
A:Reference number: A30209; MUID:88234501; PMID:3287374
A:Accession: A30209
A:Molecule type: DNA
A:Residues: 1-148 <ROL>
A:Cross-references: UNIPROT:P10148; UNIPARC:UPI0000020A69; GB:M19681; NID:g193486; PIDN:
R:Kawahara, R.S.; Deuel, T.P.
J. Biol. Chem. 264, 679-682, 1989
A:Title: Platelet-derived growth factor-inducible gene JE is a member of a family of sma
A:Reference number: A44771; MUID:89093129; PMID:2910858
A:Accession: A44771
A:Molecule type: DNA; mRNA
A:Residues: 1-148 <KA2>
A:Cross-references: UNIPARC:UPI0000020A69; GB:J04467; NID:g193488; PIDN:AAA37685.1; PID:
C:Genetics: JE
C:Superfamily: macrophage inflammatory protein
C:Keywords: cytokine; glycoprotein
F:126/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      67.1%; Score 49; DB 1; Length 148;
Best Local Similarity 62.5%; Pred. No. 0.11;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
   :||| ||||| |||
Db 43 IPMSRLSEYKRITSSR 58

RESULT 11
A54678
monocyte chemotactic protein 3 precursor - human
N:Alternate names: monocyte chemoattractant protein MCP-3
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999
C:Accession: A54678; JC1478; S32222
R:Opdenakker, G.; Fiten, P.; Nys, G.; Froyen, G.; Van Roy, N.; Speleman, F.; Laureys, G.
Genomics 21, 403-408, 1994
A:Title: The human MCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the
A:Reference number: A54678; MUID:94375065; PMID:7916328
A:Accession: A54678
A:Molecule type: DNA
A:Residues: 1-109 <OPD>
A:Cross-references: UNIPARC:UPI00000006BD; GB:X72309
R:Opdenakker, G.; Froyen, G.; Fiten, P.; Proost, P.; Van Damme, J.
Biochem. Biophys. Res. Commun. 191, 535-542, 1993
```



A;Title: Human monocyte chemotactic protein-3 (MCP-3): Molecular cloning of the cDNA and  
A;Reference number: JCL478; MUID:93213290; PMID:8461011  
A;Accession: JCL478  
A;Molecule type: mRNA  
A;Residues: 1-109 <OP2>  
A;Cross-references: UNIPARC:UPI00000006BD; GB:X72308; GB:S57464; NID:g3928270; PIDN:CAAF  
R;Minty, A.; Chalou, P.; Guillemot, J.C.; Kaghad, M.; Liauzun, P.; Magazin, M.; Miloux,  
submitted to the EMBL Data Library, March 1993  
A;Description: Molecular cloning of MCP-3: a human monocyte-derived monocyte chemoattractant  
A;Reference number: S32222  
A;Accession: S32222  
A;Molecule type: mRNA  
A;Residues: 1-109 <MIN>  
A;Cross-references: UNIPARC:UPI00000006BD; EMBL:X71087; NID:g288396; PIDN:CAAS0405.1; PID  
C;Comment: This protein induces proteinase secretion and chemotaxis by macrophages and m  
C;Genetics:  
A;Gene: GDB:SCYA7; SCYA6; MCP-3  
A;Cross-references: GDB:I38473; OMIM:158106  
A;Map position: 17q11-17q12  
A;Introns: 36/1, 75/2  
C;Superfamily: macrophage inflammatory protein  
C;Keywords: cytokine; glycoprotein; inflammation  
F;1-33/Domain: signal sequence #status predicted <SIG>  
F;34-109/Product: monocyte chemotactic protein 3 #status predicted <SIG>  
F;39/Binding site: carbohydrate (Asn) (covalent) #status predicted <MAT>  
  
Query Match 64.4%; Score 47; DB 2; Length 109;  
Best Local Similarity 73.3%; Pred. No. 0.19;  
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 1 ISVQRLASYRITSS 15  
| ||| ||| ||| |||  
Db 53 IPKQRLASYRITSS 67  
  
RESULT 12  
S07723  
Immediate-early serum-responsive protein JE precursor - rat  
N;Alternate names: monocyte chemoattractant protein-1  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
A;Accession: S07723; JN0128  
R;Timmers, H.T.M.; Pronk, G.J.; Bos, J.L.; van der Eb, A.J.  
Nucleic Acids Res. 18, 23-34, 1990  
A;Title: Analysis of the rat JE gene promoter identifies an AP-1 binding site essential  
A;Reference number: S07723; MUID:90174947; PMID:2106664  
A;Accession: S07723  
A;Molecule type: DNA  
A;Residues: 1-148 <TIM>  
A;Cross-references: UNIPROT:P14844; UNIPARC:UPI0000000187; EMBL:X17053; NID:g55530; PIDN  
R;Yoshimura, T.; Takeya, M.; Takahashi, K.  
Biochem. Biophys. Res. Commun. 174, 504-509, 1991  
A;Title: Molecular cloning of rat monocyte chemoattractant protein-1 (MCP-1) and its exp  
A;Reference number: JN0128; MUID:91128376; PMID:1704226  
A;Accession: JN0128  
A;Molecule type: mRNA  
A;Residues: 1-148 <YOS>  
A;Cross-references: UNIPARC:UPI0000000187; GB:IM57441; NID:g205333; PIDN:AAA63496.1; PID:  
A;Experimental source: spleen cells  
A;Note: the authors translated the codon GAA for residue 62 as Lys and GCT for residue 6  
C;Genetics:  
A;Introns: 26/1, 65/2  
C;Superfamily: macrophage inflammatory protein  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-148/Product: immediate-early serum-responsive protein JE #status predicted <MAT>  
  
Query Match 63.0%; Score 46; DB 1; Length 148;  
Best Local Similarity 56.2%; Pred. No. 0.41;  
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 ISVQRLASYRITSSK 16  
| : || : ||| ||| :  
Db 43 IPMGRLENYKRITSSR 58

RESULT 13  
A48093  
monocytic cytokine FIC - mouse  
N;Alternate names: intercrine/chemokine; MARC/FIC protein; monocyte chemotactic protein-  
C;Species: Mus musculus (house mouse)  
C;Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
A;Accession: A48093; JC2452; S30592; I49630  
R;Heinrich, J.N.; Ryseck, R.P.; Macdonald-Bravo, H.; Bravo, R.  
Mol. Cell. Biol. 13, 2020-2030, 1993  
A;Title: The product of a novel growth factor-activated gene, fic, is a biologically act  
A;Reference number: A48093; MUID:93204948; PMID:8455595  
A;Accession: A48093  
A;Molecule type: mRNA  
A;Residues: 1-97 <HEI>  
A;Cross-references: UNIPROT:Q03366; UNIPARC:UPI000016CCBC; GB:I04694; NID:g192925; PIDN  
A;Experimental source: NIH 3T3 cells  
R;Thirion, S.; Nys, G.; Fiten, P.; Maure, S.; Damme, J.V.; Opdenakker, G.  
Biochem. Biophys. Res. Commun. 201, 493-499, 1994  
A;Title: Mouse macrophage derived monocyte chemotactic protein-3: cDNA cloning and ident  
A;Reference number: JC2452; MUID:94271193; PMID:8002978  
A;Accession: JC2452  
A;Molecule type: mRNA  
A;Residues: 1-73, 'A', 75-97 <THI>  
A;Cross-references: UNIPARC:UPI000000028E; GB:S71251; NID:g547088; PIDN:AAB30997.1; PID:  
A;Experimental source: LPS-stimulated WEHI-3 cells  
R;Kulmburg, P.A.; Huber, N.E.; Scheer, B.J.; Wrann, M.; Baumruker, T.  
J. Exp. Med. 176, 1773-1778, 1992  
A;Title: Immunoglobulin E plus antigen challenge induces a novel intercrine/chemokine in  
A;Reference number: S30592; MUID:93094785; PMID:1281219  
A;Accession: S30592  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-73, 'A', 75-97 <KUL>  
A;Cross-references: UNIPARC:UPI000000028E; EMBL:Z12297; NID:g57937; PIDN:CAA78169.1; PID:  
C;Genetics:  
A;Gene: fic  
C;Superfamily: macrophage inflammatory protein  
C;Keywords: glycoprotein  
F;29/Binding site: carbohydrate (Asn) (covalent) #status predicted  
  
Query Match 61.6%; Score 45; DB 2; Length 97;  
Best Local Similarity 62.5%; Pred. No. 0.4;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 1 ISVQRLASYRITSSK 16  
| : ||| ||| :  
Db 41 IPKRLASYRITSSR 56  
  
RESULT 14  
JC5295  
monocyte chemotactic protein-2 precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 02-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 09-Jul-2004  
A;Accession: JC5295  
R;Van Coillie, E.; Froyen, G.; Nomiya, H.; Miura, R.; Fiten, P.; Van Aelst, I.; Van Da  
Biochem. Biophys. Res. Commun. 231, 726-730, 1997  
A;Title: Human monocyte chemotactic protein-2: cDNA cloning and regulated expression of  
A;Reference number: JC5295; MUID:97224420; PMID:9070881  
A;Accession: JC5295  
A;Molecule type: mRNA  
A;Residues: 1-99 <VAN>  
A;Cross-references: UNIPROT:P80075; UNIPARC:UPI0000030FC6; GB:Y10802; NID:g1924937; PIDN  
A;Experimental source: bone marrow  
C;Comment: This protein belongs to the beta-chemokine family which is one of the major H  
tis and in tumor biology, and contribute to the trafficking and recruitment of the respon  
C;Genetics:  
A;Gene: mcp-2  
C;Superfamily: macrophage inflammatory protein  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-99/Product: monocyte chemotactic protein-2 #status predicted <MAT>

Query Match 60.3%; Score 44; DB 2; Length 99;  
Best Local Similarity 64.3%; Pred. No. 0.63; Mismatches 2; Gaps 0;  
Matches 9; Conservative 2; Indels 3; Indels 0; Gaps 0;

Qy 1 ISVORLASVRRITSS 14  
| : | | | | | | | | | |  
Db 43 IPIQRLESYTRITN 56

RESULT 15  
S62188  
hypothetical protein 1 - Azotobacter vinelandii (fragment)  
C;Species: Azotobacter vinelandii  
C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S62188  
R;Colnaghi, R.; Pagani, S.; Kennedy, C.; Drummond, M.  
Eur. J. Biochem. 236, 240-248, 1996  
A;Title: Cloning, sequence analysis and overexpression of the rhodanese gene of Azotobacter vinelandii  
A;Reference number: S62187; MUID:96184904; PMID:8617271  
A;Accession: S62188  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-60 <COL>  
A;Cross-references: UNIPROT:Q44557; UNIPARC:UPI000013BFD9; EMBL:L42346; MUID:G1069990; PMID:8617271

Query Match 57.5%; Score 42; DB 2; Length 60;  
Best Local Similarity 60.0%; Pred. No. 0.89; Mismatches 2; Gaps 0;  
Matches 9; Conservative 2; Indels 4; Indels 0; Gaps 0;

Qy 1 ISVORLASVRRITSS 15  
| : | | | | | | | | | |  
Db 40 IQPQMASYRHILAS 54

RESULT 16  
I48147  
monocyte chemoattractant protein-1 - guinea pig  
C;Species: Cavia porcellus (guinea pig)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I48147  
R;Yoshimura, T.  
J. Immunol. 150, 5025-5032, 1993  
A;Title: cDNA cloning of guinea pig monocyte chemoattractant protein-1 and expression of the complementary DNA  
A;Reference number: I48147; MUID:93267104; PMID:8496603  
A;Accession: I48147  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-120 <RES>  
A;Cross-references: UNIPROT:Q08782; UNIPARC:UPI00001362C6; GB:L04985; MUID:G349820; PIDN:G349820; PIDN:G349820

A;Gene: MCP-1  
C;Superfamily: macrophage inflammatory protein

Query Match 56.2%; Score 41; DB 2; Length 120;  
Best Local Similarity 50.0%; Pred. No. 2.8; Mismatches 4; Indels 0; Gaps 0;  
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ISVORLASVRRITSSK 16  
| : | | | | | | | | | |  
Db 41 IPLKRVKGYERTSSR 56

RESULT 17  
F83026  
conserved hypothetical protein PA4952 [imported] - Pseudomonas aeruginosa (strain PA01)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: F83026  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B. Adams, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: F83026  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-339 <STO>  
A;Cross-references: UNIPROT:Q9HUL3; UNIPARC:UPI000000CSB8F; GB:AE004908; GB:AE004091; MUID:G349820; PIDN:G349820  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA4952  
C;Superfamily: conserved hypothetical protein H11714

Query Match 56.2%; Score 41; DB 2; Length 339;  
Best Local Similarity 60.0%; Pred. No. 8.3; Mismatches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ISVORLASVRRITSS 15  
| : | | | | | | | | | |  
Db 319 IMPQMASYRHILAS 333

RESULT 18  
S76549  
transcription-repair coupling protein - Synechocystis sp. (strain PCC 6803)  
C;Species: Synechocystis sp.  
A;Variety: PCC 6803  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: S76549  
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.  
DNA Res. 3, 109-136, 1996  
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC 6803  
A;Reference number: S74322; MUID:97061201; PMID:8905231  
A;Accession: S76549  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1199 <KAN>  
A;Cross-references: UNIPROT:Q55750; UNIPARC:UPI000012F03E; EMBL:D64002; GB:AB001339; MUID:G349820; PIDN:G349820  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C;Superfamily: transcription-repair coupling protein  
C;Keywords: ATP; DNA repair; leucine zipper; nucleotide binding; P-loop; transcription  
F;673-680/Region: nucleotide-binding motif A (P-loop)  
F;771-776/Region: nucleotide-binding motif B  
F;775-778/Region: DEAD/H motif #status atypical

Query Match 56.2%; Score 41; DB 1; Length 1199;  
Best Local Similarity 63.6%; Pred. No. 31; Mismatches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ORLASVRRITSS 14  
| : | | | | | | | | | |  
Db 1063 EKMAAYRRITSS 1073

RESULT 19  
T38233  
probable cystathionine gamma-synthase - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 05-Oct-2004  
C;Accession: T38233  
R;Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.  
Submitted to the EMBL Data Library, February 1998  
A;Reference number: Z21780  
A;Accession: T38233  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-398 <MUR>  
A;Cross-references: UNIPARC:UPI000006C358; EMBL:AL021813; PIDN:CAA16988.1; GSPDB:GN00066  
A;Experimental source: strain 972h-; cosmid c23A1  
C;Genetics:  
A;Gene: SPDB:SPAC23A1.14C  
A;Map position: 1

C;Superfamily: cystathionine gamma-synthase

Query Match 53.4%; Score 39; DB 2; Length 398;  
Best Local Similarity 53.3%; Pred. No. 23;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRTSSK 16  
||:|:|:|:|:|  
Db 354 SVESLIEWRRMTDSK 368

RESULT 20

F72253  
hypotheical protein TM1450 - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C;Accession: F72253  
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.  
Nature 399, 323-329, 1999  
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq  
A;Reference number: A72200; MUID:99287316; PMID:10360571  
A;Accession: F72253  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-893 <ARN>  
A;Cross-references: UNIPROT:Q9XIG2; UNIPARC:UPI00000D39A8; GB:AE001796; GB:AE000512; NID  
A;Experimental source: strain MSB8  
C;Genetics:  
A;Gene: TM1450

Query Match 53.4%; Score 39; DB 2; Length 893;  
Best Local Similarity 61.5%; Pred. No. 54;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 VORLASVRYTSS 15  
|:|:|:|:|:|  
Db 788 VERLRYRLASS 800

RESULT 21

JC2417  
monocyte chemoattractant protein-2 precursor - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 24-Feb-1995 #sequence\_revision 24-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: JC2417  
R;Hosang, K.; Knoke, I.; Klaudiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.  
Biochem. Biophys. Res. Commun. 205, 148-153, 1994  
A;Title: Porcine luteal cells express monocyte chemoattractant protein-2 (MCP-2): Analysis  
A;Reference number: JC2417; MUID:95091716; PMID:7999015  
A;Accession: JC2417  
A;Molecule type: mRNA  
A;Residues: 1-99 <HOS>  
A;Cross-references: UNIPROT:P49873; UNIPARC:UPI00001362D6; GB:Z48480; NID:9683718; PIDN:  
A;Experimental source: corpus luteum  
C;Superfamily: macrophage inflammatory protein  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-99/Product: monocyte chemoattractant protein-2 #status predicted <MAT>

Query Match 52.1%; Score 38; DB 2; Length 99;  
Best Local Similarity 50.0%; Pred. No. 8.4;  
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ISVORLASVRYTSSK 16  
|:|:|:|:|:|  
Db 43 IPFKKLESYTRTNSQ 58

RESULT 22

A82754  
lipoprotein XP0855 [imported] - Xylella fastidiosa (strain 9A5c)

C;Species: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C;Accession: A82754

R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer  
Nature 406, 151-157, 2000  
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717; PMID:10910347  
A;Note: for a complete list of authors see reference number A59328 below

A;Accession: A82754  
A;Status: preliminary  
A;Molecule type: DNA

A;Residues: 1-242 <SIM>

A;Cross-references: UNIPROT:Q9PE23; UNIPARC:UPI00000C2546; GB:AE003925; GB:AE003849; NID

A;Experimental source: strain 9A5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H  
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E  
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A;Reference number: A59328  
A;Contents: annotation  
C;Genetics:  
A;Gene: XF0855

Query Match 52.1%; Score 38; DB 2; Length 242;  
Best Local Similarity 43.8%; Pred. No. 21;  
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVORLASVRYTSSK 16  
::|:|:|:|:|:|  
Db 64 VAPQDLAWNRITASK 79

RESULT 23

JC5200

chemoreceptor TB334 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 27-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004

C;Accession: JC5200; PC4302

R;Thomas, M.B.; Haines, S.L.; Akesson, R.A.

Gene 178, 1-5, 1996

A;Title: Chemoreceptors expressed in taste, olfactory and male reproductive tissues.

A;Reference number: JC5200; MUID:97080538; PMID:8921883

A;Accession: JC5200

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-311 <THO1>

A;Cross-references: UNIPROT:Q62942; UNIPARC:UPI000004202D; GB:U50947; NID:gl256388; PIDN:

A;Accession: PC4302

A;Status: preliminary

A;Molecule type: protein

A;Residues: 146-153;265-272 <THO2>

A;Cross-references: UNIPARC:UPI0000178381; UNIPARC:UPI0000178382

A;Experimental source: taste bud

C;Comment: This protein is coupled to a GTP-binding protein-mediated signal transduction

C;Genetics:

A;Gene: tb334

C;Superfamily: olfactory receptor OR14

F;24-47/Domain: transmembrane #status predicted <TM1>

F;56-77/Domain: transmembrane #status predicted <TM2>

F;99-118/Domain: transmembrane #status predicted <TM3>

F;138-162/Domain: transmembrane #status predicted <TM4>

F;195-217/Domain: transmembrane #status predicted <TM5>

F;236-258/Domain: transmembrane #status predicted <TM6>

F;271-291/Domain: transmembrane #status predicted <TM7>

```
Query Match      52.1%; Score 38; DB 2; Length 311;
Best Local Similarity 57.1%; Pred. No. 28;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SVQRLASVRRITSS 15
Db 298 ALKRLSHRRILSS 311
      :|||:|||||
      :|||:|||||

RESULT 24
D37314
regulatory protein lcrR - Yersinia pseudotuberculosis (fragment)
C:Species: Yersinia pseudotuberculosis
C>Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 05-Oct-2004
C:Accession: D37314
R:Bergman, T.; Hakansson, S.; Forsberg, A.; Norlander, L.; Macellaro, A.; Baeckman, A.;
J. Bacteriol. 173, 1607-1616, 1991
A:Title: Analysis of the V antigen lcrGVH-yopBD operon of Yersinia pseudotuberculosis: e
A:Reference number: A37314; MUID:91154114; PMID:1705541
A:Accession: D37314
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-59 <BER>
A:Cross-references: UNIPROT:P19393; UNIPARC:UPI00001798AE
C:Superfamily: low calcium response locus protein R

Query Match      51.4%; Score 37.5; DB 2; Length 59;
Best Local Similarity 58.8%; Pred. No. 6.1;
Matches 10; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 1 ISVQRLAS-YRRITSSK 16
Db 14 LSTQRLAHFYRRWTGAK 30
      :|||||:|||||
      :|||||:|||||

RESULT 25
A37774
lcrR protein - Yersinia pestis
C:Species: Yersinia pestis
C>Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 05-Oct-2004
C:Accession: A37774
R:Barve, S.S.; Straley, S.C.
J. Bacteriol. 172, 4661-4671, 1990
A:Title: lcrR, a low-Ca(2+)-response locus with dual Ca(2+)-dependent functions in Yers
A:Reference number: A37774; MUID:90330579; PMID:1695896
A:Accession: A37774
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-146 <BAR>
A:Cross-references: UNIPROT:P19393; UNIPARC:UPI00001798AD; GB:M35740
C:Superfamily: low calcium response locus protein R

Query Match      51.4%; Score 37.5; DB 2; Length 146;
Best Local Similarity 58.8%; Pred. No. 16;
Matches 10; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 1 ISVQRLAS-YRRITSSK 16
Db 101 LSTQRLAHFYRRWTGAK 117
      :|||||:|||||
      :|||||:|||||

RESULT 26
T43592
low calcium response protein R - Yersinia pestis plasmid pCD1
C:Species: Yersinia pestis
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 05-Oct-2004
C:Accession: T43592; T42887
R:Hu, P.; Elliott, J.; McCreedy, P.; Skowronski, E.; Karnes, J.; Kobayashi, A.; Brubaker
J. Bacteriol. 180, 5192-5202, 1998
A:Title: Structural organization of virulence-associated plasmids of Yersinia pestis.
A:Reference number: 222578; MUID:98422474; PMID:9748454
A:Accession: T43592
A:Status: preliminary; translated from GB/EMBL/DBDJ
```

```
A:Molecule type: DNA
A:Residues: 1-146 <HUP>
A:Cross-references: UNIPROT:P19393; UNIPARC:UPI000012E2B8; EMBL:AF053946; NID:g2996222;
A:Experimental source: strain KIM
R:Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R.
Infect. Immun. 66, 4611-4623, 1998
A:Title: DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia p
A:Reference number: 222273; MUID:98427122; PMID:9746557
A:Accession: T42887
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-146 <PER>
A:Cross-references: UNIPARC:UPI000012E2B8; EMBL:AF074612; NID:g3822037; PIDN:AAC69831.1;
A:Experimental source: strain KIM5
C:Genetics:
A:Gene: lcrR
A:Genome: plasmid pCD1
C:Superfamily: low calcium response locus protein R

Query Match      51.4%; Score 37.5; DB 2; Length 146;
Best Local Similarity 58.8%; Pred. No. 16;
Matches 10; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 1 ISVQRLAS-YRRITSSK 16
Db 101 LSTQRLAHFYRRWTGAK 117
      :|||||:|||||
      :|||||:|||||

RESULT 27
T19339
hypothetical protein Cl6D2.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19339
R:Lloyd, C.
submitted to the EMBL Data Library, June 1998
A:Reference number: Z19110
A:Accession: T19339
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-194 <WIL>
A:Cross-references: UNIPROT:O62061; UNIPARC:UPI00000805A6; EMBL:AL023810; PIDN:CAA19421.
A:Experimental source: clone Cl6D2
C:Genetics:
A:Gene: CESP:Cl6D2.1
A:Map position: 2
A:Introns: 17/3; 53/2; 86/3; 137/3

Query Match      50.7%; Score 37; DB 2; Length 194;
Best Local Similarity 58.3%; Pred. No. 26;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SVQRLASVRRIT 13
Db 182 SEQQLAQFRRTV 193
      |::|:|::|
      |::|:|::|

RESULT 28
T02021
hypothetical protein T9E19.2 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C:Accession: T02021
R:Stromatt, C.; Johnson, D.; Le, T.
submitted to the EMBL Data Library, November 1998
A:Description: The sequence of A. thaliana T9E19.
A:Reference number: Z14496
A:Accession: T02021
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-374 <STR>
A:Cross-references: UNIPROT:Q9ZSH6; UNIPARC:UPI000000A530C; EMBL:AF104920; NID:g3859610;
A:Experimental source: cultivar Columbia
```

C;Genetics:  
A;Map position: 4  
A;Introns: 279/3  
A;Note: T9E19.2

Query Match 50.7%; Score 37; DB 2; Length 374;  
Best Local Similarity 53.3%; Pred. No. 52;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16  
|:|||||:|:  
Db 256 SIHRLASLRITR 270

## RESULT 29

C82112  
flagellin FlaE VC2144 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
C;Species: Vibrio cholerae  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C;Accession: C82112  
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.  
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A;Reference number: A82035; MUID:20406833; PMID:10952301  
A;Accession: C82112  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-378 <HEI>  
A;Cross-references: UNIPROT:Q9KQ60; UNIPARC:UPI000012A8A0; GB:AE004287; GB:AE003852; NID  
A;Experimental source: serogroup O1; strain N16961; biotype El Tor  
C;Genetics:  
A;Gene: VC2144  
A;Map position: 1  
C;Superfamily: flagellin

Query Match 50.7%; Score 37; DB 2; Length 378;  
Best Local Similarity 53.3%; Pred. No. 52;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16  
|:|||||:|:  
Db 28 SLERLSSGNRINSK 42

## RESULT 30

G82107  
flagellin core protein A VC2188 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
C;Species: Vibrio cholerae  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C;Accession: G82107  
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.  
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A;Reference number: A82035; MUID:20406833; PMID:10952301  
A;Accession: G82107  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-379 <HEI>  
A;Cross-references: UNIPROT:Q30858; UNIPARC:UPI000012A886; GB:AE004290; GB:AE003852; NID  
A;Experimental source: serogroup O1; strain N16961; biotype El Tor  
C;Genetics:  
A;Gene: VC2188  
A;Map position: 1  
C;Superfamily: flagellin

Query Match 50.7%; Score 37; DB 2; Length 379;  
Best Local Similarity 53.3%; Pred. No. 52;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16  
|:|||||:|:  
Db 28 SMERLSSGNRINSK 42

## RESULT 31

S52444  
flagellin - Legionella micdadei  
C;Species: Legionella micdadei  
C;Date: 08-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C;Accession: S52444  
R;Bangsberg, J.; Hindersson, P.  
submitted to the EMBL Data Library, February 1995  
A;Description: Cloning and expression of Legionella micdadei flagellin.  
A;Reference number: S52444  
A;Accession: S52444  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-474 <BAN>  
A;Cross-references: UNIPROT:P53606; UNIPARC:UPI000012A8D4; EMBL:X84699; NID:g673427; PID  
C;Superfamily: flagellin

Query Match 50.7%; Score 37; DB 2; Length 474;  
Best Local Similarity 53.3%; Pred. No. 66;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16  
|:|||||:|:  
Db 28 AIQRLSSGLRINSK 42

## RESULT 32

FLEC  
flagellin - Escherichia coli (strain K-12)  
C;Species: Escherichia coli  
A;Variety: strain K-12  
C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C;Accession: A37249; JVO018; I41270; H64955; A28187  
R;Kuwajima, G.; Asaka, J.I.; Fujiwara, T.; Fujiwara, T.; Kondo, E.  
J. Bacteriol. 168, 1479-1483, 1986  
A;Title: Nucleotide sequence of the hag gene encoding flagellin of Escherichia coli.  
A;Reference number: A37249; MUID:87057066; PMID:3536885  
A;Accession: A37249  
A;Molecule type: DNA  
A;Residues: 1-498 <KUM>  
A;Cross-references: UNIPROT:P04949; UNIPARC:UPI00000000AD; GB:M14358; NID:gl46311; PIDN:  
A;Experimental source: strain K-12  
R;Hanafusa, T.; Sakai, A.; Tomimaga, A.; Enomoto, M.  
Mol. Gen. Genet. 216, 44-50, 1989  
A;Title: Isolation and characterization of Escherichia coli hag operator mutants whose h  
A;Reference number: JVO018; MUID:89281489; PMID:2659972  
A;Accession: JVO018  
A;Molecule type: DNA  
A;Residues: 1-284, 'L', 286-498 <HAN>  
A;Cross-references: UNIPARC:UPI000016F1F5; GB:X17440; NID:g41649; PIDN:CAA35488.1; PID:9  
A;Experimental source: strain K-12  
R;Székely, E.; Simon, M.  
J. Bacteriol. 155, 74-81, 1983  
A;Title: DNA sequence adjacent to flagellar genes and evolution of flagellar- phase vari  
A;Reference number: I41269; MUID:83238225; PMID:6305924  
A;Accession: I41270  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-20 <RES>  
A;Cross-references: UNIPARC:UPI000016F1F5; GB:J01607; NID:gl46315; PIDN:AAA92491.1; PID:  
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
.A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A;Title: The complete genome sequence of Escherichia coli K-12.  
A;Reference number: A64720; MUID:97426617; PMID:9278503  
A;Accession: H64955  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA

```
C:Superfamily: flagellin

Query Match      50.7%; Score 37; DB 2; Length 565;
Best Local Similarity 53.3%; Pred. No. 79;
Matches      8; Conservative      4; Mismatches      3; Indels      0; Gaps      0;

QY    2 SVORLASYRRITSSK 16
      |:|::|||:|||:|
DB    28 SIERLSGLRLNSAK 42

RESULT 35
S61131
Probable membrane protein YGL186c - yeast (Saccharomyces cerevisiae)
N/Alternate names: Hypothetical protein Gl370
C/Species: Saccharomyces cerevisiae
C/Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C/Accession: S61131; S64203
R/Bertani, I.; Coglievina, M.; Zaccaria, P.; Klima, R.; Bruschi, C.V.
submitted to the EMBL Data Library, September 1995
A/Description: The sequence analysis of a 7.9 kb DNA fragment from the left arm
ive new genes.
A/Reference number: S61128
A/Accession: S61131
A/Molecule type: DNA
A/Residues: 1-579 <BER>
A/Cross-references: UNIPROT:P33099, UNIPARC:UPI000013B11D; EMBL:X91489; NID:gll1
R/Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Deinerl,
submitted to the Protein Sequence Database, May 1996
A/Reference number: S64183
A/Accession: S64203
A/Molecule type: DNA
A/Residues: 1-579 <BRU>
A/Cross-references: UNIPARC:UPI000013B11D; EMBL:Z72708; NID:g1322802; PID:g132282
A/Experimental source: strain S288C
C/Genetics:
A/Cross-references: SGD:S0003154
A/Map position: 7L
C/Superfamily: cytosine/purine transport protein
C/Keywords: transmembrane protein
F/127-143/Domain: transmembrane #status predicted <TM1>
F/166-182/Domain: transmembrane #status predicted <TM2>
F/200-216/Domain: transmembrane #status predicted <TM3>
F/229-245/Domain: transmembrane #status predicted <TM4>
F/312-328/Domain: transmembrane #status predicted <TM5>
F/361-377/Domain: transmembrane #status predicted <TM6>
F/399-415/Domain: transmembrane #status predicted <TM7>
F/426-442/Domain: transmembrane #status predicted <TM8>
F/517-533/Domain: transmembrane #status predicted <TM9>

Query Match      50.7%; Score 37; DB 2; Length 579;
Best Local Similarity 50.0%; Pred. No. 81;
Matches      7; Conservative      3; Mismatches      4; Indels      0; Gaps      0;

QY    3 VQRLASVRRITSSK 16
      :|::|||:|||
DB    73 IQRISPYRGTSKK 86

RESULT 36
C48658
flagellin - Escherichia coli (strain U5-41)
C/Species: Escherichia coli
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C/Accession: C48658
R/Schoenhaas, G.; Whitfield, C.
J. Bacteriol. 175, 5395-5402, 1993
A/Title: Comparative analysis of flagellin sequences from Escherichia coli stra
A/Reference number: A48658; MUID:93374833; PMID:8366026
A/Accession: C48658
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-584 <SCH>
```

A:Cross-references: UNIPROT-Q06352; UNIPARC-UPI00000B7C73; GB:L07388; NID:g290438; PIDN:  
C:Superfamily: flagellin

Query Match 50.7%; Score 37; DB 2; Length 584;  
Best Local Similarity 53.3%; Pred. No. 82;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 SVQRASYRRITSSK 16  
|:|:|:| | | |  
Db 28 SIERLSSGLRINS AK 42

RESULT 37

F85809  
hypothetical protein flic [imported] - Escherichia coli (strain O157:H7, substrain EDL933)  
C:Species: Escherichia coli  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: F85809  
F:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
iller, L.; Grotbeck, S.J.; Davis, N.W.; Lim, A.; Dimailanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: F85809  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-585 <STO>  
A:Cross-references: UNIPROT-Q9K2Y6; UNIPARC-UPI0000165819; GB:A5005174; NID:gl2516024; F:  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: flic  
C:Superfamily: flagellin

Query Match 50.7%; Score 37; DB 2; Length 585;  
Best Local Similarity 53.3%; Pred. No. 82;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 SVQRASYRRITSSK 16  
|:|:|:| | | |  
Db 28 SIERLSSGLRINS AK 42

RESULT 38

F90961  
flagellin [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)  
C:Species: Escherichia coli  
C>Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C:Accession: F90961  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: F90961  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-585 <HAY>  
A:Cross-references: UNIPROT-Q9K2Y6; UNIPARC-UPI00000D00B9; GB:BA000007; PIDN:BA836085.1;  
A:Experimental source: strain O157:H7, substrain RIMD 0509952  
C:Genetics:  
A:Gene: ECs2662  
C:Superfamily: flagellin

Query Match 50.7%; Score 37; DB 2; Length 585;  
Best Local Similarity 53.3%; Pred. No. 82;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 SVQRASYRRITSSK 16  
|:|:~|:~| | | |  
Db 28 SIERLSSGLRINS AK 42

RESULT 39



```
Qy 3 VQRLASYRRITSS 15
   |:|:|:|:|
Db 84 VESLSAYRLLSS 96

RESULT 42
D85089
hypothetical protein AT4g08880 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D85089
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: D85089
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1175 <STO>
A:Cross-references: UNIPROT:Q9ZPF3; UNIPARC:UPI000009F708; GB:NC_001268; NID:g7267530; E
C:Genetics:
A:Gene: AT4g08880
A:Map position: 4

Query Match 50.7%; Score 37; DB 2; Length 1175;
Best Local Similarity 53.3%; Pred. No. 1.7e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
   |:|:|:|:|
Db 192 SIHRLASLRITSR 206

RESULT 43
E86402
hypothetical protein F28J5.2 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86402
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86402
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1198 <STO>
A:Cross-references: UNIPROT:Q9C6N9; UNIPARC:UPI00000A5394; GB:AE005172; NID:g10998930; E
C:Genetics:
A:Map position: 1

Query Match 50.7%; Score 37; DB 2; Length 1198;
Best Local Similarity 53.3%; Pred. No. 1.7e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
   |:|:|:|:|
Db 328 SIHRLASLRITSR 342

RESULT 44
H85041
hypothetical protein AT4g03300 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: H85041
```

```
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: H85041
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1285 <STO>
A:Cross-references: UNIPROT:Q9ZR01; UNIPARC:UPI00000A72B2; GB:NC_001268; NID:g7270200; P
C:Genetics:
A:Gene: AT4g03300
A:Map position: 4

Query Match 50.7%; Score 37; DB 2; Length 1285;
Best Local Similarity 53.3%; Pred. No. 1.9e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
   |:|:|:|:|
Db 480 SIHRLASLRITSR 494

RESULT 45
H96559
hypothetical protein FSF19.8 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H96559
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H96559
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1305 <STO>
A:Cross-references: UNIPROT:Q9ZU21; UNIPARC:UPI00000AA103; GB:AE005173; NID:g4220449; P
C:Genetics:
A:Gene: FSF19.8
A:Map position: 1

Query Match 50.7%; Score 37; DB 2; Length 1305;
Best Local Similarity 53.3%; Pred. No. 1.9e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
   |:|:~|:~|:~|
Db 328 SIHRLASLRITSR 342

RESULT 46
D85066
hypothetical protein AT4g05280 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D85066
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: D85066
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1312 <STO>
A:Cross-references: UNIPROT:Q9M0W7; UNIPARC:UPI00000A5C54; GB:NC_001268; NID:g7267288; P
C:Genetics:
```



A:Gene: AT4905280  
A:Map position: 4

Query Match 50.7%; Score 37; DB 2; Length 1312;  
Best Local Similarity 53.3%; Pred. No. 1.9e+02;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 SVORLASVRRITSSK 16  
|:|||||:|:  
DB 276 SIHRLASLRARTSR 290

RESULT 47  
T47331  
hypothetical protein F7P3.20 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C:Accession: T47331  
R:Vitalle, D.; Liguori, R.; Flores, M.; Argiriou, A.; De Simone, V.; Mewes, H.W.; Rudd, S.  
submitted to the Protein Sequence Database, April 2000  
A:Reference number: Z24461  
A:Accession: T47331  
A:Status: preliminary  
A:Experimental source: cultivar Columbia; BAC clone F7P3  
C:Genetics:  
A:Map position: 3  
A:Introns: 42/1; 351/3; 416/1; 615/3; 657/3; 712/3; 754/3; 789/3; 819/3; 839/3; 873/3; 944/3  
A:Note: F7P3.20

Query Match 50.7%; Score 37; DB 2; Length 1314;  
Best Local Similarity 53.3%; Pred. No. 1.9e+02;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 SVORLASVRRITSSK 16  
|:|||||:|:  
DB 328 SIHRLASLRARTSR 342

RESULT 48  
A84470  
hypothetical protein At2g05560 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: A84470  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: A84470  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1472 <STO>  
A:Cross-references: UNIPROT:Q9SL11; UNIPARC:UPI00000A4740; GB:AE002093; NID:g4581168; PIDN:  
C:Genetics:  
A:Gene: At2g05560  
A:Map position: 2

Query Match 50.7%; Score 37; DB 2; Length 1472;  
Best Local Similarity 53.3%; Pred. No. 2.1e+02;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 SVORLASVRRITSSK 16  
|:|||||:|:  
DB 243 SIHRLASLRARTSR 257

RESULT 49  
T02599  
hypothetical protein At2g14770 [imported] - Arabidopsis thaliana  
N:Alternate names: hypothetical protein F26C24.9  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004  
C:Accession: T02599; C84521  
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,  
submitted to the EMBL Data Library, June 1998  
A:Description: Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence.  
A:Reference number: Z14680  
A:Accession: T02599  
A:Status: translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-1756 <ROU>  
A:Cross-references: UNIPROT:O80975; UNIPARC:UPI00000AA9BA; EMBL:AC004705; NID:g3252804  
A:Experimental source: cultivar Columbia  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: C84521  
A:Status: preliminary  
A:Experimental source: cultivar Columbia; BAC clone F7P3  
C:Genetics:  
A:Map position: 2  
A:Introns: 42/1; 351/3; 418/1; 617/3; 659/3; 725/1; 758/3; 778/3; 812/3; 902/2; 944/3  
A:Note: F7P3.20

Query Match 50.7%; Score 37; DB 2; Length 1756;  
Best Local Similarity 53.3%; Pred. No. 2.6e+02;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 SVORLASVRRITSSK 16  
|:|||||:|:  
DB 328 SIHRLASLRARTSR 342

RESULT 50  
B41657  
probable immunity protein - Leuconostoc gelidum plasmid pLG7.6  
C:Species: Leuconostoc gelidum  
C:Date: 13-May-1992 #sequence\_revision 12-Jun-1992 #text\_change 05-Oct-2004  
C:Accession: B41657  
R:Hastings, J.W.; Sailer, M.; Johnson, K.; Roy, K.L.; Vederas, J.C.; Stiles, M.E.  
J. Bacteriol. 173, 7491-7500, 1991  
A:Title: Characterization of leucocin A-UAL 187 and cloning of the bacteriocin gene from  
A:Reference number: A41657; MUID:92041660; PMID:1840587  
A:Accession: B41657  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-113 <HMS>  
A:Cross-references: UNIPROT:P34035; UNIPARC:UPI0000000AF8; GB:M64371; NID:g149637; PIDN:  
C:Genetics:  
A:Gene: plasmid  
C:Superfamily: immunity protein

Query Match 49.3%; Score 36; DB 2; Length 113;  
Best Local Similarity 53.8%; Pred. No. 23;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 VORLASVRRITSS 15  
|:|||||:|:  
DB 55 INRLVNYIRITAS 67

Search completed: February 6, 2006, 14:30:02  
Job time : 63 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2005, 01:09:23 ; Search time 177.048 Seconds  
(without alignments)  
1106.832 Million cell updates/sec

Title: US-10-644-277-62  
Perfect score: 2379  
Sequence: 1 QVQLQSGGLVKKPSQTLTL.....MHEALHHYTKSLSLGK 446

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2379	100.0	446	8 ADK52356	Adk52356 Human ant
2	2197.5	92.4	470	9 AEB45857	Aeb45857 Human mon
3	2187.5	92.0	464	9 AEC20880	Aec20880 Low risk
4	2186	91.9	450	6 ABP96294	Abp96294 4AS-3.1.1
5	2177	91.5	467	9 ADZ51037	Adz51037 Amino aci
6	2171	91.3	467	2 AAW14925	Aaw14925 Human gam
7	2171	91.3	467	2 ADE31589	Ade31589 Gamma 4 h
8	2164	91.0	467	2 AAW14926	Aaw14926 Human gam
9	2164	91.0	467	2 ADE31591	Ade31591 Gamma 4 h
10	2159	90.8	467	2 AAW14927	Aaw14927 Human gam
11	2159	90.8	467	7 ADE31593	Ade31593 Gamma 4 h
12	2158.5	90.7	480	9 ADZ57697	Adz57697 Anti-cMet
13	2140	90.0	473	4 AAB36206	Aab36206 Human imm
14	2136.5	89.8	580	6 AAO30915	Aao30915 di-NHS76
15	2119	89.1	442	9 ADY74807	Ady74807 Rat anti-
16	2108	88.6	463	9 ADZ57701	Adz57701 Anti-cMet
17	2106.5	88.5	466	7 ADE28479	Ade28479 Human ant
18	2104.5	88.5	466	7 ADE28471	Ade28471 Human ant
19	2096.5	88.1	466	7 ADE28419	Ade28419 Human ant
20	2090	87.9	448	9 ADW11296	Adw11296 Human C-t
21	2088.5	87.8	451	8 ADQ31884	Adq31884 Antibody
22	2088.5	87.8	451	8 ADT77643	Adt77643 Antibody
23	2088.5	87.8	451	9 AEB51162	Aeb51162 ChimERIC
24	2088	87.8	448	9 ADW11298	Adw11298 Human C-t

25	2085.5	87.7	451	8 ADT51711	Adt51711 M200 anti
26	2084.5	87.6	464	7 ADE28411	Ade28411 Human ant
27	2083	87.6	442	9 ADY74779	Ady74779 Rat anti-
28	2082.5	87.5	451	8 ADT51709	Adt51709 M200 anti
29	2082.5	87.5	451	8 ADT51710	Adt51710 M200 anti
30	2079.5	87.4	447	9 AEB46954	Aeb46954 CD1a spec
31	2079.5	87.4	451	8 ADT51712	Adt51712 M200 anti
32	2079.5	87.4	541	8 ADR10116	Adr10116 Human pro
33	2078	87.3	448	9 ADW11294	Adw11294 Human C-t
34	2077.5	87.3	451	8 ADT51713	Adt51713 M200 anti
35	2077.5	87.3	462	3 AAB26884	Aab26884 Human imm
36	2075	87.2	471	9 AEB45873	Aeb45873 Human mon
37	2071	87.1	461	9 AEA41062	Aea41062 Human ant
38	2071	87.1	465	9 AEB45849	Aeb45849 Human mon
39	2067	86.9	463	9 AEA41030	Aea41030 Human ant
40	2067	86.9	469	9 AEB45895	Aeb45895 Human mon
41	2065.5	86.8	451	8 ADQ31890	Adq31890 Antibody
42	2065.5	86.8	451	9 AEB51168	Aeb51168 ChimERIC
43	2064.5	86.8	462	9 AEB45881	Aeb45881 Human mon
44	2064	86.8	467	9 AEC20877	Aec20877 Low + mod
45	2064	86.8	469	8 ADL93669	Adl93669 Human CD4

ALIGNMENTS

RESULT 1  
ADK52356  
ID ADK52356 standard; protein; 446 AA.  
XX  
AC ADK52356;  
XX  
DT 20-MAY-2004. (first entry)  
XX  
DE Human anti-MCP-1 variable region heavy chain #16.  
XX  
KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;  
KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;  
KW Vasotropic; Immunosuppressive; Neuroprotective; Neoplastic;  
KW inflammatory condition; cancer; arthritis; multiple sclerosis;  
KW anti-MCP-1; heavy chain; light chain.  
XX  
OS Homo sapiens.  
XX  
PN WO2004016769-A2.  
XX  
PD 26-FEB-2004.  
XX  
PF 19-AUG-2003; 2003WO-US026232.  
XX  
PR 19-AUG-2002; 2002US-0404802P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;  
PI Bhakta S;  
XX  
DR WPI; 2004-203794/19.  
XX  
DR N-PSDB; ADK52355.  
XX  
PT New human monoclonal antibody that binds to monocyte chemo-attractant  
PT protein-1 and is immobilized on an insoluble matrix, useful for  
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,  
PT rheumatoid arthritis or psoriasis.  
XX  
PS Claim 1; SEQ ID NO 62; 154pp; English.  
XX  
CC The present invention relates to a human monoclonal antibody that binds  
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful  
CC for the preparation of a medicament useful for treating neoplastic or  
CC inflammatory conditions. The neoplastic disease is selected from breast  
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,

CC pancreatic cancer or prostate cancer. The inflammatory condition is  
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,  
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The  
CC antibodies are also useful for diagnosing the above diseases. It is also  
CC useful for the determining the level of MCP-1 and MCP-1 family members in  
CC patient samples. The present sequence represents a human anti-MCP-1  
CC variable region heavy chain sequence.

XX Sequence 446 AA;

SQ Query Match 100.0%; Score 2379; DB 8; Length 446;  
Best Local Similarity 100.0%; Pred. No. 3e-135;  
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGFLVKPSQTLSTCTVSGSISGGNYNNIRQHPGKLEWIGYIYSGNTY 60  
DB 1 QVQLQESGFLVKPSQTLSTCTVSGSISGGNYNNIRQHPGKLEWIGYIYSGNTY 60  
QY 61 YNPSLSKRITISIDTSKNQFSLTSSVTAADTAVVYCARDGGDDAFDIWGQTMVTVSSA 120  
DB 61 YNPSLSKRITISIDTSKNQFSLTSSVTAADTAVVYCARDGGDDAFDIWGQTMVTVSSA 120  
QY 121 STKGFSVPLAPCSRSTSESTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180  
DB 121 STKGFSVPLAPCSRSTSESTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180  
QY 181 LYSLSVSVTVPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPAPPEFLGGPSVF 240  
DB 181 LYSLSVSVTVPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPAPPEFLGGPSVF 240  
QY 241 LPPPKPDTLMSRTPETVCVVVDVQSDPEVQFNWYDGVGVHNAKTKPREEQFNSTYR 300  
DB 241 LPPPKPDTLMSRTPETVCVVVDVQSDPEVQFNWYDGVGVHNAKTKPREEQFNSTYR 300  
QY 301 VVSVLTVLHQDWLNGEKVKCKVSNKGLPSSIEKTIISKAGQPRRPQVYTLPPSQEEMTKN 360  
DB 301 VVSVLTVLHQDWLNGEKVKCKVSNKGLPSSIEKTIISKAGQPRRPQVYTLPPSQEEMTKN 360  
QY 361 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSDGSGFFLYSRLTVDKSRWQEGN 420  
DB 361 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSDGSGFFLYSRLTVDKSRWQEGN 420  
QY 421 VFSCSVMEALHNHYTKQSLSLGK 446  
DB 421 VFSCSVMEALHNHYTKQSLSLGK 446

RESULT 2

AEB45857

ID AEB45857 standard; protein; 470 AA.

XX

AC AEB45857;

XX

DT 06-OCT-2005 (first entry)

XX

DE Human monoclonal anti-MadCAM antibody #11.

XX

KW Monoclonal antibody; mucosal addressin cell adhesion molecule; MadCAM;  
KW inflammation; inflammatory bowel disease; Crohn's disease;  
KW ulcerative colitis; diverticular disease; gastritis; liver disease;  
KW primary biliary cirrhosis; primary sclerosing cholangitis;  
KW insulin dependent diabetes; graft versus host disease; antiinflammatory;  
KW gastrointestinal-gen.; antidiabetic; hepatotropic; antidiabetic;  
KW immunosuppressive; antibody.

XX

OS Homo sapiens.

XX

PN WO2005067620-A2.

XX

PD 28-JUL-2005.

XX

PF 07-JAN-2005; 2005WO-US000370.

XX

PR 09-JAN-2004; 2004US-0535490P.  
XX (PFIZ ) PFIZER INC.  
PA (ABGE-) ABGENIX INC.  
PA (PFIZ ) PFIZER LTD.  
XX  
PI Pullen N, Molloy E, Kellermann S, Green LL, Haak-Frendscho M;  
XX WPI; 2005-554958/56.  
DR N-PSDB; AEB45856.  
XX  
PT New antibody to Mucosal Addressin Cell Adhesion Molecule, useful for  
PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel  
PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or  
PT graft versus host disease.  
PS Claim 8; SEQ ID NO 22; 167pp; English.  
XX  
CC The invention relates to a human monoclonal antibody or its antigen-  
CC binding portion that specifically binds to mucosal addressin cell  
CC adhesion molecule (MadCAM). The invention also relates to a hybridoma  
CC cell line that produces the human monoclonal antibody, a pharmaceutical  
CC composition comprising an amount of the monoclonal antibody or its  
CC antigen-binding portion and a pharmaceutical carrier, a method of  
CC treating inflammatory disease in a subject, an isolated cell line that  
CC produces the monoclonal antibody or its antigen-binding portion or the  
CC heavy chain or light chain of the antibody or of its portion, an isolated  
CC nucleic acid molecule comprising a nucleotide sequence encoding the heavy  
CC chain or its antigen-binding portion or the light chain or its antigen-  
CC binding portion of an antibody described above, a vector comprising the  
CC nucleic acid molecule, where the vector optionally comprises an  
CC expression control sequence operably linked to the nucleic acid molecule,  
CC a host cell comprising the vector or the nucleic acid molecule above, a  
CC method of producing a human monoclonal antibody or its antigen-binding  
CC portion that specifically binds MadCAM, a method of isolating an antibody  
CC or its antigen-binding portion that specifically binds to MadCAM, a  
CC method of treating a subject in need of a human antibody or its antigen-  
CC binding portion that specifically binds to MadCAM and inhibits binding to  
CC alpha4beta7, a method of inhibiting alpha4beta7 binding to cells  
CC expressing human MadCAM, a method of inhibiting MadCAM-mediated leukocyte  
CC endothelial cell adhesion, migration and infiltration into tissues, a  
CC method of inhibiting alpha4beta7/MadCAM-dependent cellular adhesion,  
CC inhibiting the MadCAM-mediated recruitment of lymphocytes to  
CC gastrointestinal lymphoid tissue, a method of diagnosing a disorder  
CC characterized by circulating soluble human MadCAM and detecting  
CC inflammation in a subject. The antibody, composition and methods are  
CC useful for diagnosing and treating inflammatory disease, e.g.  
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
CC diverticular disease, gastritis, liver disease, primary biliary  
CC cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and  
CC graft versus host disease. This sequence represents a human monoclonal  
CC anti-MadCAM antibody of the invention.

XX Sequence 470 AA;

Query Match 92.4%; Score 2197.5; DB 9; Length 470;

Best Local Similarity 92.9%; Pred. No. 2.8e-124;

Matches 421; Conservative 5; Mismatches 18; Indels 9; Gaps 2;

QY 1 QVQLQESGFLVKPSQTLSTCTVSGSISGGNYNNIRQHPGKLEWIGYIYSGNTY 60  
DB 20 QVQLQESGFLVKPSQTLSTCTVSGSISGGNYNNIRQHPGKLEWIGYIYSGNTY 77  
QY 61 YNPSLSKRITISIDTSKNQFSLTSSVTAADTAVVYCARDG-----GDADFIDWGQGT 113  
DB 78 SNPSLRGRVTILADTSKNQFSLSSVTAADTAVVYCARDRTIIRGLIPSFDDYWGQGT 137  
QY 114 MVTVSSASTKGPSVFPPLAPCSRSTSESTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFP 173  
DB 138 LVTVSSASTKGPSVFPPLAPCSRSTSESTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFP 197  
QY 174 AVLQSSGLYLSVSVTVPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPAPPEF 233

198 AVLQSSGLSLSSVVTVPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPCPAPRF 257  
234 LGSPSVLPPPKPOTLMTSRTPVTCVVVDVSQEDPEVQFNNYDGVVHNAKTPREE 293  
258 LGSPSVLPPPKPOTLMTSRTPVTCVVVDVSQEDPEVQFNNYDGVVHNAKTPREE 317  
294 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAGQPREPQVYTLPPS 353  
318 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAGQPREPQVYTLPPS 377  
354 QEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDK 413  
378 QEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDK 437  
414 SRWQEGNVFSCSVHMEALHNHYTQKSLSLGLK 446  
438 SRWQEGNVFSCSVHMEALHNHYTQKSLSLGLK 470

RESULT 3  
AEC20880  
ID AEC20880 standard; protein; 464 AA.  
XX AEC20880;  
XX  
XX 20-OCT-2005 (first entry)  
XX  
XX Low risk humanized RX1 antibody heRX1-1.IgG4.  
XX endocrine-gen.; antiarthritic; antibacterial; antiinflammatory;  
XX antirheumatic; antithyroid; bone metaerases; calcium antagonist; cancer;  
XX cardiovascular-gen.; degeneration; eating-disorders-gen.; gastrointestinal-gen.;  
XX endocrine disease; endocrine-gen.; endocrine-gen.; immune disorder;  
XX genetic disorder; hepatotropic; hypercalcemia; immune disorder;  
XX immunotherapy; inflammation; monoclonal antibody; mouth disease;  
XX musculoskeletal disease; neoplasia; nephrotropic; osteopathic;  
XX osteopetrosis; osteoporosis; pagets disease; periodontal disease;  
XX pharmacuetical; rheumatoid arthritis; RX1.  
XX  
XX Homo sapiens.  
XX Mus musculus.  
XX Synthetic.  
XX  
XX W02005068503-A2.  
XX  
XX 28-JUL-2005.  
XX  
XX 06-JAN-2005; 2005WO-US000546.  
XX  
XX 07-JAN-2004; 2004US-0535181P.  
XX 02-JUN-2004; 2004US-0576417P.  
XX  
XX (CHIR ) CHIRON CORP.  
XX (XOMA ) XOMA TECHNOLOGY LTD.  
XX  
XX Liu C, Zimmerman DL, Harrowe GM, Kochs K, Kavanaugh WM, Long L;  
XX Calderon-Cacia M, Horwitz AH;  
XX WPI; 2005-597707/61.  
XX N-PSDB; AEC20878, AEC20879.  
XX  
XX Novel non-murine antibody that competes with monoclonal antibody RX1 for  
XX binding to macrophage colony stimulating factor, useful for treating  
XX hypogonadism, hypercalcemia, rickets, scurvy, homocystinuria, cancer,  
XX osteoporosis.  
XX  
XX Claim 53; SEQ ID NO 119; 269pp; English.  
XX  
XX The invention describes a non-murine antibody (I) that competes with  
XX monoclonal antibody RX1 for binding to macrophage colony stimulating  
XX factor (M-CSF) by more than 75%, where the monoclonal antibody RX1 has  
XX the heavy chain and light chain amino acid sequences having a fully  
XX defined 447 amino acids (SEQ ID No. 2) and 214 amino acids (SEQ ID No. 4)

sequences given in the specification, respectively. (I) is useful for preventing a subject afflicted with a disease that causes or contributes to osteolysis, where the antibody effectively reduces the severity of bone loss associated with the disease. The disease is chosen from metabolic bone diseases associated with relatively increased osteoclast activity, including endocrinopathies, hypercalcemia, deficiency states, chronic diseases, and hereditary diseases, cancer, osteoporosis, osteopetrosis, inflammation of bone associated with arthritis and/or rheumatoid arthritis, periodontal disease, fibrous dysplasia, and/or Paget's disease. (I) is useful for preventing or treating metastatic cancer. Antibodies of the invention are useful for preventing or reducing bone loss; osteolysis; metastatic cancer to bone and cancer. (I) is useful for manufacturing a medicament for preventing or reducing bone loss in a patient exhibiting osteolysis, manufacturing a medicament for treating a patient afflicted with a disease that causes or contributes to osteolysis, and metastatic cancer to bone in a patient suffering from metastatic cancer, for manufacturing a medicament for treating a patient having cancer. (I) in synergistic combination, is useful for preparing a medicament for treating a patient exhibiting osteolysis. This is the amino acid sequence of a low risk humanized M-CSF specific murine antibody RX1.

Query Match 92.0%; Score 2187.5; DB 9; Length 464;  
Best Local Similarity 93.9%; Pred. No. 1.1e-123;  
Matches 419; Conservative 6; Mismatches 18; Indels 3; Gaps 2;  
Sequence 464 AA;

QY 2 VOLQSGPGLVKPSQTLSTCTVSGSGISSGGNY--NNIIRHGGKLEWIGYVYSGNTY 60  
DB 21 VOLQSGPGLVKPSQTLSTCTVTDYSITS--DYANNWIRQFPGKLEWYISYSGSTS 78  
QY 61 YNPSLKSRTISIDTSKNQFSLTSSVTAADTAVYVCARDGGDDAFDIWGQGTMTVTVSSA 120  
DB 79 YNPSLKSRTISIDTSKNQFSLTSSVTAADTAVYVCARDGGDDAFDIWGQGTMTVTVSSA 138  
QY 121 STKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVYSNWSGALTSGVHTTTPAVLQSSG 180  
DB 139 STKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVYSNWSGALTSGVHTTTPAVLQSSG 198  
QY 181 LYSLSVTVTPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPCPAPFLGGPSVP 240  
DB 199 LYSLSVTVTPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPCPAPFLGGPSVP 258  
QY 241 LPPPKPOTLMTSRTPVTCVVVDVSQEDPEVQFNNYDGVVHNAKTPREEQFNSTYR 300  
DB 259 LPPPKPOTLMTSRTPVTCVVVDVSQEDPEVQFNNYDGVVHNAKTPREEQFNSTYR 318  
QY 301 VVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAGQPREPQVYTLPPSQEEMTKN 360  
DB 319 VVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAGQPREPQVYTLPPSQEEMTKN 378  
QY 361 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGN 420  
DB 379 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGN 438  
QY 421 VFSCSVMEALHNHYTQKSLSLGLK 446  
DB 439 VFSCSVMEALHNHYTQKSLSLGLK 464

RESULT 4  
ABP96294  
ID ABP96294 standard; protein; 450 AA.  
XX AC ABP96294;  
XX  
XX 20-MAY-2003 (first entry)  
XX  
XX 4A5-3.1.1-B4 antibody amino acid sequence #1.  
XX DE  
XX Anti-bTNFSP13b human antibody; antibody; human; TNFSP13b; antiulcer;  
XX immunosuppressive; antiinflammatory; dermatological; antirheumatic;

KW antiarthritic; antiaesthetic; antiallergic; antiparasitic; antiparasitic;  
KW antinfertility; antithyroid; thymomimetic; haemostatic; cytostatic;  
KW tumour necrosis factor antagonist; TNF antagonist; rheumatoid arthritis;  
KW systemic lupus erythematosus; juvenile chronic arthritis; Lyme arthritis;  
KW Crohn's disease; ulcerative colitis; inflammatory bowel disease; asthma;  
KW allergic disease; psoriasis; immune disease; organ transplant rejection;  
KW graft-versus-host disease; sarcoidosis; infectious disease; cancer;  
KW parasitic disease; female infertility; autoimmune thrombocytopenia;  
KW autoimmune thyroid disease; Hashimoto's disease; Sjogren's syndrome.

OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Region 24..34 /label= CDR1  
FT Region 50..56 /label= CDR2  
FT Region 89..97 /label= CDR3

XX WO2003016468-A2.  
XX 27-FEB-2003.  
XX 15-AUG-2002; 2002WO-US021842.  
XX 16-AUG-2001; 2001US-0312808P.  
XX (ELIL ) LILLY & CO ELI.  
XX Gelfanova VP, Hale JE, Kikly KK, Witcher DR, Rathnachalam R;  
XX WPI; 2003-268308/26.

XX New anti-HTNFSF13b human antibody, useful in manufacturing a medicament  
PT for inhibiting TNFSF13b activity in a subject suffering from a disorder  
PT in which TNFSF13b activity is detrimental, e.g. asthma, cancer or  
PT rheumatoid arthritis.

XX Example 7; Page 33; 52pp; English.

XX The present invention describes an anti-HTNFSF13b human antibody (I). (I)  
CC has immunosuppressive, antiinflammatory, dermatological, antiulcer,  
CC antirheumatic, antiarthritic, antiaesthetic, antiallergic, antiparasitic,  
CC antiparasitic, antinfertility, antithyroid, thymomimetic, haemostatic  
CC and cytostatic activities, and can be used as a tumour necrosis factor  
CC (TNF) antagonist. The anti-HTNFSF13b human antibody or an antibody that  
CC neutralises TNFSF13b activity by binding an epitope of TNFSF13b is useful  
CC in manufacturing a medicament for administering to a subject suffering  
CC from a disorder in which TNFSF13b activity is detrimental, e.g. systemic  
CC lupus erythematosus, rheumatoid arthritis, juvenile chronic arthritis,  
CC Lyme arthritis, Crohn's disease, ulcerative colitis, inflammatory bowel  
CC disease, asthma, allergic disease, psoriasis, acute or chronic immune  
CC disease associated with organ transplantation, organ transplant  
CC rejection, graft-versus-host disease, sarcoidosis, infectious diseases,  
CC parasitic diseases, female infertility, autoimmune thrombocytopenia,  
CC autoimmune thyroid disease, Hashimoto's disease, Sjogren's syndrome, or  
CC cancer. The present sequence represents a 4A5-3.1.1-B4 antibody amino  
CC acid sequence, which is used in an example from the present invention

XX Sequence 450 AA;

Query Match 91.9%; Score 2186; DB 6; Length 450;  
Best Local Similarity 92.3%; Pred. No. 1.3e-123;  
Matches 417; Conservative 9; Mismatches 18; Indels 8; Gaps 2;

QY 1 QVQLQESGFLVKPQTLSLTCTVSGSISGCGYVWVWIRQHPGKLEWIGYVYSGNTY 60  
DB 1 QVQLQWAGLTKPSETLSLTCAVYGGSF--GYVSWIRQPPGKLEWIGVNHSGSTN 58  
QY 61 YNPSLKSRITTSIDTSKNQFSLTSSVTAADTAVYVCARDGGDDA-----FDTWGQGT 114

Db 59 YNPSLKSRVTSVDTSKNQFSLKLSSTAAADTAVYVCARGYYDILTGYYYFYDWGQGT 118  
QY 115 VTSSASTKGPSVPPLAPCSRSTSESTAALGCLVKDYFPEPPTVSMNSGALTSGVHTTTPA 174  
Db 119 VTSSASTKGPSVPPLAPCSRSTSESTAALGCLVKDYFPEPPTVSMNSGALTSGVHTTTPA 178  
QY 175 VLQSSGLYSLSVVTVSPSSSLGTITTCNVVDHKPSNTKVDKRVESKYGPPCPAPPEFL 234  
Db 179 VLQSSGLYSLSVVTVSPSSSLGTITTCNVVDHKPSNTKVDKRVESKYGPPCPAPPEFL 238  
QY 235 GGPSVFLFPKPKDMLMISRTPEVTVVVDVSQSDPEVQFNWYVDGVEVHNNAKTPRE 294  
Db 239 GGPSVFLFPKPKDMLMISRTPEVTVVVDVSQSDPEVQFNWYVDGVEVHNNAKTPRE 298  
QY 295 FNSTYRVVSVLTVLHODWLNAGEYCKVSKNKGSLSSIEKTSKAGQPREPVVTLPPSQ 354  
Db 299 FNSTYRVVSVLTVLHODWLNAGEYCKVSKNKGSLSSIEKTSKAGQPREPVVTLPPSQ 358  
QY 355 EEMTKNOVSLTCLVKGFVPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSRLTV 414  
Db 359 EEMTKNOVSLTCLVKGFVPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSRLTV 418  
QY 415 RWQEGNVFSCVMHEALHNHYTQKSLSLGLK 446  
Db 419 RWQEGNVFSCVMHEALHNHYTQKSLSLGLK 450

RESULT 5  
ADZ51037  
ID ADZ51037 standard; protein; 467 AA.  
XX AC ADZ51037;  
XX DT 30-JUN-2005 (first entry)  
XX DE Amino acid sequence of heavy chain of anti-H4-1BB antibody.  
XX KW antibody therapy; H4-1BB; CD137; IgG4; cytostatic; immunosuppressive;  
KW antiinflammatory; antimicrobial; gene therapy;  
KW T cell mediated autoimmune disease; cancer; neoplasm; autoimmune disease;  
KW inflammatory disease; infectious disease; heavy chain.

OS Synthetic.  
XX Key Location/Qualifiers  
FT Peptide 1..19 /note= "leader peptide"  
XX WO2005035584-A1.  
XX PD 21-APR-2005.  
XX 12-OCT-2004; 2004WO-US033587.  
XX 10-OCT-2003; 2003US-0510193P.  
XX 08-OCT-2004; 2004US-00961567.  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX Jure-Kunkel M, Hefta LJ, Santoro M, Ganguly S;  
XX WPI; 2005-296269/30.  
XX N-PSDB; ADZ51035.

XX New monoclonal antibody that specifically binds to 4-1BB comprises a  
PT light chain variable region and a heavy chain variable region, useful for  
PT treating cancer, autoimmune diseases, inflammatory diseases, or  
PT infectious diseases.  
XX Claim 3; SEQ ID NO 3; 92pp; English.  
XX The specification describes fully human antibodies against human 4-1BB  
CC (CD137) (H4-1BB). These antibodies are especially IgG4 antibodies.

CC Antibodies for human 4-1BB are useful as immuno-enhancers of an anti-  
CC tumor or anti-viral immune response, or as immunomodulators of T cell  
CC mediated autoimmune disease. They can also be used as diagnostic tools  
CC for the detection of H4-1BB in blood or tissues of patients with cancer,  
CC autoimmunity, or other disease. The antibody can also be used for treating  
CC cancer (prostate cancer, melanoma, or epithelial cancer), autoimmune  
CC diseases (multiple sclerosis, rheumatoid arthritis, systemic lupus  
CC erythematosus, or myasthenia gravis) inflammatory diseases, and  
CC infectious diseases. AD251035, AD251036, and AD251037 represent the  
CC coding strand, complementary strand, and encoded protein of a plasmid.  
CC This plasmid encodes the heavy chain of an antibody of the invention.  
XX  
SQ Sequence 467 AA;

Query Match 91.5%; Score 2177; DB 9; Length 467;  
Best Local Similarity 92.0%; Pred. No. 4.7e-123;  
Matches 414; Conservative 11; Mismatches 19; Indels 6; Gaps 2;  
QY 1 QVQLQESGPGLVKPSQTLTCTVSGGSISSGGNYWNIHQHPGKLEWIGIYVSGNTY 60  
DB 20 QVQLQESGPGLVKPSQTLTCTVSGGSISSGGNYWNIHQHPGKLEWIGIYVSGNTY 77  
QY 61 YNPISLKRITISIDTSKNQFSLTSSVTAADTAIVYCARDGG---DDAFDINGQGTMT 116  
DB 78 YNPISLKRITISIDTSKNQFSLTSSVTAADTAIVYCARDGG---DDAFDINGQGTMT 137  
QY 117 VSSASTKGPSVFPPLAPCSRSTSESTAAALGCLVKDYPPEPVTVSWNSGALTSGVHTPPAVL 176  
DB 138 VSSASTKGPSVFPPLAPCSRSTSESTAAALGCLVKDYPPEPVTVSWNSGALTSGVHTPPAVL 197  
QY 177 QSSGLYSLSSVTVTPSSSLGTITTCNVDPKPSNTKVDKRVESKYGPPCPAPFLGG 236  
DB 198 QSSGLYSLSSVTVTPSSSLGTITTCNVDPKPSNTKVDKRVESKYGPPCPAPFLGG 257  
QY 237 PSVFLPFPKPDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN 296  
DB 258 PSVFLPFPKPDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN 317  
QY 297 STYRVVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEE 356  
DB 318 STYRVVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEE 377  
QY 357 MTNQVSLTCLVKGFPSPDIKAVESNGQPNNTKTPPVLDSGDSGFFLYSLRTVDKSRW 416  
DB 378 MTNQVSLTCLVKGFPSPDIKAVESNGQPNNTKTPPVLDSGDSGFFLYSLRTVDKSRW 437  
QY 417 QEGNVFSCSVHMEALHNHYTQKSLSLSLGK 446  
DB 438 QEGNVFSCSVHMEALHNHYTQKSLSLSLGK 467

RESULT 6  
AAW14925  
XX ID AAW14925 standard; protein; 467 AA.  
XX AC AAW14925;  
XX DT 18-OCT-1997 (first entry)  
XX DE Human gamma-4 heavy chain.  
XX KW CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;  
XX cynomolgus monkey; autoimmune disease; rheumatoid arthritis; leukaemia;  
XX lymphoma; graft-versus-host disease; asthma; transplant rejection; HIV;  
XX therapy; CE9 gamma 4.  
XX OS Homo sapiens.  
XX PN WO9709351-A1.  
XX PD 13-MAR-1997.  
XX PF 05-SEP-1996; 96WO-US014324.

XX 06-SEP-1995; 95US-00523894.  
XX (IDEC-) IDEC PHARM CORP.  
XX Hanna N, Newman RA, Reff ME;  
XX N-PSDB; AAT62868.  
XX WPI; 1997-201913/18.  
XX PT Chimeric antibody comprising monkey variable domains and human constant  
XX domains - affects CD4-mediated immune functions, esp. useful for  
XX treatment of auto-immune disease, e.g. rheumatoid arthritis.  
XX Claim 6; Page 82-84; 155pp; English.  
XX 3 Polypeptides (AAW14925-27) respectively comprise the heavy chain  
XX regions of human gamma-4, gamma-4E carrying an L236E mutation in the  
XX hinge region, and gamma-4PE carrying L236E and S229P mutations. They can  
XX be incorporated into novel monoclonal and chimeric antibodies, e.g. CE9  
XX gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in which the human IgG4 FC  
XX binding domain framework is combined with the antigen binding domains  
XX (see also AAW14922-23) of macaque anti- human CD4 monoclonal antibody  
XX E9.1. These antibodies show high affinity to human CD4, have little or no  
XX immunogenicity in humans and show reduced or absence of effector  
XX function. They can be used to treat autoimmune diseases such as  
XX rheumatoid arthritis

Query Match 91.3%; Score 2171; DB 2; Length 467;  
Best Local Similarity 91.7%; Pred. No. 1.1e-122;  
Matches 418; Conservative 7; Mismatches 13; Indels 18; Gaps 4;  
QY 1 QVQLQESGPGLVKPSQTLTCTVSGGSISSGGNYWNIHQHPGKLEWIGIYVSGNT 59  
DB 20 QVQLQESGPGLVKPSQTLTCTVSGGSISSGGNYWNIHQHPGKLEWIGIYVSGGNT 78  
QY 60 YNPISLKRITISIDTSKNQFSLTSSVTAADTAIVYCARDGGDAFDI-----WG 110  
DB 79 YNPISLKRITISIDTSKNQFSLTSSVTAADTAIVYCARDGGDAFDI-----NLT 131  
QY 111 QGTMTVTSASTKGPSVFPPLAPCSRSTSESTAAALGCLVKDYPPEPVTVSWNSGALTSGVH 170  
DB 132 QGVLTVTSASTKGPSVFPPLAPCSRSTSESTAAALGCLVKDYPPEPVTVSWNSGALTSGVH 191  
QY 171 TTPAVLQSSGLYSLSSVTVTPSSSLGTITTCNVDPKPSNTKVDKRVESKYGPPCPSCPA 230  
DB 192 TTPAVLQSSGLYSLSSVTVTPSSSLGTITTCNVDPKPSNTKVDKRVESKYGPPCPSCPA 251  
QY 231 PEFLLGSPVFLPFPKPDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 290  
DB 252 PEFLLGSPVFLPFPKPDLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 311  
QY 291 REEQFNSTYRVVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTL 350  
DB 312 REEQFNSTYRVVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTL 371  
QY 351 PPSQEMTKNQVSLTCLVKGFPSPDIKAVESNGQPNNTKTPPVLDSGDSGFFLYSLRT 410  
DB 372 PPSQEMTKNQVSLTCLVKGFPSPDIKAVESNGQPNNTKTPPVLDSGDSGFFLYSLRT 431  
QY 411 VDKSRWQEGNVFSCSVHMEALHNHYTQKSLSLSLGK 446  
DB 432 VDKSRWQEGNVFSCSVHMEALHNHYTQKSLSLSLGK 467

RESULT 7  
ADE31589  
XX ID ADE31589 standard; protein; 467 AA.  
XX AC ADE31589;  
XX PF





CC function. The gamma-4E and -4PE mutations confer activity enhanced  
CC stability and eliminate depleting activity. The antibodies can be used to  
CC treat autoimmune diseases such as rheumatoid arthritis

XX  
SQ Sequence 467 AA;  
Query Match 91.0%; Score 2164; DB 2; Length 467;  
Best Local Similarity 91.4%; Pred. No. 2.9e-122;  
Matches 417; Conservative 7; Mismatches 14; Indels 18; Gaps 4;  
QY 1 QVQLQESGFLVKPQTLSLTCTVSGGSISSGGNYNNWIRQHPGKLEWIGYIYYS-GNT 59  
DB 20 QVQLQESGFLVKPSETLSLTCSVSGSI-SGDYFWFIRQSPGKLEWIGYIYSGGGT 78  
QY 60 YNPISLKRITISIDTSKNQFSLTSSVTAADTAATVAVYCARDGDDAFDI-----WG 110  
DB 79 NNPISLNNRVISIDTSKNLFSKLRSVTAADTAATVAVYCAS-----NILKYLHMLLYWG 131  
QY 111 QGTMTVTVSSASTKGPVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTVSWNSGALTSGVH 170  
DB 132 QGVLTVTSSASTKGPVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTVSWNSGALTSGVH 191  
QY 171 TTPAVLQSSGLYSLSSVTVVPSSSLGKTYYTCNVDRHKPSNTKVDKRVESKYGPPCPSCPA 230  
DB 192 TTPAVLQSSGLYSLSSVTVVPSSSLGKTYYTCNVDRHKPSNTKVDKRVESKYGPPCPSCPA 251  
QY 231 PFELGSPVFLPPPKPDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNATKP 290  
DB 252 PEFEFGSPVFLPPPKPDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNATKP 311  
QY 291 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 350  
DB 312 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 371  
QY 351 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLRT 410  
DB 372 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLRT 431  
QY 411 VDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLGLK 446  
DB 432 VDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLGLK 467

RESULT 9  
ADE31591  
ID ADE31591 standard; protein; 467 AA.  
XX  
AC ADE31591;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Gamma 4 heavy chain variable/constant domains E mutant.  
XX  
KW chimeric antibody; CD4 antibody; Old World monkey monoclonal antibody;  
KW immunostimulant; antiasthmatic; immunosuppressive; antiarthritic;  
KW antirheumatic; cytostatic; anti-Hiv; CD4 related condition;  
KW autoimmune disorder; rheumatoid arthritis; non-autoimmune disorder;  
KW leukaemia; lymphoma; graft-versus-host diseases; asthma;  
KW transplant rejection; HIV infection; CB9.1; human; gamma 4;  
KW heavy chain variable domain; heavy chain constant domain; E mutant.

XX Homo sapiens.  
XX  
XX US2003077275-A1.  
XX  
XX 24-APR-2003.  
XX  
XX 05-AUG-2002; 2002US-00211357.  
XX  
XX 25-JUL-1991; 91US-00735064.  
XX 23-MAR-1992; 92US-00856281.  
XX 10-JUL-1992; 92US-00912292.  
XX 25-JAN-1995; 95US-00379072.

PR 07-JUN-1995; 95US-00476237.  
PR 06-SEP-1995; 95US-00523894.  
PR 10-JUL-2000; 2000US-00612914.  
XX  
PA (IDEC-) IDEC PHARM CORP.  
XX  
XX Hanna N, Newman RA, Reff ME;  
XX  
XX WPI; 2003-625537/59.  
DR N-PSDB; ADE31590.  
XX  
XX New chimeric anti-CD4 antibodies, useful for treating or preventing a CD4  
PT related conditions, e.g. rheumatoid arthritis, leukemia, lymphoma, graft-  
PT versus-host diseases, asthma, transplant rejection or HIV infection.  
XX  
PS Disclosure; SEQ ID NO 10; 85pp; English.

CC The invention describes a chimeric antibody, which is specific to human  
CC CD4. The chimeric antibody comprises the variable heavy and light chain  
CC sequences of an Old World monkey monoclonal antibody produced against  
CC human CD4, and human constant heavy and light domain sequences. The  
CC chimeric antibody has immunostimulant, antiasthmatic, immunosuppressive,  
CC antirheumatic, cytostatic and anti-HIV properties. The  
CC chimeric antibody is useful in therapy or prophylaxis, particularly for  
CC treating or preventing a CD4 related condition. This condition includes  
CC an autoimmune disorder (e.g. rheumatoid arthritis), a non-autoimmune  
CC disorder (e.g. leukaemia, lymphoma, graft-versus-host diseases, asthma,  
CC transplant rejection or HIV infection), or a condition mediated by or  
CC involving CD4+ cells. This is the amino acid sequence of human gamma 4  
CC heavy chain variable and constant domains E mutant associated with  
CC creation of CB9.1, a monkey/human chimeric antibody with specificity for  
CC CD4.

XX Sequence 467 AA;

Query Match 91.0%; Score 2164; DB 7; Length 467;  
Best Local Similarity 91.4%; Pred. No. 2.9e-122;  
Matches 417; Conservative 7; Mismatches 14; Indels 18; Gaps 4;  
QY 1 QVQLQESGFLVKPQTLSLTCTVSGGSISSGGNYNNWIRQHPGKLEWIGYIYYS-GNT 59  
DB 20 QVQLQESGFLVKPSETLSLTCSVSGSI-SGDYFWFIRQSPGKLEWIGYIYSGGGT 78  
QY 60 YNPISLKRITISIDTSKNQFSLTSSVTAADTAATVAVYCARDGDDAFDI-----WG 110  
DB 79 NNPISLNNRVISIDTSKNLFSKLRSVTAADTAATVAVYCAS-----NILKYLHMLLYWG 131  
QY 111 QGTMTVTVSSASTKGPVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTVSWNSGALTSGVH 170  
DB 132 QGVLTVTSSASTKGPVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTVSWNSGALTSGVH 191  
QY 171 TTPAVLQSSGLYSLSSVTVVPSSSLGKTYYTCNVDRHKPSNTKVDKRVESKYGPPCPSCPA 230  
DB 192 TTPAVLQSSGLYSLSSVTVVPSSSLGKTYYTCNVDRHKPSNTKVDKRVESKYGPPCPSCPA 251  
QY 231 PFELGSPVFLPPPKPDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNATKP 290  
DB 252 PEFEFGSPVFLPPPKPDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNATKP 311  
QY 291 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 350  
DB 312 REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 371  
QY 351 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLRT 410  
DB 372 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLRT 431  
QY 411 VDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLGLK 446  
DB 432 VDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLGLK 467

RESULT 10



CC chimeric antibody has immunostimulant, antiaethmatic, immunosuppressive,  
CC antiarthritic, antirheumatic, cytostatic and anti-HIV properties. The  
CC chimeric antibody is useful in therapy or prophylaxis, particularly for  
CC treating or preventing a CD4 related condition. This condition includes  
CC an autoimmune disorder (e.g. rheumatoid arthritis), a non-autoimmune  
CC disorder (e.g. leukaemia, lymphoma, graft-versus-host diseases, asthma,  
CC transplant rejection or HIV infection), or a condition mediated by or  
CC involving CD4+ cells. This is the amino acid sequence of human gamma 4  
CC heavy chain variable and constant domains PE mutant associated with  
CC creation of CE9.1, a monkey/human chimeric antibody with specificity for  
CC CD4.  
XX  
XX  
SQ Sequence 467 AA;

Query Match 90.8%; Score 2159; DB 7; Length 467;  
Best Local Similarity 91.2%; Pred. No. 5.7e-122;  
Matches 416; Conservative 7; Mismatches 15; Indels 18; Gaps 4;  
Qy 1 QVQLQESGCLVKPSQTLSTCTVSGSSISGGNGYNNWIRQHPGKLEWIGYIYVS-GNT 59  
Db 20 QVQLQESGCLVKPSQTLSTCTVSGSSISGGNGYNNWIRQHPGKLEWIGYIYVS-GGT 78  
Qy 60 YNPPLSKRITISIDTSKQFSLTSLSSVTAADTAVYYCARDDGDDAFDI-----WG 110  
Db 79 YNPPLSKRITISIDTSKQFSLTSLSSVTAADTAVYYCARDDGDDAFDI-----N 131  
Qy 111 QGTMVTSSASTKGPSVFPPLACSRSTSESTAAALGCLVKDYFPEPTVSWNSGALTSGVH 170  
Db 132 QGVLVTSSASTKGPSVFPPLACSRSTSESTAAALGCLVKDYFPEPTVSWNSGALTSGVH 191  
Qy 171 TFPVAVLQSSGLYSLSSVTVFPSSSLGKTKYTCNVHDKPSNTKYDKVESKYGPCCPCA 230  
Db 192 TFPVAVLQSSGLYSLSSVTVFPSSSLGKTKYTCNVHDKPSNTKYDKVESKYGPCCPCA 251  
Qy 231 PEFLLGSPVLPFPKPKDLMISRTPEVTCVVDVSOEDPEVQFNMYVDGVEVHNARTKP 290  
Db 252 PEFEGGSPVLPFPKPKDLMISRTPEVTCVVDVSOEDPEVQFNMYVDGVEVHNARTKP 311  
Qy 291 REQFNSTYRVSVLTVLHQDLNGLKEYCKCKVSNKGLPSSIEKTIKAKGQPREPQVYTL 350  
Db 312 REQFNSTYRVSVLTVLHQDLNGLKEYCKCKVSNKGLPSSIEKTIKAKGQPREPQVYTL 371  
Qy 351 PPQSEMTKQVSLTCLVKFGYPSDIAVEENSGQPENNYKTPPVLDSDGSPFLYSRLT 410  
Db 372 PPQSEMTKQVSLTCLVKFGYPSDIAVEENSGQPENNYKTPPVLDSDGSPFLYSRLT 431  
Qy 411 VDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLGLK 446  
Db 432 VDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLGLK 467

RESULT 12  
ADZ57697 standard; protein; 480 AA.  
XX AC ADZ57697;  
XX AC ADZ57697;  
DT 30-JUN-2005 (first entry)  
XX DE Anti-cMet antibody 9.1.2 heavy chain protein.  
XX antibody engineering; cytostatic; vulnary; vasotropic; cardiant;  
KW monoclonal antibody; heavy chain; light chain; wound healing; skin ulcer;  
KW gastrointestinal ulcer; ischemia; transplant rejection;  
KW myocardial infarction; reperfusion injury; restenosis; angioplasty;  
KW vascular disease; cancer; retinopathy; endometriosis; arthritis;  
KW Alzheimers disease; tumor; glioblastoma; sarcoma; carcinoma; diagnosis;  
KW antibody.  
XX  
OS Homo sapiens.  
XX Key Location/Qualifiers  
FH Peptide 1. .19  
FT

FT Protein /note= "signal peptide"  
FT 20. .480  
FT /note= "mature antibody 9.1.2. heavy chain protein"  
FT 50. .56  
FT /note= "complementarity determining region 1"  
FT 71. .86  
FT /note= "complementarity determining region 2"  
FT 119. .143  
FT /note= "complementarity determining region 3"  
PN GB2404660-A.  
XX  
XX 09-FEB-2005.  
XX 04-AUG-2004; 2004GB-00017384.  
XX 04-AUG-2003; 2003US-0492432P.  
XX (PFIZ ) PFIZER PROD INC.  
XX (ABGE-) ABGENIX INC.  
PI Michaud NR, Kajiji S, Borzillo G, Bedian V, Coleman K, Green LB;  
PI Jia X;  
XX WPI; 2005-145169/16.  
XX N-PSDB; ADZ57696.  
XX Human monoclonal antibody or antigen-binding portion that specifically  
XX binds to c-Met, useful for treating cancer by inhibiting c-Met or for  
XX promoting tissue regeneration and wound healing by activating c-Met.  
PS Claim 6; SEQ ID NO 6; 128pp; English.  
XX The invention relates to a human monoclonal antibody (I) or its antigen-  
XX binding portion that specifically binds to c-Met, comprises a heavy chain  
XX having a fully defined sequence (S1) of 13.3.2 heavy chain, where X2 is  
XX lysine and X4 is threonine, and a light chain having a fully defined  
XX sequence (S2) of 13.3.2 light chain, where X8 is threonine, where both  
XX chains are without a signal sequence. All the sequences are fully defined  
XX in the specification. (I) is useful for the manufacture of a medicament  
XX for treating a hyperproliferative disorder in a subject, where the  
XX antibody or its portion is a c-Met antagonist. (I) is useful for  
XX manufacture of a medicament for promoting wound healing or tissue  
XX regeneration in a subject, where the antibody, antigen-binding portion or  
XX the composition activates c-Met. (I) which has a c-Met agonist activity  
XX is useful in tissue regeneration or wound healing (skin ulcers or gastric  
XX ulcers), or treating ischemia associated with kidney transplant  
XX rejection, for attenuating toxicity associated with cyclosporin treatment  
XX after transplant surgery, for treating myocardial infarction, cardiac  
XX ischemia due to reperfusion injury, restenosis after angioplasty or  
XX vascular diseases. (I) which has a c-Met antagonist activity is useful  
XX for treating cancers of brain, lung, squamous cell, bladder, neck, liver,  
XX prostate, etc., proliferative vitreoretinopathy, proliferative plaque  
XX retinopathy, endometriosis, and arthritis, for inhibiting cellular mitogenic  
XX formation in Alzheimer's disease, inhibiting cellular mitogenic  
XX responses, or for treating tumor, glioblastoma, sarcomas, or carcinomas.  
XX (I) is useful for detecting c-Met in a biological sample in vitro or in  
XX vivo, thus useful for diagnosing c-Met-expressing tumor. (I) has  
XX selectivity for c-Met that is at least 100 times greater than their  
XX selectivity for insulin like growth factor I receptor. This sequence  
XX corresponds to the antibody 9.1.2 heavy chain used in the invention.  
XX  
XX Sequence 480 AA;

Query Match 90.7%; Score 2159.5; DB 9; Length 480;  
Best Local Similarity 88.5%; Pred. No. 6.3e-122;  
Matches 409; Conservative 17; Mismatches 19; Indels 17; Gaps 3;  
Qy 1 QVQLQESGCLVKPSQTLSTCTVSGSSISGGNGYNNWIRQHPGKLEWIGYIYVSQNTY 60  
Db 20 QVQLQESGCLVKPSQTLSTCTVSGSSISGGNGYNNWIRQHPGKLEWIGYIYVSQNTY 79  
Qy 61 YNPPLSKRITISIDTSKQFSLTSLSSVTAADTAVYYCARDDGDDAFDI-----GDDAF- 106

Db 80 YNPSLKSRVTIISVDISKNOFSLKLSVTHAADTAVYICARDGPGKVCSSSTSCVPTGEYYY 139  
QY 107 --DIMGQGTMTVSSASTKGPVFLPLAPCSRSTSESTAALGCLVKDYPPPEVTVSWNSGA 164  
Db 140 GMDVNGQGTTVTVSSASTKGPVFLPLAPCSRSTSESTAALGCLVKDYPPPEVTVSWNSGA 199  
QY 165 LTSGVHTTFAVLQSSGLYLSVTVVPPSSSLGTQYTCNVHDHKPNTKVDKXVESKYGPP 224  
Db 200 LTSGVHTTFAVLQSSGLYLSVTVVPPSSSLGTQYTCNVHDHKPNTKVDKXVESKYGPP 259  
QY 225 CPSCAPEFLGPGSVFLPPPKDITLMISRTPEVTCVVVDVSOEDPEVQFNWYDGVVH 284  
Db 260 CPSCAPP-VAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVQFNWYDGVVH 318  
QY 285 NAKTPREBQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPISIETKISKAKGQPRE 344  
Db 319 NAKTPREBQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPISIETKISKAKGQPRE 378  
QY 345 PQVYTLPPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFF 404  
Db 379 PQVYTLPPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFF 438  
QY 405 LYSRLTVDKSRWQEGNVFSCSVWHEALHNHYTQKSLSLGLK 446  
Db 439 LYSRLTVDKSRWQEGNVFSCSVWHEALHNHYTQKSLSLSPGK 480

RESULT 13

ID AAB36206  
XX AAB36206 standard; protein; 473 AA.  
AC AAB36206;  
XX  
DT 15-FEB-2001 (first entry)  
XX  
DE Human immune system associated protein HISAP-4.  
XX  
KW Human; immune system associated protein; HISAP-4; immune disorder;  
KW infection; autoimmune disease; cancer.  
XX  
OS Homo sapiens.  
XX  
PN US6135941-A.  
XX  
PD 24-OCT-2000.  
XX  
PF 27-MAR-1998; 98US-00049672.  
XX  
PR 27-MAR-1998; 98US-00049672.  
XX  
PA (INCY-) INCYTE PHARM INC.  
PI Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;  
PI Hillman JL, Au-Young J;  
XX  
DR WPI; 2001-030926/04.  
DR N-PSDB; AAC66522.

PT New human immune system associated proteins (HISAP) and polynucleotides  
PT encoding the HISAP, useful for diagnosing, treating or preventing immune  
PT or cell proliferative disorders or infections.  
XX  
PS Claim 1; Col 53-56; 54pp; English.

CC The present invention provides the coding and protein sequences for a  
CC number of human immune system associated proteins (HISAPs). These can be  
CC used in the diagnosis and treatment of various autoimmune disorders,  
CC infections and cell proliferation diseases. The diseases include AIDS,  
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,  
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia  
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus  
CC erythematosus, arteriosclerosis, cirrhosis and cancer

XX Sequence 473 AA;  
SQ  
Query Match 90.0%; Score 2140; DB 4; Length 473;  
Best Local Similarity 89.2%; Pred. No. 8.1e-121;  
Matches 405; Conservative 18; Mismatches 23; Indels 8; Gaps 2;  
QY 1 QVQLQESGPGLVKPSQSLTCTVSGGSISGGNYWMIROHPGKGLGWICVYYSGNTY 60  
Db 20 QVQLQESGPGLVKPSQSLTCTVSGGSISGGNYWMIROHPGKGLGWICVYYSGNTL 79  
QY 61 YNPSLKSRVTIISVDISKNOFSLKLSVTHAADTAVYICARDGPGKVCSSSTSCVPT 115  
Db 80 YNPSLKSRVTIISVDISKNOFSLKLSVTHAADTAVYICARDGPGKVCSSSTSCVPT 139  
QY 116 TVSSASTKGPVFLPLAPCSRSTSESTAALGCLVKDYPPPEVTVSWNSGALTSGVHTTFAV 175  
Db 140 TVSSASTKGPVFLPLAPCSRSTSESTAALGCLVKDYPPPEVTVSWNSGALTSGVHTTFAV 199  
QY 176 LQSSGLYLSVTVVPPSSSLGTQYTCNVHDHKPNTKVDKXVESK---YGPCCSCAPE 232  
Db 200 LQSSGLYLSVTVVPPSSSLGTQYTCNVHDHKPNTKVDKXVESKCDKTHTCPPCAPE 259  
QY 233 FLGGPSVFLPPPKDITLMISRTPEVTCVVVDVSOEDPEVQFNWYDGVVHNAKTGPRE 292  
Db 260 LLGGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVQFNWYDGVVHNAKTGPRE 319  
QY 293 EQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPISIETKISKAKGQPREQVYTLPP 352  
Db 320 EQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPISIETKISKAKGQPREQVYTLPP 379  
QY 353 SQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSRLTV 412  
Db 380 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSRLTV 439  
QY 413 KSRWQEGNVFSCSVWHEALHNHYTQKSLSLGLK 446  
Db 440 KSRWQEGNVFSCSVWHEALHNHYTQKSLSLSPGK 473

RESULT 14

AAO30915  
ID AAO30915 standard; protein; 580 AA.  
XX  
AC AAO30915;  
XX  
DT 22-SEP-2003 (first entry)  
XX  
DE dI-NHS76 (gamma4h) (FN>AQ) -ala-IL2 (D20T) variant protein.  
XX  
KW Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;  
KW gene therapy; immunoglobulin; Ig; fusion protein; human; variant.  
XX  
OS Homo sapiens.  
OS Unidentified.  
OS Chimeric.  
XX  
PN WO2003048334-A2.  
XX  
PD 12-JUN-2003.  
XX  
PF 04-DEC-2002; 2002WO-US038780.  
XX  
PR 04-DEC-2001; 2001US-0337113P.  
PR 12-APR-2002; 2002US-0371966P.  
XX  
XX (EMDL-) EMD LEXIGEN RES CENT CORP.  
XX  
PI Gillies SD;  
XX  
DR WPI; 2003-513757/48.  
XX  
PT New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2



Qy	301	VVS	VT	VL	VL	HQ	DL	NG	KE	YK	CK	V	SN	K	G	L	P	S	S	I	E	K	T	I	S	K	A	G	O	P	R	E	P	O	V	T	L	P	P	S	O	E	E	M	T	K	N	360													
Db	297	VVS	VT	VL	VL	HQ	DL	NG	KE	YK	CK	V	SN	K	G	L	P	S	S	I	E	K	T	I	S	K	A	G	O	P	R	E	P	O	V	T	L	P	P	S	O	E	E	M	T	K	N	356													
Qy	361	QV	S	L	T	C	L	V	K	G	F	Y	P	S	D	I	A	V	E	W	E	S	N	G	O	P	E	N	N	Y	K	T	T	P	P	V	L	D	S	D	G	S	F	F	L	Y	S	R	L	T	V	D	K	S	R	W	Q	E	G	N	420
Db	357	QV	S	L	T	C	L	V	K	G	F	Y	P	S	D	I	A	V	E	W	E	S	N	G	O	P	E	N	N	Y	K	T	T	P	P	V	L	D	S	D	G	S	F	F	L	Y	S	R	L	T	V	D	K	S	R	W	Q	E	G	N	416
Qy	421	VF	S	C	S	V	M	H	E	A	L	H	N	H	Y	T	Q	K	S	L	S	L	G	K	446																																				
Db	417	VF	S	C	S	V	M	H	E	A	L	H	N	H	Y	T	Q	K	S	L	S	L	G	K	442																																				

Search completed: December 17, 2005, 01:18:31  
Job time : 180.048 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 17, 2005, 01:10:58 ; Search time 33.7879 Seconds  
(without alignments)  
1270.061 Million cell updates/sec

Title: US-10-644-277-62  
Perfect score: 2379  
Sequence: 1 QVQLQESGPGLVKPSQTLSL.....MHEALHNHYTQKSLSLGLK 446

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*

- 1: PIR1.\*
- 2: PIR2.\*
- 3: PIR3.\*
- 4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1743	73.3	327	1 G4HU	Ig gamma-4 chain C
2	1605.5	67.5	326	1 G2HU	Ig gamma-2 chain C
3	1590.5	66.9	330	1 GHU	Ig gamma-1 chain C
4	1585	66.6	377	2 A60764	Ig gamma-3 chain C
5	1575	66.2	377	2 A23511	Ig gamma-3 chain C
6	1562.5	65.7	470	2 S22080	Ig heavy chain pre
7	1521.5	64.0	472	2 S31459	Ig gamma-1 chain r
8	1427.5	60.0	374	2 S69339	Ig heavy chain V r
9	1422	59.8	469	2 S37483	Ig gamma-2a chain
10	1411.5	59.3	446	2 S40295	Ig gamma-2a chain
11	1367	57.5	444	2 PC4336	monoclonal antibody
12	1311.5	55.1	474	1 G2M511	Ig gamma-2b chain
13	1303	54.8	475	2 S01321	Ig gamma-2b chain
14	1289.5	54.0	328	2 I47159	Ig gamma 2a chain
15	1283.5	54.0	328	2 I47160	Ig gamma 2b chain
16	1264.5	53.2	328	2 I47161	Ig gamma 3 chain c
17	1240.5	52.1	328	2 I47158	Ig gamma 1 chain c
18	1199	50.4	323	1 GHRB	Ig gamma chain C r
19	1162	48.8	329	1 G2GP	Ig gamma-2 chain C
20	1147	48.2	308	2 C30554	Ig heavy chain C r
21	1139.5	47.9	255	4 S31866	Ig gamma-1 chain C
22	1129.5	47.5	234	2 PT0207	Ig gamma chain C r
23	1124	47.2	333	2 PS0018	Ig gamma-2b chain C
24	1118.5	47.0	326	2 PS0017	Ig gamma-1 chain C
25	1108.5	46.6	289	1 G3HUM1	Ig gamma-3 heavy c
26	1108	46.6	329	2 S00847	Ig gamma-2c chain
27	1106.5	46.5	324	1 GIMS	Ig gamma-1 chain C
28	1106.5	46.5	330	1 G2MSA	Ig gamma-2a chain
29	1103	46.4	327	2 S06611	Ig gamma-2 chain C

ALIGNMENTS

RESULT 1

G4HU

Ig gamma-4 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text\_change 09-Jul-2004

C:Accession: A90933; A90249; A02150

R:Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A:Reference number: A90933; MUID:83157104; PMID:6299662

A:Accession: A90933

A:Molecule type: DNA

A:Residues: 1-327 <ELL>

A:Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190

A>Note: The sequence was determined from the germline gene

R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A:Title: Human immunoglobulin subclases. Partial amino acid sequence of the constant r

A:Reference number: A90249; MUID:70207560; PMID:4192699

A:Accession: A90249

A:Molecule type: protein

A:Residues: 1-30;81-326 <PIN>

A:Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796

C:Genetics:

A:Gene: GDB:IGHG4

A:Cross-references: GDB:119340; OMIM:147130

A:Map position: 14q32.33-14q32.33

A:Introns: 99/1; 111/1; 221/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F;20-85/Domain: immunoglobulin homology <IM1>

F;99-110/Region: hinge

F;134-203/Domain: immunoglobulin homology <IM2>

F;240-307/Domain: immunoglobulin homology <IM3>

F;14/disulfide bonds: interchain (to light chain) #status experimental

F;27-83,141-201,247-305/Disulfide bonds: #status predicted

F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 73.3%; Score 1743; DB 1; Length 327;

Best Local Similarity 100.0%; Pred. No. 3.3e-93;

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVWSNLSGALTSGVHTFPAVLQSS 179

Db 1 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVWSNLSGALTSGVHTFPAVLQSS 60

QY 180 GLYSLSVVTVPSSSLGTQTYTCNDVHKPSNTKVDKRVESKYGPPCPAPFELGPPSV 239

Db 61 GLYSLSVVTVPSSSLGTQTYTCNDVHKPSNTKVDKRVESKYGPPCPAPFELGPPSV 120



QY 240 FLPPKPKDTLMISRTPEVTCVVVDVSDPEDEVQFNWYVDGVGVNAKTKEPPEQFNSTY 299  
DB 121 FLPPKPKDTLMISRTPEVTCVVVDVSDPEDEVQFNWYVDGVGVNAKTKEPPEQFNSTY 180  
QY 300 RVSVLTVLHQLDNLGKEYCKVSKNGKLPSSISIEKTSKAKGQPREPQVYVTLPPSQEEMTK 359  
DB 181 RVSVLTVLHQLDNLGKEYCKVSKNGKLPSSISIEKTSKAKGQPREPQVYVTLPPSQEEMTK 240  
QY 360 NQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSLRTVDKSRWQEG 419  
DB 241 NQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSLRTVDKSRWQEG 300  
QY 420 NVFSCSVNHEALHNHYTQKSLSLGLK 446  
DB 301 NVFSCSVNHEALHNHYTQKSLSLGLK 327

RESULT 2  
G2HU  
Ig gamma-2 chain C region - human  
A:Species: Homo sapiens (man)  
C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text\_change 09-Jul-2004  
A:Accession: A93906; A92809; A90752; A93132; A02148  
R:Ellison, J.; Hood, L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con  
A:Reference number: A93906; MUID:82197621; PMID:6804948  
A:Accession: A93906  
A:Molecule type: DNA  
A:Residues: 1-326 <ELL>  
A:CROSS-references: UNIPROT:P01859; UNIPARC:UPI000003BFCC; GB:V00554; GB:J00230; NID:g32  
A:Note: Lys-326 is probably removed posttranslationally  
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f  
A:Reference number: A92809; MUID:81007873; PMID:6774012  
A:Contents: myeloma protein Til  
A:Accession: A92809  
A:Molecule type: protein  
A:Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>  
A:CROSS-references: UNIPARC:UPI0000173791  
A:Note: Trp-156 is at or near the complement-binding site  
R:Connell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A:Title: The amino acid sequences of the three heavy chain constant region domains of a  
A:Reference number: A90752; MUID:80001357; PMID:113060  
A:Contents: myeloma protein Zie  
A:Accession: A90752  
A:Molecule type: protein  
A:Residues: 1-24,'B',26-57,'EV',60-85,132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-  
A:CROSS-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793  
A:Note: this sequence has since been revised  
R:Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin G  
A:Reference number: A93132; MUID:80114419; PMID:118920  
A:Contents: Zie  
A:Accession: A93132  
A:Molecule type: protein  
A:Residues: 238-275 <HOF>  
A:CROSS-references: UNIPARC:UPI0000173794  
R:Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A:Reference number: A94591  
A:Contents: annotation: Zie, revisions to residues 25, 59, 60, and 264-268  
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidati  
ned  
R:Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.  
A:Reference number: A90253; MUID:72033500; PMID:4940472  
A:Contents: annotation; myeloma protein Sa, disulfide bonds

R:Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A:Title: Structural studies of immunoglobulin G.  
A:Reference number: A93157; MUID:69064124; PMID:5782707  
A:Contents: annotation; Sa, disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG2  
A:CROSS-references: GDB:119338; OMIM:147110  
A:Map position: 14q32.33-14q32.33  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lai  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:133-202/Domain: immunoglobulin homology <IM2>  
F:239-306/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83,140-200,246-304/Disulfide bonds: #status experimental  
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.5%; Score 1605.5; DB 1; Length 326;  
Best Local Similarity 92.4%; Pred. No. 2.6e-85;  
Matches 302; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

QY 120 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSNWSGALTSGVHTFPAVLQSS 179  
DB 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSNWSGALTSGVHTFPAVLQSS 60  
QY 180 GLYSLSSVTVTPSSSLGKTKVTCNVDPKSNSTKVDRVESKYGPPCPSCPAPEFLGGPSV 239  
DB 61 GLYSLSSVTVTPSSNFGTQVTCNVDPKSNSTKVDRVERKCCVCEPCPAPP-VAGPSV 119  
QY 240 FLPPKPKDTLMISRTPEVTCVVVDVSDPEDEVQFNWYVDGVGVNAKTKEPPEQFNSTY 299  
DB 120 FLPPKPKDTLMISRTPEVTCVVVDVSDPEDEVQFNWYVDGVGVNAKTKEPPEQFNSTF 179  
QY 300 RVSVLTVLHQLDNLGKEYCKVSKNGKLPSSISIEKTSKAKGQPREPQVYVTLPPSQEEMTK 359  
DB 180 RVSVLTVLHQLDNLGKEYCKVSKNGKLPSSISIEKTSKAKGQPREPQVYVTLPPSQEEMTK 239  
QY 360 NQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSLRTVDKSRWQEG 419  
DB 240 NQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSLRTVDKSRWQEG 299  
QY 420 NVFSCSVNHEALHNHYTQKSLSLGLK 446  
DB 300 NVFSCSVNHEALHNHYTQKSLSLSPGK 326

RESULT 3  
G2HU  
Ig gamma-1 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text\_change 09-Jul-2004  
A:Accession: A93433; S36861; S3887; B90563; A90564; B91688; A91723; A02146  
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.  
Nucleic Acids Res. 10, 4071-4079, 1982  
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.  
A:Reference number: A93433; MUID:82274238; PMID:6287432  
A:Accession: A93433  
A:Molecule type: DNA  
A:Residues: 1-330 <ELL>  
A:CROSS-references: UNIPROT:P01857; UNIPARC:UPI0000034C0E; EMBL:Z17370  
A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers, ;  
A:Note: Lys-330 is removed after translation  
R:Harris, L.J.  
submitted to the EMBL Data Library, October 1992  
A:Reference number: S33904  
A:Accession: S36861  
A:Molecule type: DNA  
A:Residues: 2-330 <HAR>  
A:CROSS-references: UNIPARC:UPI0000013C6FE; EMBL:Z17370



R;Takahaehi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.  
Cell 29, 671-679, 1982  
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a  
A;Reference number: S33887; MUID:83001943; PMID:6811139  
A;Accession: S33887  
A;Molecule type: DNA  
A;Residues: 88-113;235-330 <TAK>  
A;Cross-references: UNIPARC:UPI0000173788; UNIPARC:UPI000017378C; EMBL:Z17370  
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,  
Biochemistry 9, 3161-3170, 1970  
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen  
A;Reference number: A90563; MUID:71064024; PMID:5489771  
A;Contents: myeloma protein Eu  
A;Accession: B90563  
A;Molecule type: protein  
A;Residues: 1-96, 'R', 98-135 <CUN>  
A;Cross-references: UNIPARC:UPI000017378D  
A;Note: this sequence has the G1m(3) marker, 97-Arg  
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
Biochemistry 9, 3171-3181, 1970  
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen  
A;Reference number: A90564; MUID:71064025; PMID:5530842  
A;Contents: Eu  
A;Accession: A90564  
A;Molecule type: protein  
A;Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,  
A;Cross-references: UNIPARC:UPI000017378E  
A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met  
R;Ponstingl, H.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
A;Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),  
igen Primärstruktur.  
A;Reference number: A91668; MUID:77070269; PMID:826475  
A;Contents: myeloma protein Nie  
A;Accession: B91668  
A;Molecule type: protein  
A;Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'O', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27  
A;Cross-references: UNIPARC:UPI000017378F  
A;Note: this sequence has the G1m(17) and G1m(1) markers  
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A;Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL  
A;Reference number: A91723; MUID:83289131; PMID:6884994  
A;Contents: myeloma protein KOL; disulfide bonds  
A;Accession: A91723  
A;Molecule type: protein  
A;Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH  
A;Cross-references: UNIPARC:UPI0000173790  
A;Note: this sequence has the G1m(3) and G1m(non-1) markers  
R;Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
A;Reference number: A90565; MUID:71064027; PMID:4923144  
A;Contents: annotation; disulfide bonds  
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
enbromide cleavage products, and the disulfide bridges.  
A;Reference number: A91667; MUID:77070267; PMID:1002129  
A;Contents: annotation; disulfide bonds  
A;Genetics:  
A;Gene: GDB:IGHG1  
A;Cross-references: GDB:120085; OMIM:147100  
A;Map position: 14q32.33-14q32.33  
A;Introns: 99/1; 114/1; 224/1  
A;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IM1>  
F;137-206/Domain: immunoglobulin homology <IM2>  
F;243-310/Domain: immunoglobulin homology <IM3>  
F;27-83, 144-204, 250-308/Disulfide bonds: #status experimental

F;103/Disulfide bonds: interchain (to light chain) #status experimental  
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F;180/Binding site: carbohydrate (Aen) (covalent) #status experimental

Query Match 66.9%; Score 1590.5; DB 1; Length 330;  
Best Local Similarity 90.9%; Pred. No. 1.9e-84;  
Matches 300; Conservative 12; Mismatches 15; Indels 3; Gaps 1;

QY 120 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179  
Db 1 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
QY 180 GLYSLSSVTVTPSSSLGTTTCNVDPKPSNTKVDKRVESK---YGPCPCSPAPPEFLGG 236  
Db 61 GLYSLSSVTVTPSSSLGTTTCNVDPKPSNTKVDKRVESKCDKTHTCPPCAPPELLGG 120  
QY 237 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNAKTKPREEQFN 296  
Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQFN 180  
QY 297 SYRIVVSVLTQLHQQDLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQBE 356  
Db 181 SYRIVVSVLTQLHQQDLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSRDE 240  
QY 357 MTKNQVSLTCLVKGYFIPSDIAVEWESNGOPENNYKTTTPPVLSDSGSFFLYSLRTVDDKSRW 416  
Db 241 LTKNQVSLTCLVKGYFIPSDIAVEWESNGOPENNYKTTTPPVLSDSGSFFLYSLRTVDDKSRW 300  
QY 417 QGQNVFSCVMHEALHNNHYTKLSLSLQK 446  
Db 301 QGQNVFSCVMHEALHNNHYTKLSLSLQK 330

RESULT 4  
A60764  
Ig gamma-3 chain C region, form LAT - human  
C;Species: Homo sapiens (man)  
C;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 31-Dec-2004  
C;Accession: A60764  
R;Huck, S.; Lefranc, G.; Lefranc, M.P.  
Immunogenetics 30, 250-257, 1989  
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, bl, c3, c5, u) with an IGHG4 convert  
A;Reference number: A60764; MUID:90007613; PMID:2571587  
A;Accession: A60764  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-377 <HUC>  
A;Cross-references: UNIPROT:Q9N4Y9; UNIPARC:UPI0000176F0B  
C;Superfamily: immunoglobulin homology  
C;Keywords: immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 66.8%; Score 1585; DB 2; Length 377;  
Best Local Similarity 80.6%; Pred. No. 4.6e-84;  
Matches 304; Conservative 8; Mismatches 15; Indels 50; Gaps 1;

QY 120 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179  
Db 1 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
QY 180 GLYSLSSVTVTPSSSLGTTTCNVDPKPSNTKVDKRVESK----- 220  
Db 61 GLYSLSSVTVTPSSSLGTTTCNVDPKPSNTKVDKRVESKPLDGTTHTCPCPEPKSC 120  
QY 221 -----YGPCPCSPAPPEFLGGPSVFLPPPKPDT 249  
Db 121 DTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPEPKPDT 180  
QY 250 LMTSRTPETCVVVDVSDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTVTVSVLTVLH 309  
Db 181 LMTSRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQFNSTVTVSVLTVLH 240  
QY 310 QDMLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQBEIMTKNQVSLTCLVK 369

Db 241 QDWLNGKEYKCVSNKALPAPIEKIISKTKGQPRFPQVYTLPPSREEMTKQVSLTCLVK 300  
QY 370 GYPYSDIAVEWESNGQPNYYKTTTPVLDSDGFFLYSLRTVDKSRWQEGNVFSCVMHE 429  
Db 301 GFYPYSDIAVEWESSGQPNYYNTTPVLDSDGFFLYSLRTVDKSRWQEGNVFSCVMHE 360  
QY 430 ALHNHYTQKSLSLSLGK 446  
Db 361 ALHNRFQKSLSLSPGK 377  
RESULT 5  
A23511  
Ig gamma-3 chain C region (allotype G3m(b)) - human  
C:Species: Homo sapiens (man)  
C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999  
C:Accession: A23511  
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.  
Nucleic Acids Res. 14, 1779-1789, 1986  
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: c  
A:Reference number: A23511; MUID:86148507; PMID:3081877  
A:Accession: A23511  
A:Molecule type: DNA  
A:Residues: 1-377 <HUC>  
A:Cross-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12958; NID:G33070; PIDN:CAA272  
C:Genetics:  
A:Gene: GDB:IGHG3  
A:Cross-references: GDB:119339; OMIM:147120  
A:Map position: 14q32.33-14q32.33  
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IMM>  
Query Match 66.2%; Score 1575; DB 2; Length 377;  
Best Local Similarity 79.6%; Pred. No. 1.7e-83;  
Matches 300; Conservative 12; Mismatches 15; Indels 50; Gaps 1;  
QY 120 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 179  
Db 1 ASTKGPSVFPLAPCSRSTSGGTAAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 60  
QY 180 GLYSLSVVTVPSLSLGTYYTCNVVDHKPSNTKVDKRVESK----- 220  
Db 61 GLYSLSVVTVPSLSLGTYYTCNVNHHKPSNTKVDKRVELKTPPLGDTHTTCPRCEPKSC 120  
QY 221 -----YGPSPCPAPEFLGGPSVFLFPKPKDT 249  
Db 121 DTPPPCPCEPKSCDTPPPCPCEPKSCDTPPPCPAPELGGPSVFLFPKPKDT 180  
QY 250 LMISRTPEVTCVVVDVSDPEQFNWYVDGVEFHNAKTKPREQFNSTYRVVSVLTVLIH 309  
Db 181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEFHNAKTKPREQFNSTYRVVSVLTVLIH 240  
QY 310 QDWLNGKEYKCKVSNKGLPSSTEKTIISKAKGQPRFPQVYTLPPSREEMTKQVSLTCLVK 369  
Db 241 QDWLNGKEYKCKVSNKALPAPIEKIISKTKGQPRFPQVYTLPPSREEMTKQVSLTCLVK 300  
QY 370 GYPYSDIAVEWESNGQPNYYKTTTPVLDSDGFFLYSLRTVDKSRWQEGNVFSCVMHE 429  
Db 301 GFYPYSDIAVEWESSGQPNYYNTTPVLDSDGFFLYSLRTVDKSRWQEGNVFSCVMHE 360  
QY 430 ALHNHYTQKSLSLSLGK 446  
Db 361 ALHNRFQKSLSLSPGK 377

RESULT 6  
S22080  
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine  
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)  
C:Species: Bos primigenius taurus (cattle)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S22080; S06610; A31303  
R:Sanders, P.G.  
submitted to the EMBL Data Library, November 1991  
A:Reference number: S22080  
A:Accession: S22080  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-470 <SAN>  
A:Cross-references: UNIPARC:UPI0000116007; EMBL:X62916; NID:G439; PIDN:CAA44699.1; PID:G4  
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.  
Mol. Immunol. 26, 841-850, 1989  
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma  
A:Reference number: S06610; MUID:90097956; PMID:2513487  
A:Accession: S06610  
A:Molecule type: DNA  
A:Residues: 142-470 <SYM>  
A:Cross-references: UNIPARC:UPI0000176F36; EMBL:X16701  
A>Note: the sequence was determined from the germline gene  
C:Genetics:  
A:Gene: IG CH gamma-1  
A:Introns: 98/1; 111/1; 221/1  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein  
F:161-225/Domain: immunoglobulin homology <IMM>  
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 65.7%; Score 1562.5; DB 2; Length 470;  
Best Local Similarity 66.5%; Pred. No. 1.2e-82;  
Matches 302; Conservative 49; Mismatches 92; Indels 11; Gaps 6;  
QY 1 QVQLQESGPGLVKPSQTLSTLTCTVSGGSISSGNGYNNWIRQHPGKLEWIGYIYSGNTY 60  
Db 20 QVQLRESGPGLVKPSQTLSTLTCTVSGFSLSSYA--LTMVROAPKALEWVGGITSGGTTY 77  
QY 61 YNPILKSRITISIDTSKNQFSLTLSSVTAADTAVVYCAR----DGGDDAF-DINGQGTMV 115  
Db 78 YNPALKSRLSITKENSQVSLSVSTPEDTATYYCARSTYGEVGDGAIADANGQGLLV 137  
QY 116 TVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVWNSGALTSGVHTFPAV 175  
Db 138 TVSSASTTAPKVPYPLSLSCCGDKSSSTVTLGCLVSYMPPEPTVTWNSGALKSGVHTFPAV 197  
QY 176 LQSSGLYSLSVVTVPSLSLGTYYTCNVVDHKPSNTKVDKEVSKYGP-PCPSCPAPEFL 234  
Db 198 LQSSGLYSLSVVTVPSLSTGSG--QTFTCNVAHPASSTKVDKAVDPTCKPSPCDCCPPPELP 256  
QY 235 GGPSVFLFPKPKDPTLMISRTPEVTCVVVDVSDPEQFNWYVDGVEFHNAKTKPREEQ 294  
Db 257 GGPSVFLFPKPKDPTLISGTPEVTCVVVDVGHDDPEVKSFWFVDDVEVNTATYKPREEQ 316  
QY 295 FNSTYRVVSVLTVLIHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPRFPQVYTLPPSQ 354  
Db 317 FNSTYRVVSVLARIHQDWLTGSGEKPKVHNEGLPAPIVRTISRTKGPAREPQVYVLAPPQ 376  
QY 355 EEMTKNQVSLTCLVKGYFSPDSIAVEWESNGCP--ENNYKITPPVLDSDGSFSLSLRTVD 412  
Db 377 EELSKSTVSLTCLVKGYFSPDSIAVEWESNGCP--ENNYKITPPVLDSDGSFSLSLRTVD 436  
QY 413 KSRWQEGNVFSCVMHEALHNHYTQKSLSLSLGK 446  
Db 437 RNSWQEGDYYTCVVNHEALHNHYTQKSLSLGK 470  
RESULT 7  
S31459  
Ig gamma-1 chain - sheep (fragment)  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Jul-1999  
C:Accession: S31459  
R:Patric, S.; Nau, F.  
submitted to the EMBL Data Library, December 1992  
A:Reference number: S31459

A:Accession: S31459  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-472 <PAT>  
C:Cross-references: UNIPARC:UPI0000176F35; EMBL:X69797  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:277-346/Domain: immunoglobulin homology <IMM>

Query Match 64.0%; Score 1521.5; DB 2; Length 472;  
Best Local Similarity 63.6%; Pred. No. 2.6e-80;  
Matches 293; Conservative 54; Mismatches 93; Indels 21; Gaps 5;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYNNWIRQHPGKLEWIGYIYSGNTY 60  
DB 18 QVRLQESGPGSLATLLQTLSTVCTTCTSSLNYYG--VDWVRQAPGKALEWIGSGYDEDID 75  
QY 61 YNPPLSKRITISIDTSKNQFSLTSSVTAADTAAYVYCARDGGDD-----AFDIWGQGT 113  
DB 76 YNPVLKSRISITKDTSKSQVSLTSLVTTEDTAAYVYCARVDYDSSHAPAYASYDFMGPG 135  
QY 114 MVTVSASTKGPSVFPPLAPCSRSTSTAAALGCLVKDYPPPEPTVSWNSGALTSVGHVTP 173  
DB 136 LISVLSASTTPPKVYELTSCGDTSSIVTLGCLVSSYMPPEPTVTVNSGALTSVGHVTP 195  
QY 174 AVLOSSGLYSLSSVTVPPSSLTGKTYTCNVDRHKPSNTKVDKVESKYGPPCP 227  
DB 196 AILQSSGLYSLSSVTVPPASTSGAQTFICNVHPASSTKVDKRVE-----PGCPDPCKHCR 251  
QY 228 CPAPEFLGGPSVFLFPKPKDLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAK 287  
DB 252 CPPPELPGGPSVFIFFPKPKDITISGTEVTCVVVDVQDDPEVQFNFVDNVEVTRAR 311  
QY 288 TKPREQFNSTYRWSVLTVLHQQDLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQV 347  
DB 312 TKPREQFNSTYRWSVLTVLHQQDLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQV 371  
QY 348 YTLPPQSEMTKNQVSLTCLVKGFYPSDIAVEWESNGP--ENNYKTTTPVLDSDSGSFFL 405  
DB 372 YVLAPEQELSKSLTSLVTLVTFYFDYIAVEWQKNGQPESEDKYGTITTSQLDADGSYFL 431  
QY 406 YSRLLTVDKSRWQSGNWFSCSVMEALHNNHYTKQSLSLSLGK 446  
DB 432 YSRLLTVDKSRWQSGNWFSCSVMEALHNNHYTKQSLSLSLGK 472

RESULT 8  
S69339  
IG heavy chain V region precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C:Accession: S69339; S72664  
R:Khamilich, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A:Reference number: S69339; PMID:95262687; PMID:7744049  
A:Accession: S69339  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-374 <KHA>  
C:Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695  
R:Khamilich, A.A.  
submitted to the EMBL Data Library, September 1994  
A:Reference number: S72664  
A:Accession: S72664  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140, 'C', 142-374 <KH2>  
C:Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 60.0%; Score 1427.5; DB 2; Length 374;  
Best Local Similarity 62.7%; Pred. No. 5e-75;

Matches 282; Conservative 27; Mismatches 42; Indels 99; Gaps 4;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYNNWIRQHPGKLEWIGYIYSGNTY 60  
DB 20 QITLKESGPTLVKPTQTLTCTTSGFSLSKSGVGVWIRQPPGQALEWALIFWDDDKR 79  
QY 61 YNPPLSKRITISIDTSKNQFSLTSSVTAADTAAYVYCARD-----CGDDAFDIWGQGTMTV 116  
DB 80 YSPSLRTRLTITKDTSKNQVVLTMVNDPADTATYCYGYSVEGYGQYRFHSGQGTTLV 139  
QY 117 VSSASTKGPSVFPPLAPCSRSTSTAAALGCLVKDYFPEPTVTVSWNSGALTSVGHVTPAVL 176  
DB 140 VSS-----EPKSCD----- 148  
QY 177 QSSGLYSLSSVTVPPSSLTGKTYTCNVDRHKPSNTKVDKVESKYGPPCPSPAPPEFLGG 236  
DB 149 -----KTHT----- 164  
QY 237 PSVFLFPPKPKDLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPREEQN 296  
DB 165 PSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQN 224  
QY 297 STYRVSVLTVLHQQDLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVTVLPPSQE 356  
DB 225 STYRVSVLTVLHQQDLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVTVLPPSQE 284  
QY 357 MTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDSGSFFLYSLTVDKSRW 416  
DB 285 MTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDSGSFFLYSLTVDKSRW 344  
QY 417 QSGNWFSCSVMEALHNNHYTKQSLSLSLGK 446  
DB 345 QSGNWFSCSVMEALHNNHYTKQSLSLSLGK 374

RESULT 9  
S37483  
IG gamma-2a chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S37483  
R:Ducancel, F.F.D.  
submitted to the EMBL Data Library, February 1993  
A:Reference number: S37483  
A:Accession: S37483  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-469 <DUC>  
C:Cross-references: UNIPARC:UPI000002FB47; EMBL:X70423; NID:G406252; PIDN:CAA49868.1; PII:61  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 59.8%; Score 1422; DB 2; Length 469;  
Best Local Similarity 59.7%; Pred. No. 1.3e-74;  
Matches 271; Conservative 71; Mismatches 100; Indels 12; Gaps 7;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYNNWIRQHPGKLEWIGYIY-YSNGT 59  
DB 20 QIQLQSGPELVKPGASVKISCKASGYTFTD--YYINWVQKPGQGLKIGWIGLYPASGNT 77  
QY 60 YNPPLSKRITISIDTSKNQFSLTSSVTAADTAAYVYCARDGGDDA--FDIWGQGTMTV 117  
DB 78 KTNENFKGATLTVDTSSTAYKQLSSLTSEDVAVFCARANGATATLLDYMGGQGTTLV 137  
QY 118 SSASTKGPSVFPPLAPCSRSTSTAAALGCLVKDYFPEPTVTVSWNSGALTSVGHVTPAVLQ 177  
DB 138 SSAKTTAPSVYPLAPVCGDTGSSVTLGCLVKGYFPEPTVTLTWSGSLSSGVTTPAVLQ 197  
QY 178 SSGLYSLSSVTVPPSSLTGKTYTCNVDRHKPSNTKVDKVESKYGP---PCP---SCPAP 232  
DB 198 SD-LYTLSSSVTVTSWPSQITCNVAHPASSTKYDKKIEPR-GPTIKPCPPCKCPAPN 255

Qy	233	FLGGSPVFLPPPKPKD	TLMISRTPEVTCVVVDVQSD	DEPQVFNWYGVGVHN	AKTKPRE	292
Db	256	LLGGSPVFIFPPKIKD	VLMISSLPTTCVVVDVSD	EDPDVQISWFN	VNNVHFAQTQTHR	315
Qy	293	EQNSTYRVVSVLTVL	HWDLNGKVKCKVSKG	LPSIEKTI	SKAKGQPREPVVTLPP	352
Db	316	EDYNTLRVVSALP	IQHDSWGRFKCKV	NNKDLPA	PIERTISKPGSVRA	PVVVLP 375
Qy	353	SOEEMTKNOVSLTCL	VKGYPYSDIAV	EWESNGQPN	NYKTPVPLDS	SGSFYLSRLTVD 412
Db	376	PEEEMTKQVTLCT	WTDMPEDIV	YEWTTNGK	TELNYKTEPVL	DSDSGSFYMSKLVE 435
Qy	413	KSRQEGNVFSCV	MHEALH	NYHTOK	SLSLGK	446
Db	436	KKWVBRNYSYCS	VVHGGV	LHNHTTK	SPSRTPGK	469

RESULT 10

S40295  
Ig gamma-2a chain (mAb735) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 09-Jul-2004  
C/Accession: S40295  
R/Kiebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bi  
submitted to the EMBL Data Library, January 1993  
A/Description: Primary structure of the murine monoclonal Ig2a antibody mAb735 against  
A/Reference number: S40295  
A/Accession: S40295  
A/Molecule type: protein  
A/Residues: 1-446 <KLE>  
A/Cross-references: UNIPROT:Q99L25; UNIPARC:UPI0000176F38  
C/Genetics:  
A/Map position: 12  
C/Superfamily: immunoglobulin C region; immunoglobulin homology  
C/Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid  
F/1-446/Product: Ig gamma-2a chain #status experimental <WAT>  
F/1-117/Domain: V-D-J region <VDJ>  
F/118-446/Domain: C region <CHR>  
F/118-214/Domain: C1 region <CH1>  
F/215-230/Region: hinge  
F/231-340/Domain: C2 region <CH2>  
F/341-446/Domain: C3 region <CH3>  
F/360-427/Domain: immunoglobulin homology <IMM>  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F/22-96,144-199,281-321,367-425/Disulfide bonds: #status predicted  
F/132/disulfide bonds: interchain (to light chain) #status predicted  
F/224,227,229/Disulfide bonds: interchain #status predicted  
F/297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 59.3%; Score 1411.5; DB 2; Length 446;  
Best Local Similarity 59.6%; Pred. No. 5.1e-74;  
Matches 269; Conservative 71; Mismatches 100; Indels 11; Gaps 7

	Qy	1	OQLOQSGPGLVYKPGQTLSLTCVTWSGGSISSGNNWNIROHCKGLEWTGYIV--YSGNT	59
	Dd	1	OQLOQSGPELVPRGASVKISCKAGSYFTFD--YYIIHWQRPGEGLEWLGWIYPGSGNT	58
	Qy	60	YNPNLSKRITISIDITSKNQFSLTSSVTAADTAVYICARDGGDDAFDIWGQGTMTVTSS	119
	Dd	59	KYNEKPKGRATLTVDTSSTAYMQLSSLTSEDSAVYFCAR-GGKFAMDYGQGTSTVTSS	117
	Qy	120	ASTKGSPVEPLAPCSRSTSESTAALGCGLVKQYFPPEPTVTVSNSGALTSGVHTTPAVLQSS	179
	Dd	118	AKTAPESVYPLAPVCGDITGGSVTLGCGLVKGYFPPEPTVLTWNSSGLSSGVHTTPAVLQSD	177
	Qy	180	GLYSLSVVTVTPSSLSGTIKTCNVNDHKPSNTKVDKVESKYGP---PCP--SCPAPFL	234
	Dd	178	-LYLTSSSVTVTSSWPQSQISTCNVAHPASTTKVDKKIEPR-GPTIKPCDPCCKCAPNULL	235
	Qy	235	GBSVELFPKPDKDTLMISRTPENTCVVVDVSQEDPEVQNWWYVDGVHEVNNAKTKPREQ	294
	Dd	236	GGPSVIPFPKPIKDVLMLSLSPMTVCVVYDVSEDPPQVISFWFNANVELIATAQTHRED	295

Qy	295	FNSTRVVRVSVLTVLHODWLNGKEYCKVSNKGLPSS	TEKTLISKAKQDREPQVYTLPPSQ	354
Db	296	FNSTRVVRVSVLPIQHODWMSGKFKCVNNKDL	PAPTELTISKPKGSVRAPQVYVLPPE	355
Qy	355	EEMTKNQVSLTCLVKGYPSDIAVEWSNGQENNYKT	PVLDSGSGFFLYSRLTVDKKS	414
Db	356	EEMTKKQVLTUCMVYDPMPEDIYVEWTNNGKTEL	NYKNTPEVLDSGSGYFMYSKLURVEKK	415
Qy	415	RWQEGNVFSCSVMEALHNHYTKQSLSLSG		445
Db	416	NWVERNSYSCSVVHGEGLNHHHTKFSFRTPG		446

RESULT 11

PC4436  
monoclonal antibody 13-1 heavy chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jan-2000  
C:Accession: PC4436  
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.;  
Biochem. Biophys. Res. Commun. 240, 566-572, 1997  
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against  
A:Reference number: JC5810; MUID:98063277; PMID:9398605  
A:Accession: PC4436  
A:Molecule type: protein  
A:Residues: 1-444 <AKA>  
A:Cross-references: UNIPARC:UPI0000176F41  
C:Comment: This catalytic antibody has peroxidase oxidase activity. It is directed  
C:Superfamily: immunoglobulin Cregion; immunoglobulin homology  
F:251-320/Domain: immunoglobulin homology <IMM>  
F:22/Disulfide bonds: interchain (to 98) #status predicted  
F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match	57.5%;	Score 1367;	DB 2;	Length 444;
Best Local Similarity	58.0%;	Pred. No. 1.8e-71;		
Matches 262;	Conservative	69;	Mismatches 107;	
			Indels 14;	Gaps 7

Qy	1	QVQLQESGGPGVLRPSPQTLSTCTVSGSISGGNY--NWNIHQHPGKGLIEWIGYIYSGNT	59
Db	1	EVQVETGGGLVRPGNSLKLSCLTSGTFS---NYRHWLRLQPPGKRLIEWTAIVTVKSDN	57
Qy	60	Y---YNPSLKSRIITISDTSKNQPSLTLSSTVAADTAIVYCARGGDDAFDIWGQGTMTV	116
Db	58	YGAKYAESVGRFTIISRDDSKSVYLQMNRLREEDTATYYCCRPWVYAMDGCGGTSVI	117
Qy	117	VSSASTKGPSVFPLAPCSRSTSESTAALGCLLVKQYFPEPVTVVSNNSGALTTSGVHTFPVL	176
Db	118	VSSAKTTPPSVPLAPGSAAGTNSMTLGLLVKGYFPEPVTVTVSNSSGLSSGVHTFPVL	177
Qy	177	QSGLYSLSSVTVPSSSLGTHKTVTCNVDDHKPSNTKVDKRVESK--YGPSPSCPAPRPL	234
Db	178	QSD--LYTLSSSVTPSSTWSPSTETCNVAHPASSTKVDKVLPRDCGCKPC-ICTVPEV-	234
Qy	235	GGPSVLFPPPKDITLMSITPEVTCVVVDVSDPEQFQWYVDGVVHNAKTKPRREQ	294
Db	235	--SSVFPPPKDVLITITLPKTVCCVVDDISKDDPEQVQSFVDDVHVHTAQTPREQ	292
Qy	295	FNSTYRVVSVLTVLDHDLINGKEYCKVSNKGLPSSIEKTTISKAKGPREEPOVYTLPPSQ	354
Db	293	FNSTFRSVSELPINHDQWLNGKEFKRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPTPPK	352
Qy	355	EEMTKQVSLTCLVKGPYPSPDIAVEWESNGSPENNYKTTTPVLVDSGGSFFLYSRILTVDKS	414
Db	353	EQMAKQKVSITCMITDFPEDIITVEQWNGQPAENYKNTQIPMDTDGSAFYVYKLVNQKS	412
Qy	415	RWQEGNVFSPCSVMHEALHNHYTQKSLSLGLK	446
Db	413	NWEAGNTFTCSVLHSEGLHNHTTKSLSHSPK	444

RESULT 12  
G2MS11  
Ig gamma-2b chain - mouse

C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1980 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C;Accession: S25057; A02157; A26235; A26233; A26235; A26233; A26235  
R;Pischer, R.; Voss, A.; Nierbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
submitted to the EMBL Data Library, July 1992  
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m  
A;Reference number: S25057  
A;Accession: S25057  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-474 <FIS>  
A;Cross-references: UNIPROT:P01866; UNIPARC:UPI0000116095; EMBL:X67210; NID:G54826; PIDN  
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.  
Nature 288, 786-789, 1990  
A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from m  
A;Reference number: A02157; MUID:80120716; PMID:6766534  
A;Contents: a allele  
A;Accession: A02157  
A;Molecule type: DNA  
A;Residues: 138-161, 'L', 163-189, 'FP', 193-376, 'T', 378-474 <YAM>  
A;Cross-references: UNIPARC:UPI00000272D2; GB:J00461  
A;Note: the sequence was determined from the germline gene  
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.  
Science 206, 1299-1303, 1979  
A;Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea  
A;Reference number: A26235; MUID:80081501; PMID:117548  
A;Contents: MPC 11  
A;Accession: A26235  
A;Molecule type: mRNA  
A;Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>  
A;Cross-references: UNIPARC:UPI00001737AF  
A;Note: Lys-474 is probably removed posttranslationally  
R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.  
Science 206, 1303-1306, 1979  
A;Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglob  
A;Reference number: A26232; MUID:80081502; PMID:117549  
A;Accession: A26232  
A;Molecule type: DNA  
A;Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU2>  
A;Cross-references: UNIPARC:UPI00001737AF  
R;Ollio, R.; Rougeon, F.  
Nature 296, 761-763, 1982  
A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma  
A;Reference number: A26233; MUID:82173203; PMID:6803173  
A;Contents: b allele  
A;Accession: A26233  
A;Molecule type: DNA  
A;Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>  
A;Cross-references: UNIPARC:UPI00001737B0; GB:J00461  
R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahash  
J. Biol. Chem. 269, 12345-12350, 1994  
A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.  
A;Reference number: A53598; MUID:94216359; PMID:7512967  
A;Accession: A53598  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 234-251 <KIM>  
A;Cross-references: UNIPARC:UPI00001737B1  
A;Comment: The a allele sequence is shown.  
C;Genetics:  
A;Introns: 138/1; 236/1; 258/1; 368/1  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa  
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobul  
F;152-222/Domain: immunoglobulin homology <IM1>  
F;236-257/Region: hinge  
F;281-350/Domain: immunoglobulin homology <IM2>  
F;387-454/Domain: immunoglobulin homology <IM3>  
F;152/Disulfide bonds: interchain (to light chain) #status predicted  
F;164-220,288-348,394-452/Disulfide bonds: #status predicted  
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted  
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 55.1%; Score 1311.5; DB 1; Length 474;  
Best Local Similarity 55.0%; Pred. No. 3e-68;  
Matches 252; Conservative 72; Mismatches 119; Indels 15; Gaps 5;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGSGNWNWIRHQHPGKLEWIGYIY-YSGNT 59  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 20 EVQLQSGPELVNPGASVKMSCKASGYTFT--YVMHWVKQKPGQGLEWIGYINPKDGT 77  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 60 YNPISLKSRTISIDTSKNQFSLTLSSTVAADTAIVYVCARDGGDDAFDIWGQGTMTVVS 119  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 78 KNEKFKGKATLTSDKSNNTATMELSSLTSDSAVYCARDYDYDFWYWGQGTMTVVS 137  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 120 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 138 AKTTPSPVPLAPGCGDITGSSVTSGLVKGYFPEPVTVSWNSGSLSSVHTLSQALLQS 197  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 180 GLYSLSGVVTVPSSSLGKTKTYTCNDVHKPSNTKYDKRVESKYGPD-----PCP 228  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 198 GLYTSSSVTVPSSTWPSQTVCVAHPASSTTVDKLEPS-GPISTINPCPPCKECHKC 256  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 229 PAPEFLGSPVFLPPKPKDTLMISRTPEVTCVVVDVSDPEDEVQFNWYVDGVEVHNAKT 288  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 257 PAPNLEGGPSVFIPFPNTIKQVLMISLTLPKVCVVVDVSEDDPDVQLISWFWNVVEVHTAQT 316  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 289 KPRESQFNSTYRVSVLTVLVHODWLNKGEYCKVSNKGLPSSIEKTIKAKGQPREPQVY 348  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 317 QTHREDYNTIRVSTLPLIQHODWMSGEFKCKVNNKDLPSPIERTISKIQLVRAPQVY 376  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 349 TLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSR 408  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 377 ILPPPAEQLSRKVDLSLTCLVGFNPGDISVEMTSNGHTEENYKDTAPVLDSDGSYFIYSK 436  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 409 LTVDSRWQEGNVFSCSVNHEALHNHYTQKSLSLGLK 446  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 437 LNMKTSKMEKTSFSCNVRHGLKNYLLKKTISRSPGK 474  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
RESULT 13  
S01321  
Ig gamma-2b chain precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 23-Jul-1999  
C;Accession: S01321  
R;de Vaele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.  
Eur. J. Biochem. 176, 287-295, 1988  
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed at  
A;Reference number: S01320; MUID:88329081; PMID:3138116  
A;Accession: S01321  
A;Molecule type: mRNA  
A;Residues: 1-475 <DE1>  
A;Cross-references: UNIPARC:UPI0000115DDB; EMBL:X13188; NID:951780; PIDN:CAA31580.1; PID  
A;Note: this sequence was determined from the differentiated gene  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-475/Product: Ig gamma-2b chain #status predicted <MAT>  
F;159-223/Domain: immunoglobulin homology <IMM>  
Query Match 54.8%; Score 1303; DB 2; Length 475;  
Best Local Similarity 55.2%; Pred. No. 9.3e-68;  
Matches 254; Conservative 77; Mismatches 111; Indels 18; Gaps 7;  
QY 1 QVQLQSGPGLVKPSQTLSTCTVSGSISGSGNWNWIRHQHPGKLEWIGYIY-YSGNT 59  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 20 QVQLQSGAELARPASVKLSCKASGYTFTSYG--ISWVKQRTGQGLEWIGIYPSGNS 77  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 60 YNPISLKSRTISIDTSKNQFSLTLSSTVAADTAIVYVCARDGGDDAFDIWGQGTMTV 117  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 78 YFNEKFKGKATLTVDKSSSTAYLHLSLTSDSAVYFCAGPROVGLLPGYWGQGTMTV 137  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 118 SSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 177  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||





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OM protein - protein search, using sw model

Run on: December 17, 2005, 01:10:08 ; Search time 204.079 Seconds  
(without alignments)  
1541.883 Million cell updates/sec

Title: US-10-644-277-62  
Perfect score: 2379  
Sequence: 1 QVQLQESGGLVKPSQTL...MHEALNHVYTKLSLSLQK 446

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2146	90.2	476	Q6MZ7_HUMAN	Q6mz7 homo sapien
2	2144.5	90.1	473	Q8T63_HUMAN	Q8tc63 homo sapien
3	2127.5	89.4	476	Q6GMX1_HUMAN	Q6gm1 homo sapien
4	2074	87.2	465	Q6GMX6_HUMAN	Q6gm6 homo sapien
5	1919.5	80.7	466	Q6IN78_HUMAN	Q6in78 homo sapien
6	1918.5	80.6	470	Q6PJA4_HUMAN	Q6pj4 homo sapien
7	1900	79.9	473	Q6MZV7_HUMAN	Q6mzv7 homo sapien
8	1896.5	79.7	464	Q6MZU6_HUMAN	Q6mzu6 homo sapien
9	1893.5	79.6	478	Q6PI81_HUMAN	Q6pi81 homo sapien
10	1893	79.6	478	Q6P6C4_HUMAN	Q6p6c4 homo sapien
11	1892	79.5	475	Q5EP85_HUMAN	Q5ef85 homo sapien
12	1886.5	79.3	470	Q7Z5W1_HUMAN	Q7z5w1 homo sapien
13	1883	79.2	469	Q569F4_HUMAN	Q569f4 homo sapien
14	1880.5	79.0	472	Q6N089_HUMAN	Q6n089 homo sapien
15	1879	79.0	475	Q6MZQ6_HUMAN	Q6mzq6 homo sapien
16	1875.5	78.8	480	Q6N094_HUMAN	Q6n094 homo sapien
17	1874	78.8	544	Q6PJ95_HUMAN	Q6pj95 homo sapien
18	1871.5	78.7	482	Q7Z3S1_HUMAN	Q7z3s1 homo sapien
19	1863.5	78.3	466	Q6N096_HUMAN	Q6n096 homo sapien
20	1862.5	78.3	470	Q68CN4_HUMAN	Q68cn4 homo sapien
21	1859	78.1	473	Q6P055_HUMAN	Q6p055 homo sapien
22	1855	78.0	475	Q6GMW7_HUMAN	Q6gmw7 homo sapien
23	1850	77.8	521	Q8N4Y9_HUMAN	Q8n4y9 homo sapien
24	1844	77.5	417	Q8N093_HUMAN	Q8n093 homo sapien
25	1839.5	77.3	518	Q8N030_HUMAN	Q8n030 homo sapien
26	1838.5	77.3	480	Q6PJF1_HUMAN	Q6pjf1 homo sapien
27	1835	77.1	475	Q6N095_HUMAN	Q6n095 homo sapien
28	1830	76.9	469	Q7Z7P5_HUMAN	Q7z7p5 homo sapien
29	1826	76.8	519	Q5EBM2_HUMAN	Q5ebm2 homo sapien
30	1804	75.8	475	Q3RE17_PONPY	Q3re17 pongo pygma
31	1804	75.8	481	Q6N097_HUMAN	Q6n097 homo sapien

32	1743	73.3	327	1	IGHG4_HUMAN	P01861 homo sapien
33	1661.5	69.8	348	2	Q6PYX1_HUMAN	Q6pyx1 homo sapien
34	1605.5	67.5	326	1	IGHG2_HUMAN	P01859 homo sapien
35	1590.5	66.9	230	1	IGHG1_HUMAN	P01857 homo sapien
36	1571	66.0	509	2	Q8NF17_HUMAN	Q8nf17 homo sapien
37	1501	63.1	469	2	Q8M839_RAT	Q8m839 rattus norv
38	1470	61.8	354	2	Q86TT2_HUMAN	Q86tt2 homo sapien
39	1450.5	61.0	458	2	Q5M842_RAT	Q5m842 rattus norv
40	1416	59.5	467	2	Q4VBH1_RAT	Q4vbh1 rattus norv
41	1408	59.2	465	2	Q5I0J0_RAT	Q5i0j0 rattus norv
42	1407	59.1	473	2	Q9D8L4_MOUSE	Q9d8l4 mus musculu
43	1405.5	59.1	468	2	Q569B4_RAT	Q569b4 rattus norv
44	1399.5	58.8	468	2	Q569W9_MOUSE	Q569w9 mus musculu
45	1395	58.6	463	2	Q99LC4_MOUSE	Q99lc4 mus musculu

ALIGNMENTS

RESULT 1  
Q6MZ7\_HUMAN PRELIMINARY; PRT; 476 AA.  
ID Q6MZ7; AC Q6MZ7;  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DE Hypothetical protein DKFZp686M24218.  
GN Name=DKFZp686M24218;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Human rectum tumor;  
RG The German Human cDNA Consortium;  
RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Robo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640824; CAE45900.1; -; mRNA.  
DR HSSP; P01861; 1ADQ.  
DR SMR; Q6MZ7; 28-472.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_C1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00230; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 476 AA; 52420 MW; 0D3D1FFE5853958F CRC64;

Query Match 90.2%; Score 2146; DB 2; Length 476;  
Best Local Similarity 89.8%; Pred. No. 3.2e-143;  
Matches 404; Conservative 13; Mismatches 29; Indels 4; Gaps 1;

QY	1	QVQLQESGGLVKPSQTLSTCTVSGGSISSGGYNNWIRQHPGKGLIEWIYISGNTY	60
DB	27	QLQLQESGGLVKASATLSLTCVPPGYLSDSSSYGWINRQPPQGLIEWIGTVSYSGTPY	86
QY	61	YNPLSKSRITISIDTSKNQFSLTSSVTADTAATVAYVCARDGG-----DDAPDIWGQGTMTV	116
DB	87	YTFSLKSLRLTIHVDPKSKQIFLNLTSTVTAADTAATVAYVCVRHGGYSFASAYPFPGQCAPVT	146
QY	117	VSSASTKGSGVFPLAPCSRSTSESTAALGLVKDYPEPPTVTSWNSGALTSGVHTTPAVL	176
DB	147	VSSASTKGSGVFPLAPCSRSTSESTAALGLVKDYPEPPTVTSWNSGALTSGVHTTPAVL	206

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QY 177 QSSGLYSSVVTVPSSSLGTCTYTCNVDPKSNKTKVDRVSKYGPCCBPAPFELGG 236
Db 207 QSSGLYSSVVTVPSSSLGTCTYTCNVDPKSNKTKVDRVSKYGPCCBPAPFELGG 266
QY 237 PSVFLFPKPKDMLISRTPEVTCVVDVDSQEDPEVQFNWYDGVVEVHNAKTKPREEQFN 296
Db 267 PSVFLFPKPKDMLISRTPEVTCVVDVDSQEDPEVQFNWYDGVVEVHNAKTKPREEQFN 326
QY 297 STYRVVSVTLVHQDLWNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEE 356
Db 327 STYRVVSVTLVHQDLWNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEE 386
QY 357 MTKNOVSLTCLVKGFPSPDIAVWESNGOPENNYYKTPPVLDSGSPFLYSRLTVDKSRW 416
Db 387 MTKNOVSLTCLVKGFPSPDIAVWESNGOPENNYYKTPPVLDSGSPFLYSRLTVDKSRW 446
QY 417 QSGNVFSCVMHEALHNHYTKLSLSLKG 446
Db 447 QSGNVFSCVMHEALHNHYTKLSLSLKG 476

RESULT 2
Q8TC63 HUMAN
ID Q8TC63 HUMAN PRELIMINARY; PRT; 473 AA.
AC Q8TC63
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG4 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smalius D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -, mRNA.
DR HSSP; P01861; 1ADO.
DR InterPro; IPR000923; BlueCu 1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.C1.
DR InterPro; IPR003006; Ig.MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
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DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 90.1%; Score 2144.5; DB 2; Length 473;
Best Local Similarity 90.6%; Pred. No. 4e-143;
Matches 405; Conservative 14; Mismatches 27; Indels 1; Gaps 1;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYNNIRHQHKGLEWIGYIYSGNTY 60
Db 27 RLQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYNNIRHQHKGLEWIGYIYSGNTY 86
QY 61 YNPSLKSRITISIDTSKNQPSLTLSSTVAADTAIYTCARDGGDAFDI-WQOQTMTVTS 119
Db 87 YSPSLSRVTSADMSSENFYKLDLSVTAADTAIYCAAGHLVNGFGAHWGQGLVSVSP 146
QY 120 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 179
Db 147 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 206
QY 180 GLYSLSVVTVPSSSLGTCTYTCNVDPKSNKTKVDRVSKYGPCCBPAPFELGGPSV 239
Db 207 GLYSLSVVTVPSSSLGTCTYTCNVDPKSNKTKVDRVSKYGPCCBPAPFELGGPSV 266
QY 240 FLFPKPKDMLISRTPEVTCVVDVDSQEDPEVQFNWYDGVVEVHNAKTKPREEQFNSTY 299
Db 267 FLFPKPKDMLISRTPEVTCVVDVDSQEDPEVQFNWYDGVVEVHNAKTKPREEQFNSTY 326
QY 300 RVSVLTVLHQDLWNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEEMTK 359
Db 327 RVSVLTVLHQDLWNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEEMTK 386
QY 360 NQVSLTCLVKGFPSPDIAVWESNGOPENNYYKTPPVLDSGSPFLYSRLTVDKSRWQEG 419
Db 387 NQVSLTCLVKGFPSPDIAVWESNGOPENNYYKTPPVLDSGSPFLYSRLTVDKSRWQEG 446
QY 420 NVFSCVMHEALHNHYTKLSLSLKG 446
Db 447 NVFSCVMHEALHNHYTKLSLSLKG 473

RESULT 3
Q6GMX1 HUMAN
ID Q6GMX1 HUMAN PRELIMINARY; PRT; 476 AA.
AC Q6GMX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smalius D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -, mRNA.
DR HSSP; P01861; 1ADO.
DR InterPro; IPR000923; BlueCu 1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.C1.
DR InterPro; IPR003006; Ig.MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
```



RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073773; AAH73773.1; -; mRNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 3.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match 89.4%; Score 2127.5; DB 2; Length 476;  
Best Local Similarity 88.2%; Pred. No. 6.5e-142;  
Matches 403; Conservative 20; Mismatches 23; Indels 11; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYNNWIRQHPGKGLEWIGYIYSGNTY 60  
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYNNWIRQHPGKGLEWIGYIYSGNTY 79  
QY 61 YNPILSKRITISIDTSKNQPSLTSSVTAADTAIVYCARDG-----GDDAFDIWGOG 112  
DB 80 YNPILSKRITISIDTSKNQPSLTSSVTAADTAIVYCARDG-----GDDAFDIWGOG 139  
QY 113 TMVTSSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYPPEPTVSMNSGALTSVGHFT 172  
DB 140 TMVTSSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYPPEPTVSMNSGALTSVGHFT 199  
QY 173 PAVLQSGSLYSLSVTVTPSSSLGKTCTYCNVDHKSNTKVDKRVESK---YGPPECSCP 229  
DB 200 PAVLQSGSLYSLSVTVTPSSSLGKTCTYCNVDHKSNTKVDKRVESK---YGPPECSCP 259  
QY 230 APFLGSGPSVFLPAPKPKDLMISRTPEVTCVVDVSDPEVQFNWYDGVVHNKTK 289  
DB 260 APFLGSGPSVFLPAPKPKDLMISRTPEVTCVVDVSDPEVQFNWYDGVVHNKTK 319  
QY 290 PREEQFNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIIEKTIKAKGQPREPQVYT 349  
DB 320 PREEQFNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIIEKTIKAKGQPREPQVYT 379  
QY 350 LPSPQEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSRL 409  
DB 380 LPSPQEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSRL 439  
QY 410 TVDKSRQEGNVFSCSVNHEALHNHYTQKSLSLSPGK 446  
DB 440 TVDKSRQEGNVFSCSVNHEALHNHYTQKSLSLSPGK 476

RESULT 4  
Q6GMX6 HUMAN PRELIMINARY; PRT; 465 AA.  
AC Q6GMX6;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M.J., Udell T.B., Toshlyuk S., Carninci P., Prange C.,  
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Raha S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.L.  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073766; AAH73766.1; -; mRNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 87.2%; Score 2074; DB 2; Length 465;  
Best Local Similarity 88.4%; Pred. No. 3.8e-138;  
Matches 397; Conservative 19; Mismatches 27; Indels 6; Gaps 3;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYNNWIRQHPGKGLEWIGYIYSGNTY 60  
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYNNWIRQHPGKGLEWIGYIYSGNTY 77  
QY 61 YNPILSKRITISIDTSKNQPSLTSSVTAADTAIVYCARDGDDAFDIWGQTMVTSSA 120  
DB 78 YNPILSKRITISIDTSKNQPSLTSSVTAADTAIVYCARDGDDAFDIWGQTMVTSSA 136  
QY 121 STKGPSVFLPAPCSRSTSESTAALGCLVKDYPPEPTVSMNSGALTSVGHFTFPVQLQSSG 180  
DB 137 STKGPSVFLPAPCSRSTSESTAALGCLVKDYPPEPTVSMNSGALTSVGHFTFPVQLQSSG 196  
QY 181 LYSLSVTVTPSSSLGKTCTYCNVDHKSNTKVDKRVESK---YGPPECSCPAPEFLGGP 237  
DB 197 LYSLSVTVTPSSSLGKTCTYCNVDHKSNTKVDKRVESK---YGPPECSCPAPEFLGGP 256  
QY 238 SVFLPFPKPKDLMISRTPEVTCVVDVSDPEVQFNWYDGVVHNKTKPREQFNS 297  
DB 257 SVFLPFPKPKDLMISRTPEVTCVVDVSDPEVQFNWYDGVVHNKTKPREQFNS 316

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QY 298 TYRVSVTLVHODWLNKGYCKVSKNGLPSSIEKTIISKAKGQPREQVYTLPPSQEEM 357
DB 317 TYRVSVTLVHODWLNKGYCKVSKNGLPSSIEKTIISKAKGQPREQVYTLPPSRDEL 376
QY 358 TKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSRLTVDKSRWQ 417
DB 377 TKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQ 436
QY 418 EGNVFCSCVMHEALHNHYTQKSLSLSPGK 466
DB 437 QGNVFCSCVMHEALHNHYTQKSLSLSPGK 465

RESULT 5
Q6IN78 HUMAN
ID Q6IN78_HUMAN PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -, mRNA.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50854 MW; 53EB0BCDE81076E CRC64;

Query Match 80.7%; Score 1919.5; DB 2; Length 466;
Best Local Similarity 81.5%; Pred. No. 3.2e-127;

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Matches 366; Conservative 28; Mismatches 50; Indels 5; Gaps 2;
QY 1 QVQLQESGPGLVKPQSQTLSLTCTVSGSISGNGYWMWIRHPOKGLIEWIYISGNTY 60
DB 20 EVQLVDSGGGIQPGGSLTSLCAASGLTVSS--NYMHWVRQAPGKGLWSVLYIGGATY 77
QY 61 YNPGLKRIITISIDTSKNQPSLTSLSSVTAADTAIVYCARDDGDDAFDIDWGQGTWTVSSA 120
DB 78 YADSVKGRFTISRDNKNTLYLQWNSLRADETAIVYCARGVYVPAAPWGQGTIVTVSSA 137
QY 121 STKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
DB 138 STKGPSVFPPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 197
QY 181 LYSLSVSVTVPPSSSLGTYTTCNVDPHPSNTKVDKRVESK---YGPCCPSCPAPBEFLGGP 237
DB 198 LYSLSVSVTVPPSSSLGTQTCVNVNHRKPSNTKVDKRVKPSKCDTKTCTCPCPAPELLGGP 257
QY 238 SVFLFPPPKPKDITLMISRTPEVTCVVVDVSDPEQFNWYVDGVEVHNAKTKPRREQFNS 297
DB 258 SVFLFPPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRREQFNS 317
QY 298 TYRVSVTLVHODWLNKGYCKVSKNGLPSSIEKTIISKAKGQPREQVYTLPPSQEEM 357
DB 318 TYRVSVTLVHODWLNKGYCKVSKNGLPSSIEKTIISKAKGQPREQVYTLPPSRDEL 377
QY 358 TKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSRLTVDKSRWQ 417
DB 378 TKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQ 437
QY 418 EGNVFCSCVMHEALHNHYTQKSLSLSPGK 466
DB 438 QGNVFCSCVMHEALHNHYTQKSLSLSPGK 466

RESULT 6
Q6PJN4 HUMAN
ID Q6PJN4_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6PJN4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

```

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[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC018747; AAH18747.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR SMR; Q6FJA4; 20-470.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 470 AA; 51716 MW; 7B49556A11FD7D99 CRC64;

Query Match      80.6%; Score 1918.5; DB 2; Length 470;
Best Local Similarity 81.5%; Pred. No. 3.8e-127;
Matches 370; Conservative 27; Mismatches 46; Indels 11; Gaps 5;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGNYW-NHROHPGKLEWIGYIYSGN- 58
DB 20 EVQLVESGGGLVQPGGSLRLSCVSGFTFS--YMSWVRQAPGKLEWVANIKDGGSE 76

QY 59 TYNPSLKRITISIDTSKNQPSLTLSVTAADTAVVYCARDGGD---DAFDIWGQGTWV 115
DB 77 KYVDVSKGRFTISRDNKNSLYLQNSLRAEDTAVVYCARDGSSWYRDFDPWGQGTLV 136

QY 116 TVSSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
DB 137 TVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 196

QY 176 LQSSGLYSLSVTVPSRSSLGTYTCNVHDKSNTKVDKRVESK---YGPCCPCPAE 232
DB 197 LQSSGLYSLSVTVPSRSSLGTYTCNVNHKPSNTKVDKRVESK---YGPCCPCPAE 256

QY 233 FLGGPSVFLPAPKPKDTLMISRTPEVTCVVVDVSDPEQVFNWYVDGVEVHNAKTKPRE 292
DB 257 LLGGPSVFLPAPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316

QY 293 EQFNSTYRVVSVLTVLDHQMNLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPP 352
DB 317 EQFNSTYRVVSVLTVLDHQMNLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPP 376

QY 353 SQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSEFFLYSLRTVD 412
DB 377 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSEFFLYSLRTVD 436

QY 413 KSRWQEGNVFSCSVHMEALHNHYTQKSLSLGLK 446
DB 437 KSRWQEGNVFSCSVHMEALHNHYTQKSLSLSPGK 470

RESULT 7
Q6MZU7_HUMAN
ID Q6MZU7_HUMAN PRELIMINARY; PRT; 473 AA.
AC Q6MZU7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C11235.
GN Name=DKFZp686C11235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Small intestine;
RG The German cDNA Consortium;
RA Bloeker H., Boeher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640853; CAE45920.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 52121 MW; 9476EAE4C0BFC447 CRC64;

Query Match      79.9%; Score 1900; DB 2; Length 473;
Best Local Similarity 80.7%; Pred. No. 7.7e-126;
Matches 368; Conservative 25; Mismatches 51; Indels 12; Gaps 4;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGNYW-NHROHPGKLEWIGYIYSGN- 59
DB 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFS--FEMNWVRQAPGKLEWLSYITRSNTV 77

QY 60 YYNPSLKRITISIDTSKNQPSLTLSVTAADTAVVYCARDGGD---FDIWGQGT 113
DB 78 YYADSLQGRFTISRDNKNSLYLQNSLRAEDTAVVYCARDQNEHTSPWYPSFDFYWGQGI 137

QY 114 MVTVSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 173
DB 138 LVTVSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 197

QY 174 AVLSGGLYSLSVTVPSRSSLGTYTCNVHDKPSNTKVDKRVESK---YGPCCPCPA 230
DB 198 AVLSGGLYSLSVTVPSRSSLGTYTCNVNHKPSNTKVDKRVESKCDKTHTCPCPA 257

QY 231 PFLLGSPSVFLPAPKPKDTLMISRTPEVTCVVVDVSDPEQVFNWYVDGVEVHNAKTKP 290
DB 258 PELLGSPSVFLPAPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 317

QY 291 REEQFNSTYRVVSVLTVLDHQMNLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTL 350
DB 318 REEQFNSTYRVVSVLTVLDHQMNLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTL 377

QY 351 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSEFFLYSLRT 410
DB 378 PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSEFFLYSKLT 437

QY 411 VDKSRWQEGNVFSCSVHMEALHNHYTQKSLSLGLK 446
DB 438 VDKSRWQEGNVFSCSVHMEALHNHYTQKSLSLSPGK 473

RESULT 8
Q6MZU6_HUMAN
ID Q6MZU6_HUMAN PRELIMINARY; PRT; 464 AA.
AC Q6MZU6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C15213.
GN Name=DKFZp686C15213;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]

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QY 345 PQVYTLPPSQBETKNOVSLTCLVKGFPSPDI AVEWESNGQPNKYKTPPVLDSDGSPF 404
DB 377 PQVYTLPPSREETKNOVSLTCLVKGFPSPDI AVEWESNGQPNKYKTPPVLDSDGSPF 436
QY 405 LYSRLTVDKSRQEGNVFSCVMHEALHNHYTKSLSLGK 446
DB 437 LYSKLTVDKSRQEGNVFSCVMHEALHNHYTKSLSPGK 478

RESULT 10
Q6P6C4_HUMAN PRELIMINARY; PRT; 465 AA.
ID Q6P6C4_HUMAN PRELIMINARY; PRT; 465 AA.
AC Q6P6C4; 2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krzywicki M.J., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062335; AAF62335.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR SMR; Q6P6C4; 20-465.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51325 MW; FDD89348ADC3786D CRC64;

Query Match 79.6%; Score 1893; DB 2; Length 465;
Best Local Similarity 80.7%; Pred. No. 2.4e-125;
Matches 363; Conservative 28; Mismatches 51; Indels 8; Gaps 5;

QY 1 QVQLQESGPGLVKPSQTLSTCTVGSISGGNYW-NWIRQHPGKGLGWNIYYSGN- 58
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DB 20 EVQLMESAGLVKPGGSLRLCAASGFFS---EYVMSWVRQAPGKGLGWNIYKDDGSA 76
QY 59 TYYPNLSKSLRTISDTSKNQFSLTSSVTAADTAIVVYCARD--GGDDAFDITWGOGTWT 116
DB 77 THLDSSVKGRTISRDNARNTLYLQMSLRVEDTANYICAREIPGRCFYDFWGHGTLVT 136
QY 117 VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKQYFPEPTVSMNSGALTSGVHTFPAVL 176
DB 137 VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKQYFPEPTVSMNSGALTSGVHTFPAVL 196
QY 177 QSSGLYSLSVVTPSSSLGKTKYTCNVDHPSNTKYDKRVESKYGPPCPSPCAPEFLGG 236
DB 197 QSSGLYSLSVVTPSSSNGFTQYTCNVDHPSNTKYDKRVESKYGPPCPSPCAPEFLGG 255
QY 237 PSVFLPPKPKDLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNNAKTKPREEQFN 296
DB 256 PSVFLPPKPKDLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNNAKTKPREEQFN 315
QY 297 STYRVSVLTCLVKGFPSPDI AVEWESNGQPNKYKTPPVLDSDGSPFLYSLTVDKSRW 356
DB 316 STYRVSVLTCLVKGFPSPDI AVEWESNGQPNKYKTPPVLDSDGSPFLYSLTVDKSRW 375
QY 357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPNKYKTPPVLDSDGSPFLYSLTVDKSRW 416
DB 376 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPNKYKTPPVLDSDGSPFLYSLTVDKSRW 435
QY 417 QGQNVFSCVMHEALHNHYTKSLSLGK 446
DB 436 QGQNVFSCVMHEALHNHYTKSLSPGK 465

RESULT 11
Q6P6C4_HUMAN PRELIMINARY; PRT; 475 AA.
ID Q6P6C4_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6P6C4; 2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Anti-Rhd monoclonal T125 gammal heavy chain precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gaucher C., Klein P., Beliard R.;
RT "Sequence determination of the recombinant human anti-Rhd monoclonal
antibody T125."
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY849992; AAW82028.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW SIGNAL.
FT SIGNAL.
FT CHAIN 1 19 Potential.
FT CHAIN 20 475 anti-Rhd monoclonal T125 gammal heavy
chain.
SQ SEQUENCE 475 AA; 52362 MW; 1367D400DC7D2859 CRC64;

Query Match 79.5%; Score 1892; DB 2; Length 475;
Best Local Similarity 80.0%; Pred. No. 2.9e-125;
Matches 367; Conservative 27; Mismatches 49; Indels 16; Gaps 5;
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QY 60 YNPSLKSRIITISIDTSKNQFSLTSSVTAADTAVVYCARDDGDDAFDI-----WG 110
Db 79 NYNPSLNKRVSIISIDTSKNLFSKLRSVTAADTAVVYCAS-----NILKYLHMLLYWG 131
QY 111 QGTMVTVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYPPPEPVTVSWNSGALTSGVH 170
Db 132 QGVLTVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYPPPEPVTVSWNSGALTSGVH 191
QY 171 TPAVLQSSGLYSLSSVTVTPSSSLGTITYTCNVDPKPSNTKVDKRVESKYGPPCPSCPA 230
Db 192 TPAVLQSSGLYSLSSVTVTPSSSLGTITYTCNVDPKPSNTKVDKRVESKYGPPCPSCPA 251
QY 231 PEFLLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 290
Db 252 PEFLLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 311
QY 291 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 350
Db 312 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 371
QY 351 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLT 410
Db 372 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLT 431
QY 411 VDKSRWQEGNVFSCSVMHREALHNYHTOKSLSLSLGK 446
Db 432 VDKSRWQEGNVFSCSVMHREALHNYHTOKSLSLSLGK 467
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## RESULT 2

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US-08-523-894-10
; Sequence 12, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-523-894-10
Query Match 91.0%; Score 2164; DB 2; Length 467;
Best Local Similarity 91.4%; Pred. No. 2.9e-160;
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Matches 417; Conservative 7; Mismatches 14; Indels 18; Gaps 4;
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSGSISSGGNYYNWIRHPGKGLIEWIGIYYIS-GNT 59
Db 20 QVQLQESGPGLVKPESETLSLTCSVSGSI-SGDYYWFWIRQSPGKGLIEWIGIYVSGGGT 78
QY 60 YNPSLKSRIITISIDTSKNQFSLTSSVTAADTAVVYCARDDGDDAFDI-----WG 110
Db 79 NYNPSLNKRVSIISIDTSKNLFSKLRSVTAADTAVVYCAS-----NILKYLHMLLYWG 131
QY 111 QGTMVTVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYPPPEPVTVSWNSGALTSGVH 170
Db 132 QGVLTVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYPPPEPVTVSWNSGALTSGVH 191
QY 171 TPAVLQSSGLYSLSSVTVTPSSSLGTITYTCNVDPKPSNTKVDKRVESKYGPPCPSCPA 230
Db 192 TPAVLQSSGLYSLSSVTVTPSSSLGTITYTCNVDPKPSNTKVDKRVESKYGPPCPSCPA 251
QY 231 PEFLLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 290
Db 252 PEFLLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 311
QY 291 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 350
Db 312 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 371
QY 351 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLT 410
Db 372 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLT 431
QY 411 VDKSRWQEGNVFSCSVMHREALHNYHTOKSLSLSLGK 446
Db 432 VDKSRWQEGNVFSCSVMHREALHNYHTOKSLSLSLGK 467

RESULT 3
US-08-523-894-12
; Sequence 12, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-523-894-12

Query Match 90.8%; Score 2159; DB 2; Length 467;
Best Local Similarity 91.2%; Pred. No. 7.1e-160;
Matches 416; Conservative 7; Mismatches 15; Indels 18; Gaps 4;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSCGNYWNIHQHPGKLEWIGYIYS-GNT 59
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGGSI-SGDYWFWRQSPGKLEWIGYIYSGG 78
QY 60 YNPSSLKSRITISIDTSKNQFSLTSSVTAADTAATVYVYCARDGDDAFDI- 110
DB 79 YNPSSLKSRITISIDTSKNQFSLTSSVTAADTAATVYVYCARDGDDAFDI- 131
QY 111 QGTMVTVSSASTKGPSVFLPAPCSRSTSESTAAALGCLVKDYFPEPTVTSWNSGALTSGVH 170
DB 132 QGVLTVTVSSASTKGPSVFLPAPCSRSTSESTAAALGCLVKDYFPEPTVTSWNSGALTSGVH 191
QY 171 TTPAVLQSSGLYSLSVTVTPSSSLGTQYTCNVDHKPKNTKVDKRVESKYGPPCPSCPA 230
DB 192 TTPAVLQSSGLYSLSVTVTPSSSLGTQYTCNVDHKPKNTKVDKRVESKYGPPCPSCPA 251
QY 231 PEPFGSPVFLPPPKPDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTP 290
DB 252 PEPFGSPVFLPPPKPDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTP 311
QY 291 REQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 350
DB 312 REQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 371
QY 351 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLT 410
DB 372 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLT 431
QY 411 VDKSRQEGNVFSCSVMEALHNNHYTKQSLSLSGK 446
DB 432 VDKSRQEGNVFSCSVMEALHNNHYTKQSLSLSGK 467

RESULT 4
US-09-049-672A-4
; Sequence 4, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049.672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

;
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Certone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 473 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PANTU01
; CLONE: 1513264
; US-09-049-672A-4

Query Match 90.0%; Score 2140; DB 2; Length 473;
Best Local Similarity 89.2%; Pred. No. 2.2e-158;
Matches 405; Conservative 18; Mismatches 23; Indels 8; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSCGNYWNIHQHPGKLEWIGYIYS-GNT 60
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSCGNYWNIHQHPGKLEWIGYIYS-GNT 79
QY 61 YNPSSLKSRITISIDTSKNQFSLTSSVTAADTAATVYVYCARD- 115
DB 80 YNPSSLKSRITISIDTSKNQFSLTSSVTAADTAATVYVYCARD- 139
QY 116 TVSSASTKGPSVFLPAPCSRSTSESTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAV 175
DB 140 TVSSASTKGPSVFLPAPCSRSTSESTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAV 199
QY 176 LOSSGLYSLSVTVTPSSSLGTQYTCNVDHKPKNTKVDKRVESK- 232
DB 200 LOSSGLYSLSVTVTPSSSLGTQYTCNVNHKPSNTKVDKRVESKCDKTHTCPPCPAPE 259
QY 233 FLGGPSVFLPPPKPDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTPRE 292
DB 260 LLGGPSVFLPPPKPDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTPRE 319
QY 293 EQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPP 352
DB 320 EQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPP 379
QY 353 SOEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLTVD 412
DB 380 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLTVD 439
QY 413 KSRWQEGNVFSCSVMEALHNNHYTKQSLSLSGK 446
DB 440 KSRWQEGNVFSCSVMEALHNNHYTKQSLSLSGK 473

RESULT 5
PCT-US96-13152-4
; Sequence 4, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
```

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-13152-4
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Query Match 86.7%; Score 2062.5; DB 4; Length 443;  
Best Local Similarity 88.1%; Pred. No. 2.1e-152;  
Matches 393; Conservative 16; Mismatches 34; Indels 3; Gaps 2;

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Qy 1 QVQLQESGPGLVKPSQTLTLCTVSGGISISSGNNYMWIRQHPGKGLWIGYIYSGNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSQAASGFTSTYA--MSWVRQAPGKGLWVASISTGGSTY 58
Qy 61 YNPISLKSRTISIDTSKNQFSLTSSVTAADTAVYVCARDGGDDAFDIWGQGTWVTVSSA 120
Db 59 YPDSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYVCARD-YDGYFDYWGQGTWVTVSSA 117
Qy 121 STKGSPVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180
Db 118 STKGSPVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 177
Qy 181 LYSLSVSVTVFSSSLGTITYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPEFLGGPSVF 240
Db 178 LYSLSVSVTVFSSSLGTITYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPEFLGGPSVF 237
Qy 241 LFPPPKPDKTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYR 300
Db 238 LFPPPKPDKTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYR 297
Qy 301 VVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTSKAGQPRPQVYTLPPSQQEEMTKN 360
Db 298 VVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTSKAGQPRPQVYTLPPSQQEEMTKN 357
Qy 361 QVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQSGN 420
Db 358 QVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQSGN 417
Qy 421 VFSCSWMEALHNHYTQKSLSLGLK 446
Db 418 VFSCSWMEALHNHYTQKSLSLGLK 443
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RESULT 6  
US-08-704-744-81  
; Sequence 81, Application US/08704744  
; Patent No. 5705154

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;
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5.3
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,744
; FILING DATE: 06-SEPT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208886
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: PCT/US/95/02400
; FILING DATE: 08-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2987
; TELEFAX: (908) 298-5388
; TELEX:
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-704-744-81
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Query Match 86.5%; Score 2057; DB 1; Length 467;  
Best Local Similarity 87.6%; Pred. No. 6.2e-152;  
Matches 395; Conservative 13; Mismatches 35; Indels 8; Gaps 4;

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Qy 1 QVQLQESGPGLVKPSQTLTLCTVSGGISISSGNNYMWIRQHPGKGLWIGYIYSG-N 58
Db 20 EVQLVESGGGLVQPGGSLRLSQAASGFTSFRS--YWMTWVRQAPGKGLWVASISISGDN 76
Qy 59 TYNPISLKSRTISIDTSKNQFSLTSSVTAADTAVYVCARDG---GDADFINGQGTWV 115
Db 77 TYPDSVKGRFTISRDDSKSTLYLQMNLSRAEDTAVYVCVRDPYFSGHYDFWQGQTLV 136
Qy 116 TVSSASTKGSVPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 175
Db 137 TVSSASTKGSVPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 196
Qy 176 LQSSGLYSLSVTVFSSSLGTITYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPEFLG 235
Db 197 LQSSGLYSLSVTVFSSSLGTITYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPEFLG 256
Qy 236 GPSVFLFPPPKPDKTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF 295
Db 257 GPSVFLFPPPKPDKTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF 316
Qy 296 NSTYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTSKAGQPRPQVYTLPPSQE 355
Db 317 NSTYRVSVLTVLHQDLNKGKEYKCKVSNKGLPSSIEKTSKAGQPRPQVYTLPPSQE 376
Qy 356 EMTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSR 415
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Db 377 EMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSLFLYSLRLTVDKSR 436  
Qy 416 WQEGNVFSCVMHEALHNNHYTKQSLSLGK 446  
Db 437 WQEGNVFSCVMHEALHNNHYTKQSLSLGK 467  
RESULT 7  
US-08-487-550-12  
; Sequence 12, Application US/08487550  
; Patent No. 6113898  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 476 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-487-550-12  
Query Match 85.9%; Score 2044.5; DB 2; Length 476;  
Best Local Similarity 85.6%; Pred. No. 5.9e-151;  
Matches 392; Conservative 21; Mismatches 32; Indels 13; Gaps 4;  
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGNYNNWIRQHPGKLEWIGYIY-YSGNT 59  
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGSISGGNYNNWIRQHPGKLEWIGYIY-YSGNT 78  
Qy 60 YNPSLKSRTITSDTSKNQFSLTSSVTAADTAAYVYCARDG-----GDDAFDIWQ 111  
Db 79 YNPSLKSQVTTISDTSKNQFSLKLSNMTAADTAAYVYCVDRDLFSVVGMYNNWFDVWGP 138  
Qy 112 GTMTVTSASSTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVYSWNSGALTSGVHT 171  
Db 139 GVLTVTSASSTKGPSVFLPAPCSRSTSGTAALGCLVKDYFPEPTVYSWNSGALTSGVHT 198  
Qy 172 FPAVLQSGSLYSLSSVTVTPSSSLGTQTYTCNVDPKPSNTKVDKRVESK---YGPCPCSC 228  
Db 199 FPAVLQSGSLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKAEPKSCDKTHTTTPC 258  
Qy 229 PAPFLQSGPSVFLPAPKQDTLMISRTPEVTCVVVDYSDQEDPEVQFNNYVDGVVHNAKT 288  
Db 259 PAPFLQSGPSVFLPAPKQDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 318

Qy 289 KPRBEQFNSTYRVSVLTVLHQDMLNGKEYKCKVSNKGLPSSIEKTIISKAKGPQEPQY 348  
Db 319 KPREQYNSTYRVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKTIISKAKGPQEPQY 378  
Qy 349 TLPPSQEEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSLFLYSR 408  
Db 379 TLPPSRDBLTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSLFLYSK 438  
Qy 409 LTVDKSRWQEGNVFSCVMHEALHNNHYTKQSLSLGK 446  
Db 439 LTVDKSRWQEGNVFSCVMHEALHNNHYTKQSLSLSPGK 476  
RESULT 8  
US-09-526-098-12  
; Sequence 12, Application US/09526098  
; Patent No. 6492134  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09526,098  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/383,916  
; FILING DATE:  
; APPLICATION NUMBER: US 08/487,550  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 476 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-526-098-12  
Query Match 85.9%; Score 2044.5; DB 2; Length 476;  
Best Local Similarity 85.6%; Pred. No. 5.9e-151;  
Matches 392; Conservative 21; Mismatches 32; Indels 13; Gaps 4;  
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGNYNNWIRQHPGKLEWIGYIY-YSGNT 59  
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGSISGGNYNNWIRQHPGKLEWIGYIY-YSGNT 78  
Qy 60 YNPSLKSRTITSDTSKNQFSLTSSVTAADTAAYVYCARDG-----GDDAFDIWQ 111  
Db 79 YNPSLKSQVTTISDTSKNQFSLKLSNMTAADTAAYVYCVDRDLFSVVGMYNNWFDVWGP 138

[illegible]

## RESULT 9

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US-09-383-916-12
; Sequence 12, Application US/09383916
; Patent No. 6709654
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; AND USE THEREOF AS
; PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/383,916
; FILING DATE: 26-AUG-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-383-916-12

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## RESULT 10

RESULT 10  
 US-09-758-173-12  
 ; Sequence 12, Application US/09758173  
 ; Patent No. 6893638  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, Darrell R.  
 ; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
 ; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
 ; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
 ; STREET: 699 Prince Street  
 ; CITY: Alexandria  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22314  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/758,173  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/383,916  
 ; FILING DATE:  
 ; APPLICATION NUMBER: US 08/487,550  
 ; FILING DATE: 07-JUN-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Teskin, Robin L.  
 ; REGISTRATION NUMBER: 35,030  
 ; REFERENCE/DOCKET NUMBER: 012712-131  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 703-836-6620  
 ; TELEFAX: 703-836-2021





Db 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFS----DYWMSNVRQAPCKGLEWVADIKNDGSY 76  
QY 59 TYNPSLSKRITITSDTSKNQSLTSSVTAADTAVYICARDGGDDAFDINGQGGMVTVS 118  
Db 77 TNYAPSLNTRFTISRDNAKNSLYLQWNSLRABDTAVYICAR----ELGTGWGQGGMVTVS 132  
QY 119 SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTPFAVLQS 178  
Db 133 SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTPFAVLQS 192  
QY 179 SGLYSLSVVTVPPSSSLGKTKYTCNVDHKPSNTKVDKRVESYGPSPCPAPFELGGPS 238  
Db 193 SGLYSLSVVTVPPSSSLGKTKYTCNVDHKPSNTKVDKRVESYGPSPCPAPFELGGPS 252  
QY 239 VFLFPPKPKDTLMISRTPEVTCVVVDVQEDDEVDQFNQVVDGVEVHNKATPKPRQFNMST 298  
Db 253 VFLFPPKPKDTLMISRTPEVTCVVVDVQEDDEVDQFNQVVDGVEVHNKATPKPRQFNMST 312  
QY 299 YRVVSVLTVLHODWLNKGEYKCKVSKGLPSSIEKTIKAKGQPREPOVYTLPPSQEEMT 358  
Db 313 YRVVSVLTVLHODWLNKGEYKCKVSKGLPSSIEKTIKAKGQPREPOVYTLPPSQEEMT 372  
QY 359 KNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQE 418  
Db 373 KNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQE 432  
QY 419 GNVFCSVMHEALHNHYTQKSLSLGLK 446  
Db 433 GNVFCSVMHEALHNHYTQKSLSLGLK 460

## RESULT 13

US-08-793-450-8  
; Sequence 8, Application US/08793450  
; Patent No. 6312690  
; GENERAL INFORMATION:  
; APPLICANT: EDELMAN, LENA  
; APPLICANT: MARGARITTE, CHRISTEL  
; APPLICANT: KACZOREK, MICHEL  
; APPLICANT: CHAABIHI, HASSAN  
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 03-MAR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94/10566  
; FILING DATE: 02-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 472 amino acids

; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-793-450-8

Query Match 84.8%; Score 2018.5; DB 2; Length 472;

Best Local Similarity 85.1%; Pred. No. 6.2e-149;

Matches 387; Conservative 22; Mismatches 35; Indels 11; Gaps 3;

QY 1 QVQLQESGPGLVKPQSQTLSLTCTVSGSISGGNYYWNIHQHPKGLEWIGIYYSGNTY 60

Db 20 QVQLQESGAGLLKPSLSETLSLTCTVYGSFSS--GYWWSWIRQPPGKLEWIGEINHSSTN 77

QY 61 YNPSLSKRITITSDTSKNQSLTSSVTAADTAVYICAR-----DGGDDAFDINGQGM 114

Db 78 YNPSLSKRITISVDTSKNQSLKLSVTAADTAVYICARAPYKWKYHGMDFDPWQGT 137

QY 115 VTVSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 174

Db 138 VTVSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 197

QY 175 VLOSGLYSLSVVTVPPSSSLGKTKYTCNVDHKPSNTKVDKRVESK---YGPSPCPCAP 231

Db 198 VLOSGLYSLSVVTVPPSSSLGKTKYTCNVNHKPSNTKVDKKAEPKSCDKTQTCCPCAP 257

QY 232 EFLGSPSVFLFPPKPKDTLMISRTPEVTCVVVDVQEDDEVDQFNQVVDGVEVHNKATKPR 291

Db 258 ELLGSPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPR 317

QY 292 EEQFNSTYRVVSVLTVLHODWLNKGEYKCKVSKGLPSSIEKTIKAKGQPREPOVYTL 351

Db 318 EEQFNSTYRVVSVLTVLHODWLNKGEYKCKVSKGLPAPIEKTIKAKGQPREPOVYTL 377

QY 352 PSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTV 411

Db 378 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTV 437

QY 412 DKSRWQGNVFCSCVMHEALHNHYTQKSLSLGLK 446

Db 438 DKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 472

## RESULT 14

US-07-916-098A-45  
; Sequence 45, Application US/07916098A  
; Patent No. 5871732  
; GENERAL INFORMATION:  
; APPLICANT: BURKLY, LINDA C.  
; APPLICANT: CHISHOLM, PATRICIA L.  
; APPLICANT: THOMAS, DAVID W.  
; APPLICANT: ROSA, MARGARET D.  
; APPLICANT: ROSA, JOSEPH J.  
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN  
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.  
; STREET: 10 SOUTH WACKER DRIVE  
; CITY: CHICAGO  
; STATE: ILLINOIS  
; COUNTRY: U.S.A.  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07916,098A  
; FILING DATE: July 24, 1992  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US91/08843



FILING DATE: No. 5871732ember 27, 1991  
CLASSIFICATION: 424  
APPLICATION NUMBER: 07/618,542  
FILING DATE: No. 5871732ember 27, 1990  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: JOHN J. MC DONNELL  
REGISTRATION NUMBER: 26,949  
REFERENCE/DOCKET NUMBER: 92,310-G  
TELEPHONE: (312) 715-1000  
TELEFAX: (312) 715-1234  
TELEX: 910/221-5317  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-916-098A-45

STATE: D. C.  
COUNTRY: U.S.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage  
COMPUTER: IBM AT compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2  
SOFTWARE: WordPerfect 5.0 (Dos Text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/030,175  
FILING DATE: 17-MAY-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB91/01578  
FILING DATE: 13-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Ernst, Barbara G.  
REGISTRATION NUMBER: 30,377  
REFERENCE/DOCKET NUMBER: 1768-113  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)783-6040  
TELEFAX: (202)783-6031  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-030-175-42

Query Match 84.3%; Score 2005; DB 1; Length 467;  
Best Local Similarity 85.4%; Pred. No. 6.9e-148;  
Matches 385; Conservative 22; Mismatches 36; Indels 8; Gaps 4;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYNNWIRQHPGKLEWIGYIY-YSGNT 59  
DB 20 QVQLQESGAEVKKPGASVKVSCKASGYTFTS--YVHWVRQAPFGQGLEWIGYINPNDGT 77

QY 60 YNPISLKRITISIDTSKQFSLTSSVTAADTAAYVYCARDGGDDA---FDIWGQGTWV 115  
DB 78 DYDEKFGKATVLDPSNTAYWELSLRSEDYAVYCARCKDNYATGAWFAYWGQGTLV 137

QY 116 TVSSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAV 175  
DB 138 TVSSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAV 197

QY 176 LQSSGLYSLSVTVPSSSISLTCTYTCNVDPKSNKVDKRVESKYGPPCPAPAEFLG 235  
DB 198 LQSSGLYSLSVTVPSSSISLTCTYTCNVDPKSNKVDKRVESKYGPPCPAPAEFLG 257

QY 236 GPSVFLPAPKPTLMISRTPEVTCVVDVYQSDPEVQFNWYVDGVEVHNAKTKPREEQF 295  
DB 258 GPSVFLPAPKPTLMISRTPEVTCVVDVYQSDPEVQFNWYVDGVEVHNAKTKPREEQF 317

QY 296 NSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAKGPQRPQVYTLPPSQE 355  
DB 318 NSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAK-QPREPQVYTLPPSQE 376

QY 356 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSLRTVYDKSR 415  
DB 377 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSLRTVYDKSR 436

QY 416 WQGNVFSCSVMHEALHNHYTQKSLSLGLK 446  
DB 437 WQGNVFSCSVMHEALHNHYTQKSLSLGLK 467

Query Match 83.6%; Score 1990; DB 2; Length 467;  
Best Local Similarity 84.7%; Pred. No. 1e-146;  
Matches 381; Conservative 26; Mismatches 37; Indels 6; Gaps 3;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYNNWIRQHPGKLEWIGYIYSG-NT 59  
DB 20 QVQLQESGGLVRRPSQTLSTCTVSGFTSFNYG--MAWVRQPPGRGLEWIGTISHDGSDI 77

QY 60 YNPISLKRITISIDTSKQFSLTSSVTAADTAAYVYCARDGGDDAFDIWQGTWVTVSS 119  
DB 78 YFRDSVKGKVTMLVDTSKQFSLRSLSSVTAADTAAYVYCARQGTIAGIRHWGQSLTVSS 137

QY 120 ASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQSS 179  
DB 138 ASTKGPSVFLPAPCSRSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQSS 197

QY 180 GLYSLSVTVPSSSISLTCTYTCNVDPKSNKVDKRVESK---YGPCCPAPAEFLGG 236  
DB 198 GLYSLSVTVPSSSISLTCTYTCNVDPKSNKVDKRVESK---YGPCCPAPAEFLGG 257

QY 237 PSVFLPAPKPTLMISRTPEVTCVVDVYQSDPEVQFNWYVDGVEVHNAKTKPREEQFN 296  
DB 258 PSVFLPAPKPTLMISRTPEVTCVVDVYQSDPEVQFNWYVDGVEVHNAKTKPREEQFN 317

QY 297 STYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAKGPQRPQVYTLPPSQE 356  
DB 318 STYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAKGPQRPQVYTLPPSRDE 377

QY 357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSLRTVYDKSRW 416  
DB 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSLRTVYDKSRW 437

QY 417 QEGNVFSCSVMHEALHNHYTQKSLSLGLK 446  
DB 438 QEGNVFSCSVMHEALHNHYTQKSLSLSPGK 467

Query Match 84.3%; Score 2005; DB 1; Length 467;  
Best Local Similarity 85.4%; Pred. No. 6.9e-148;  
Matches 385; Conservative 22; Mismatches 36; Indels 8; Gaps 4;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYNNWIRQHPGKLEWIGYIY-YSGNT 59  
DB 20 QVQLQESGAEVKKPGASVKVSCKASGYTFTS--YVHWVRQAPFGQGLEWIGYINPNDGT 77

QY 60 YNPISLKRITISIDTSKQFSLTSSVTAADTAAYVYCARDGGDDA---FDIWGQGTWV 115  
DB 78 DYDEKFGKATVLDPSNTAYWELSLRSEDYAVYCARCKDNYATGAWFAYWGQGTLV 137

QY 116 TVSSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAV 175  
DB 138 TVSSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAV 197

QY 176 LQSSGLYSLSVTVPSSSISLTCTYTCNVDPKSNKVDKRVESKYGPPCPAPAEFLG 235  
DB 198 LQSSGLYSLSVTVPSSSISLTCTYTCNVDPKSNKVDKRVESKYGPPCPAPAEFLG 257

QY 236 GPSVFLPAPKPTLMISRTPEVTCVVDVYQSDPEVQFNWYVDGVEVHNAKTKPREEQF 295  
DB 258 GPSVFLPAPKPTLMISRTPEVTCVVDVYQSDPEVQFNWYVDGVEVHNAKTKPREEQF 317

QY 296 NSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAKGPQRPQVYTLPPSQE 355  
DB 318 NSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAK-QPREPQVYTLPPSQE 376

QY 356 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSLRTVYDKSR 415  
DB 377 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSLRTVYDKSR 436

QY 416 WQGNVFSCSVMHEALHNHYTQKSLSLGLK 446  
DB 437 WQGNVFSCSVMHEALHNHYTQKSLSLGLK 467

RESULT 15  
US-08-030-175-42  
Sequence 42, Application US/08030175  
Patent No. 6767996  
GENERAL INFORMATION:  
APPLICANT: Gorman, Scott D.  
APPLICANT: Clark, Michael R.  
APPLICANT: Cobbold, Stephen P.  
APPLICANT: Waldmann, Herman  
TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.  
STREET: 555 13TH ST., NW Suite 701 East  
CITY: Washington

Search completed: December 17, 2005, 01:25:45  
Job time : 46.6 secs

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OM protein - protein search, using sw model

Run on: December 17, 2005, 01:14:05 ; Search time 147.315 Seconds  
(without alignments)  
1264.988 Million cell updates/sec

Title: us-10-644-277-62  
Perfect score: 2379  
Sequence: 1 QVQLQSGGLVVKPSQTLSTL.....MHEALHHYTKLSLSLCK 446

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pap:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pap:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pap:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pap:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pap:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2379	100.0	446	5	US-10-644-277-62
2	2197.5	92.4	470	6	US-11-031-485-22
3	2180	91.6	450	5	US-10-484-790A-17
4	2177	91.5	467	5	US-10-961-567A-3
5	2171	91.3	467	4	US-10-211-357-8
6	2164	91.0	467	4	US-10-211-357-10
7	2159	90.8	467	4	US-10-211-357-12
8	2158.5	90.7	480	5	US-10-910-901-6
9	2136.5	89.8	580	4	US-10-310-719-37
10	2119	89.1	442	5	US-10-937-596-32
11	2108	88.6	463	5	US-10-910-901-10
12	2106.5	88.5	466	4	US-10-292-088-86
13	2104.5	88.5	466	4	US-10-292-088-70
14	2096.5	88.1	466	4	US-10-292-088-30
15	2088.5	87.8	464	5	US-10-818-068-25
16	2088.5	87.8	451	5	US-10-724-274-25
17	2088.5	87.8	451	5	US-10-830-956-25
18	2085.5	87.7	451	5	US-10-822-300-144
19	2084.5	87.6	464	4	US-10-292-088-22
20	2083	87.6	442	5	US-10-937-596-4
21	2082.5	87.5	451	5	US-10-822-300-142
22	2082.5	87.5	451	5	US-10-822-300-143
23	2079.5	87.4	451	5	US-10-822-300-145
24	2077.5	87.3	451	5	US-10-822-300-146
25	2075	87.2	471	6	US-11-031-485-38
26	2071	87.1	461	5	US-10-938-353-70
27	2071	87.1	465	6	US-11-031-485-14

28	2067	86.9	463	5	US-10-938-353-18	Sequence 18, Appl
29	2067	86.9	469	6	US-11-031-485-60	Sequence 60, Appl
30	2065.5	86.8	451	5	US-10-724-274-31	Sequence 31, Appl
31	2065.5	86.8	451	5	US-10-830-956-31	Sequence 31, Appl
32	2064.5	86.8	462	6	US-11-031-485-45	Sequence 46, Appl
33	2064	86.8	469	4	US-10-663-244-164	Sequence 164, Appl
34	2062.5	86.7	443	3	US-09-917-410-4	Sequence 4, Appl
35	2062.5	86.7	462	5	US-10-938-353-46	Sequence 46, Appl
36	2060	86.6	469	5	US-10-805-177-137	Sequence 137, Appl
37	2059	86.5	444	5	US-10-492-228-57	Sequence 57, Appl
38	2059	86.5	469	4	US-10-663-244-157	Sequence 157, Appl
39	2059	86.5	469	6	US-11-031-485-18	Sequence 18, Appl
40	2057.5	86.5	462	5	US-10-938-353-86	Sequence 86, Appl
41	2055.5	86.4	462	5	US-10-938-353-50	Sequence 50, Appl
42	2054.5	86.4	466	4	US-10-663-244-162	Sequence 162, Appl
43	2054	86.3	461	5	US-10-938-353-38	Sequence 38, Appl
44	2054	86.3	461	5	US-10-938-353-78	Sequence 78, Appl
45	2049.5	86.1	464	4	US-10-663-244-158	Sequence 158, Appl

ALIGNMENTS

RESULT 1  
US-10-644-277-62  
; Sequence 62, Application US/10644277  
; Publication No. US20050058639A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudae, Jean M.  
; APPLICANT: Haak-Frendscho, Mary  
; APPLICANT: Foord, Orit  
; APPLICANT: Liang, Meina L.  
; APPLICANT: Ahluwalia, Kiran  
; APPLICANT: Bhakta, Sunil  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE  
; FILE REFERENCE: CHEMO-ATTRACTANT PROTEIN-1 (MCP-1) AND USES THEREOF  
; FILE REFERENCE: ABGENIX.091A  
; CURRENT APPLICATION NUMBER: US/10/644,277  
; CURRENT FILING DATE: 2003-08-19  
; PRIOR APPLICATION NUMBER: 60/404,802  
; PRIOR FILING DATE: 2002-08-19  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 62  
; LENGTH: 446  
; TYPE: PRT  
; ORGANISM: Homosapien  
US-10-644-277-62

Query Match	100.0%	Score 2379;	DB 5;	Length 446;
Best Local Similarity	100.0%	Pred. No. 1.7e-152;		
Matches 446;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	QVQLQSGGLVVKPSQTLSTLTCTVSGGSISSGGNYNNWIRQHPGKLEWIGIYYSGNTY	60	
Db	1	QVQLQSGGLVVKPSQTLSTLTCTVSGGSISSGGNYNNWIRQHPGKLEWIGIYYSGNTY	60	
Qy	61	YNPSLSRITISIDTSKNQFSLTSSVTADTAIVYCARDGGDDAFDIWGQGTMTVSSA	120	
Db	61	YNPSLSRITISIDTSKNQFSLTSSVTADTAIVYCARDGGDDAFDIWGQGTMTVSSA	120	
Qy	121	STKGPSVFPPLACSRSTSESTAALGLVKDYFPPEPTVSNWNSGALTSGVHTFPFVLQSSG	180	
Db	121	STKGPSVFPPLACSRSTSESTAALGLVKDYFPPEPTVSNWNSGALTSGVHTFPFVLQSSG	180	
Qy	181	LYSLSSVTVTPSSSLGTKTYTCNVDHKPSNTKVDKVESKYGPCCSCAPELGGPSVF	240	
Db	181	LYSLSSVTVTPSSSLGTKTYTCNVDHKPSNTKVDKVESKYGPCCSCAPELGGPSVF	240	
Qy	241	LFPFKPKDTLMISRTPEVTCVVDVDSQDEPQFNWYVDGVEVHNAKTKPREEQFNSTYR	300	
Db	241	LFPFKPKDTLMISRTPEVTCVVDVDSQDEPQFNWYVDGVEVHNAKTKPREEQFNSTYR	300	

QY 301 VVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEMTKN 360  
DB 301 VVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEMTKN 360  
QY 361 QVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSGFFLYSRLTVDKSRWQEN 420  
DB 361 QVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSGFFLYSRLTVDKSRWQEN 420  
QY 421 VFSCVMHEALHNHYTQKSLSLGLK 446  
DB 421 VFSCVMHEALHNHYTQKSLSLGLK 446  
RESULT 2  
US-11-031-485-22  
; Sequence 22, Application US/11031485  
; Publication No. US20050232917A1  
; GENERAL INFORMATION:  
; APPLICANT: PULLEN, NICHOLAS  
; APPLICANT: MOLLOY, ELIZABETH  
; APPLICANT: KELLERMANN, SIRID-AIMEE  
; APPLICANT: GREEN, LARRY L.  
; APPLICANT: HAAK-FRIENDSCHO, MARY  
; TITLE OF INVENTION: ANTIBODIES TO MADCAM  
; FILE REFERENCE: ABX-PF6  
; CURRENT APPLICATION NUMBER: US/11/031,485  
; CURRENT FILING DATE: 2005-01-07  
; PRIOR APPLICATION NUMBER: 60/535,490  
; PRIOR FILING DATE: 2004-01-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: Patentin Ver. 3.3  
; SEQ ID NO 22  
; LENGTH: 470  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-031-485-22

Query Match 92.4%; Score 2197.5; DB 6; Length 470;  
Best Local Similarity 92.9%; Pred. No. 3.2e-140;  
Matches 421; Conservative 5; Mismatches 18; Indels 9; Gaps 2;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYMNIROHPGKLEWIGVIYVSGNTY 60  
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGDLSI--NYSWIRQAPGKLEWIGRIYTSGGTN 77  
QY 61 YNPSLKSRITISIDTSKNQFSLTSSVTAADTAVYYCARDG-----GDDAFDIWGQGT 113  
DB 78 SNPSLRGRVTILADTSKNQFSLKLSVTAADTAVYYCARDRTIIRGLIPFFDYWGQGT 137  
QY 114 MVTVSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 173  
DB 138 LVTVSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 197  
QY 174 AVQLQSGLYSLSSVTVVPSSISLGTYYTCNVDPKSNKVDKRVESKYGPPCPSPAPPEF 233  
DB 198 AVQLQSGLYSLSSVTVVPSSISLGTYYTCNVDPKSNKVDKRVESKYGPPCPSPAPPEF 257  
QY 234 LGGPSVFLPPPKPDITLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNKATKPREE 293  
DB 258 LGGPSVFLPPPKPDITLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNKATKPREE 317  
QY 294 QNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPS 353  
DB 318 QNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPS 377  
QY 354 QSEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSGFFLYSRLTVDK 413  
DB 378 QSEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSGFFLYSRLTVDK 437  
QY 414 SRWQEGNVFSCVMHEALHNHYTQKSLSLGLK 446  
DB 438 SRWQEGNVFSCVMHEALHNHYTQKSLSLGLK 470

RESULT 3  
US-10-484-790A-17  
; Sequence 17, Application US/10484790A  
; Publication No. US20050070694A1  
; GENERAL INFORMATION:  
; APPLICANT: Gelfanova, et al., Valentina  
; TITLE OF INVENTION: Antagonistic Anti-htNPSF13b Human Antibodies  
; FILE REFERENCE: X-15239  
; CURRENT APPLICATION NUMBER: US/10/484,790A  
; CURRENT FILING DATE: 2004-01-22  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 17  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-484-790A-17

Query Match 91.6%; Score 2180; DB 5; Length 450;  
Best Local Similarity 92.0%; Pred. No. 4.7e-139;  
Matches 416; Conservative 9; Mismatches 19; Indels 8; Gaps 2;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYMNIROHPGKLEWIGVIYVSGNTY 60  
DB 1 QVQLQQWAGLTKPSETLSLTCAVYGGFS--GYTWSWIRQPPGKLEWIGEINHSSTN 58  
QY 61 YNPSLKSRITISIDTSKNQFSLTSSVTAADTAVYYCARDGDDA-----FDIWGQGT 114  
DB 59 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGYYDILTGYYYFDYWGQGT 118  
QY 115 VTVSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 174  
DB 119 VTVSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 178  
QY 175 VLQSSGLYSLSSVTVVPSSISLGTYYTCNVDPKSNKVDKRVESKYGPPCPSPAPPEFL 234  
DB 179 VLQSSGLYSLSSVTVVPSSISLGTYYTCNVDPKSNKVDKRVESKYGPPCPSPAPPEFL 238  
QY 235 GGPSVFLPPPKPDITLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNKATKPREE 294  
DB 239 GGPSVFLPPPKPDITLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNKATKPREE 298  
QY 295 FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQ 354  
DB 299 FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQ 358  
QY 355 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSGFFLYSRLTVDKS 414  
DB 359 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSGFFLYSRLTVDKS 418  
QY 415 RWQEGNVFSCVMHEALHNHYTQKSLSLGLK 446  
DB 419 RWQEGNVFSCVMHEALHNHYTQKSLSLGLK 450

RESULT 4  
US-10-961-567A-3  
; Sequence 3, Application US/10961567A  
; Publication No. US20050095244A1  
; GENERAL INFORMATION:  
; APPLICANT: Jure-Kunkel, Maria  
; APPLICANT: Hefta, Laura  
; APPLICANT: Santoro, Marc  
; APPLICANT: Ganguly, Subinay  
; TITLE OF INVENTION: FULLY HUMAN ANTIBODIES AGAINST HUMAN 4-1BB  
; FILE REFERENCE: 10060 NP  
; CURRENT APPLICATION NUMBER: US/10/961,567A  
; CURRENT FILING DATE: 2004-10-08  
; PRIOR APPLICATION NUMBER: US 60/510193  
; PRIOR FILING DATE: 2003-10-10  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patentin version 3.2

SEQ ID NO 3  
LENGTH: 467  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: pd17-20H4.9.h4a amino acid sequence  
US-10-961-567A-3

Query Match  
Best Local Similarity 91.5%; Score 2177; DB 5; Length 467;  
Matches 414; Conservative 11; Mismatches 19; Indels 6; Gaps 2;

1 QVQLQESGPGLVKPSQTLSLTCTVSGSISGGNYNNIRQHPGKLEWIGYIYSGNTY 60  
20 QVQLQESGPGLVKPSQTLSLTCTVSGSISGGNYNNIRQHPGKLEWIGYIYSGNTY 77  
61 YNPISKSRITISIDTSKNQFSLTSSVTAADTAAYVYCARDGG----DDAFDIWGQGTWVT 116  
78 YNPISKSRITISIDTSKNQFSLTSSVTAADTAAYVYCARDGG----DDAFDIWGQGTWVT 137  
117 VSSASTKGPSVFLPACSRSTSESTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 176  
138 VSSASTKGPSVFLPACSRSTSESTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 197  
177 QSSGLYSLSVTVTPSSSLGTITKTCNVDPKPSNTKVDKRVESKYGPPCPAPFLGG 236  
198 QSSGLYSLSVTVTPSSSLGTITKTCNVDPKPSNTKVDKRVESKYGPPCPAPFLGG 257  
237 PSVFLPFPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNVDGVVHNATKPREEQFN 296  
258 PSVFLPFPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNVDGVVHNATKPREEQFN 317  
297 STYRVVSVLTVLHODMNLNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPS 356  
318 STYRVVSVLTVLHODMNLNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPS 377  
357 MTNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLRTVDPK 416  
378 MTNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLRTVDPK 437  
417 QEGNVFSCSVHMEALHNHYTQKSLSLGLK 446  
438 QEGNVFSCSVHMEALHNHYTQKSLSLGLK 467

APPLICATION NUMBER: US/09/612,914A  
FILING DATE: 10-Jul-2000  
APPLICATION NUMBER: US 08/523,894  
FILING DATE: 06-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-165  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-10-211-357-8

Query Match  
Best Local Similarity 91.3%; Score 2171; DB 4; Length 467;  
Matches 418; Conservative 7; Mismatches 13; Indels 18; Gaps 4;

1 QVQLQESGPGLVKPSQTLSLTCTVSGSISGGNYNNIRQHPGKLEWIGYIYSGNT 59  
20 QVQLQESGPGLVKPSQTLSLTCTVSGSISGGNYNNIRQHPGKLEWIGYIYSGNT 78  
60 YNPISKSRITISIDTSKNQFSLTSSVTAADTAAYVYCARDGGDAFDI-----WG 110  
79 YNPISKSRITISIDTSKNQFSLTSSVTAADTAAYVYCARDGGDAFDI-----WG 131  
111 QGTMVTVSASTKGPSVFLPACSRSTSESTAAALGCLVKDYFPEPVTVSWNSGALTSGV 170  
132 QGTMVTVSASTKGPSVFLPACSRSTSESTAAALGCLVKDYFPEPVTVSWNSGALTSGV 191  
171 TTPAVLQSSGLYSLSVTVTPSSSLGTITKTCNVDPKPSNTKVDKRVESKYGPPCP 230  
192 TTPAVLQSSGLYSLSVTVTPSSSLGTITKTCNVDPKPSNTKVDKRVESKYGPPCP 251  
231 PEFLLGSPVFLPFPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNVDGVVHNATKP 290  
252 PEFLLGSPVFLPFPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNVDGVVHNATKP 311  
291 REEQNSTYRVVSVLTVLHODMNLNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVY 350  
312 REEQNSTYRVVSVLTVLHODMNLNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVY 371  
351 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSL 410  
372 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSL 431  
411 VDKSRWQEGNVFSCSVHMEALHNHYTQKSLSLGLK 446  
432 VDKSRWQEGNVFSCSVHMEALHNHYTQKSLSLGLK 467

RESULT 6  
US-10-211-357-10  
Sequence 10, Application US/10211357  
Publication No. US2003007275A1  
GENERAL INFORMATION:  
APPLICANT: Hanna, Nabil  
Newman, Roland A.  
Reff, Mitchell E.  
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
Therapy  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
ZIP: 22314-3187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/211,357  
FILING DATE: 05-Aug-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

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;
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/211,357
; FILING DATE: 05-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/612,914A
; FILING DATE: 10-Jul-2000
; APPLICATION NUMBER: US 08/523,894
; FILING DATE: 06-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-211-357-10
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Query Match 91.0%; Score 2164; DB 4; Length 467;
Best Local Similarity 91.4%; Pred. No. 5,9e-138;
Matches 417; Conservative 7; Mismatches 14; Indels 18; Gaps 4;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIROHPGKLEWIGVIYYS-GNT 59
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVQLQESGPGLVKPSQTLSTCTVSGGSI-SGDYYWFWIRSPGKLEWIGVIYSGGGT 78
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
60 YNPSSLKSRITISIDTSKNQFSLTSSVTAADTAVYYCARDGGDAFDI-----WG 110
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
79 NYNPSLNRRVSIIDTSKNLFSKLRSVTAADTAVYYCAS-----NILKYLHLLYWG 131

QY 111 QGTWTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH 170
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
132 QGVLTVTSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH 191
QY 171 TTPAVLQSSGLYSLSVTVTPSSSLGTKTTCNVDPKPSNTKVDKRVSCKYGPCCPCPA 230
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
192 TTPAVLQSSGLYSLSVTVTPSSSLGTKTTCNVDPKPSNTKVDKRVSCKYGPCCPCPA 251
QY 231 PFLGSGPSVFLPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKP 290
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
252 PFEFGSPVFLPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKP 311
QY 291 REEQFNSTYRVVSVLTVLHQLWLNKKEYCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 350
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
312 REEQFNSTYRVVSVLTVLHQLWLNKKEYCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 371
QY 351 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLT 410
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
372 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLT 431
QY 411 VDKSRWQEGNVFSCSWMEALHNHYTQKSLSLSLGK 446
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
432 VDKSRWQEGNVFSCSWMEALHNHYTQKSLSLSLGK 467
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RESULT 7
US-10-211-357-12
; Sequence 12, Application US/10211357
; Publication No. US2003007725A1
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;
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; Newman, Roland A.
; Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/211,357
; FILING DATE: 05-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/612,914A
; FILING DATE: 10-Jul-2000
; APPLICATION NUMBER: US 08/523,894
; FILING DATE: 06-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-211-357-12

Query Match 90.8%; Score 2159; DB 4; Length 467;
Best Local Similarity 91.2%; Pred. No. 1.3e-137;
Matches 416; Conservative 7; Mismatches 15; Indels 18; Gaps 4;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIROHPGKLEWIGVIYYS-GNT 59
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVQLQESGPGLVKPSQTLSTCTVSGGSI-SGDYYWFWIRSPGKLEWIGVIYSGGGT 78
QY 60 YNPSSLKSRITISIDTSKNQFSLTSSVTAADTAVYYCARDGGDAFDI-----WG 110
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
79 NYNPSLNRRVSIIDTSKNLFSKLRSVTAADTAVYYCAS-----NILKYLHLLYWG 131

QY 111 QGTWTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH 170
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
132 QGVLTVTSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH 191
QY 171 TTPAVLQSSGLYSLSVTVTPSSSLGTKTTCNVDPKPSNTKVDKRVSCKYGPCCPCPA 230
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
192 TTPAVLQSSGLYSLSVTVTPSSSLGTKTTCNVDPKPSNTKVDKRVSCKYGPCCPCPA 251
QY 231 PFLGSGPSVFLPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKP 290
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
252 PFEFGSPVFLPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKP 311
QY 291 REEQFNSTYRVVSVLTVLHQLWLNKKEYCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 350
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
312 REEQFNSTYRVVSVLTVLHQLWLNKKEYCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 371
QY 351 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLT 410
```

Db 372 PPSQEMTKNQSLTCLVKGFPSPDIWVWESNGQPNKYKTPPVLDSGSGFFLYSLRT 431  
Qy 411 VDKSRWQEGNVFSCVMHEALHNNHYTKSLSLSGK 446  
Db 432 VDKSRWQEGNVFSCVMHEALHNNHYTKSLSLSGK 467

RESULT 8

US-10-910-901-6  
; Sequence 6, Application US/10910901  
; Publication No. US20050054019A1  
; GENERAL INFORMATION:  
; APPLICANT: MICHAUD, NEIL R., et al.  
; TITLE OF INVENTION: ANTIBODIES TO c-MET  
; FILE REFERENCE: ABX-PF5  
; CURRENT APPLICATION NUMBER: US/10/910,901  
; PRIOR FILING DATE: 2004-08-03  
; PRIOR APPLICATION NUMBER: US 60/492,432  
; PRIOR FILING DATE: 2003-08-04  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 6  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-910-901-6

Query Match 90.7%; Score 2158.5; DB 5; Length 480;  
Best Local Similarity 88.5%; Pred. No. 1.4e-137;  
Matches 409; Conservative 17; Mismatches 19; Indels 17; Gaps 3;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYNNWIRQHPGKGLWIGYIYSGNTY 60  
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYNNWIRQHPGKGLWIGYIYSGNTY 79  
Qy 61 YNPISLRSRTISIDTSKNQFSLTSSVTAADTAIVYCARDG-----GDADF- 106  
Db 80 YNPISLRSRTISIDTSKNQFSLTSSVTAADTAIVYCARDGPGLYGCSSTSCPTVGYIY 139  
Qy 107 --DIWGGTMTVTVSSASTKPSVFLPAPCSRSTSESTAALGCLVKDYFPEPVTVSNWSGA 164  
Db 140 GMDVWGQGTITVSSASTKPSVFLPAPCSRSTSESTAALGCLVKDYFPEPVTVSNWSGA 199  
Qy 165 LTSGVHTFPVAVLQSSGLYSSVTVVPSNFGITQYTCNVDPKPSNTKVDKRVESKGGPP 224  
Db 200 LTSGVHTFPVAVLQSSGLYSSVTVVPSNFGITQYTCNVDPKPSNTKVDKRVESKGGPP 259  
Qy 225 CPSCPAPEFLGGPSVFLPAPKPDTLMSRTPEVTCVVDVSOEDPEVQFNWYVDGVEVH 284  
Db 260 CPSCPAPEFLGGPSVFLPAPKPDTLMSRTPEVTCVVDVSOEDPEVQFNWYVDGVEVH 318  
Qy 285 NAKTKPREQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAGQPRE 344  
Db 319 NAKTKPREQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPAPIEKTIISKAGQPRE 378  
Qy 345 PQVYTLPPSQEMTKNQSLTCLVKGFPSPDIWVWESNGQPNKYKTPPVLDSGSGFF 404  
Db 379 PQVYTLPPSQEMTKNQSLTCLVKGFPSPDIWVWESNGQPNKYKTPPVLDSGSGFF 438  
Qy 405 LYSRLTVDKSRWQEGNVFSCVMHEALHNNHYTKSLSLSGK 446  
Db 439 LYSRLTVDKSRWQEGNVFSCVMHEALHNNHYTKSLSLSGK 480

RESULT 9

US-10-310-719-37  
; Sequence 37, Application US/10310719  
; Publication No. US20030166163A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity  
; FILE REFERENCE: LEX-020

; CURRENT APPLICATION NUMBER: US/10/310,719  
; CURRENT FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/337,113  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/371,966  
; PRIOR FILING DATE: 2002-04-12  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 37  
; LENGTH: 580  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: di-NHS76(gamma4h) (FN>AQ) -ala-IL2 (D20T) heavy chain fused to  
; OTHER INFORMATION: IL-2 variant  
US-10-310-719-37

Query Match 89.8%; Score 2136.5; DB 4; Length 580;  
Best Local Similarity 91.3%; Pred. No. 5.5e-136;  
Matches 409; Conservative 11; Mismatches 23; Indels 5; Gaps 3;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYNNWIRQHPGKGLWIGYIYSGNTY 60  
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGYNNWIRQHPGKGLWIGYIYSGNTY 59  
Qy 61 YNPISLRSRTISIDTSKNQFSLTSSVTAADTAIVYCARDGDDAFDIWQGGTMTVTVSSA 120  
Db 60 YNPISLRSRTISIDTSKNQFSLTSSVTAADTAIVYCAR-GKWSKFDYWGQGLTVTVSSA 118  
Qy 121 STKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPVTVSNWSGALTSGVHTTTPAVLQSSG 180  
Db 119 STKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPVTVSNWSGALTSGVHTTTPAVLQSSG 178  
Qy 181 LYSLSVTVVPSNFGITQYTCNVDPKPSNTKVDKRVESK-----YGPCCPCPAPEFLGGP 237  
Db 179 LYSLSVTVVPSNFGITQYTCNVDPKPSNTKVDKRVESKCDKTHCTCPCPAPEFLGGP 238  
Qy 238 SVFLPAPKPDTLMSRTPEVTCVVDVSOEDPEVQFNWYVDGVEVHNAKTKPREQAQS 297  
Db 239 SVFLPAPKPDTLMSRTPEVTCVVDVSOEDPEVQFNWYVDGVEVHNAKTKPREQAQS 298  
Qy 298 TYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAGQPREQVYTLPPSQEM 357  
Db 299 TYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAGQPREQVYTLPPSQEM 358  
Qy 358 TKNQVSLTCLVKGFPSPDIWVWESNGQPNKYKTPPVLDSGSGFFLYSLTVDKSRMQ 417  
Db 359 TKNQVSLTCLVKGFPSPDIWVWESNGQPNKYKTPPVLDSGSGFFLYSLTVDKSRMQ 418  
Qy 418 EGNVFSQVMHEALHNNHYTKSLSLSG 445  
Db 419 QGNIFSCVMHEALHNNHYTKSATATPG 446

RESULT 10

US-10-937-596-32  
; Sequence 32, Application US/10937596  
; Publication No. US20050118169A1  
; GENERAL INFORMATION:  
; APPLICANT: BARTKE, ILSE  
; APPLICANT: CARR, FRANCIS  
; APPLICANT: CHIZZONITE, RICHARD ANTHONY  
; APPLICANT: EUGUI, ELSIE M.  
; APPLICANT: FERTIG, GEORG  
; APPLICANT: HAMILTON, ANITA  
; APPLICANT: LANZENDORFER, MARTIN  
; APPLICANT: RUEGER, PETRA  
; APPLICANT: SCHUMACHER, RALF  
; APPLICANT: TRUITT, THERESA PATRICIA  
; TITLE OF INVENTION: ANTIBODIES AGAINST INTERLEUKIN-1 RECEPTOR AND USES THEREOF  
; FILE REFERENCE: CD21842-US1  
; CURRENT APPLICATION NUMBER: US/10/937,596  
; CURRENT FILING DATE: 2004-09-09

; PRIOR APPLICATION NUMBER: 60/501,681
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: EP 03029659.4
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy
; OTHER INFORMATION: Chain Of DEI 5/8
US-10-937-596-32

Query Match 89.1%; Score 2119; DB 5; Length 442;
Best Local Similarity 90.8%; Pred. No. 6.1e-135;
Matches 405; Conservative 16; Mismatches 21; Indels 4; Gaps 2;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIROHPGKLEWIGYIYSGNTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIROHPGKLEWIGYIYSGNTY 58
Qy 61 YNPISLKRITISIDTSKNQFSLTSSVTAADTAAYVYCARDGGDDAFDIWGQGTMTVTVSSA 120
Db 59 YSTLSKSRITISIDTSKNQFSLTSSVTAADTAAYVYCARDGGDDAFDIWGQGTMTVTVSSA 116
Qy 121 STKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSG 180
Db 117 STKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSG 176
Qy 181 LYSLSVTVTPSSSLGTYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPEFLGGPSVF 240
Db 177 LYSLSVTVTPSSSLGTYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPEFLGGPSVF 236
Qy 241 LPPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYR 300
Db 237 LPPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYR 296
Qy 301 VVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQRPQVYTLPPSQEEMTKN 360
Db 297 VVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQRPQVYTLPPSQEEMTKN 356
Qy 361 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQSGN 420
Db 357 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQSGN 416
Qy 421 VFSCSVMEALHNHYTKSLSLSLKG 446
Db 417 VFSCSVMEALHNHYTKSLSLSLKG 442

RESULT 11
US-10-910-901-10
; Sequence 10, Application US/10910901
; Publication No. US20050054019A1
; GENERAL INFORMATION:
; APPLICANT: MICHAUD, NEIL R., et al.
; TITLE OF INVENTION: ANTIBODIES TO C-MET
; FILE REFERENCE: ABX-PF5
; CURRENT APPLICATION NUMBER: US/10/910,901
; PRIOR FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: US 60/492,432
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-910-901-10

Query Match 88.6%; Score 2108; DB 5; Length 463;

Best Local Similarity 89.7%; Pred. No. 3.6e-134;
Matches 400; Conservative 16; Mismatches 28; Indels 2; Gaps 2;
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIROHPGKLEWIGYIYSGNTY 60
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIROHPGKLEWIGYIYSGNTY 79
Qy 61 YNPISLKRITISIDTSKNQFSLTSSVTAADTAAYVYCARDGGDDAFDIWGQGTMTVTVSSA 120
Db 80 YNPISLKRITISIDTSKNQFSLTSSVTAADTAAYVYCARDGGDDAFDIWGQGTMTVTVSSA 138
Qy 121 STKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSG 180
Db 139 STKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSG 198
Qy 181 LYSLSVTVTPSSSLGTYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPEFLGGPSVF 240
Db 199 LYSLSVTVTPSSSLGTYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPEFLGGPSVF 257
Qy 241 LPPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYR 300
Db 258 LPPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYR 317
Qy 301 VVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQRPQVYTLPPSQEEMTKN 360
Db 318 VVSVLTVLHODWLNKGEYKCKVSNKGLPAPIEKTIISKAKGQRPQVYTLPPSQEEMTKN 377
Qy 361 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQSGN 420
Db 378 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQSGN 437
Qy 421 VFSCSVMEALHNHYTKSLSLSLKG 446
Db 438 VFSCSVMEALHNHYTKSLSLSLKG 463

RESULT 12
US-10-292-088-86
; Sequence 86, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-86

Query Match 88.5%; Score 2106.5; DB 4; Length 466;
Best Local Similarity 89.3%; Pred. No. 4.5e-134;
Matches 402; Conservative 16; Mismatches 25; Indels 7; Gaps 3;
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIROHPGKLEWIGYIYSGNTY 60
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIROHPGKLEWIGYIYSGNTY 77
Qy 61 YNPISLKRITISIDTSKNQFSLTSSVTAADTAAYVYCARDGG---DDAFDIWGQGTMTV 116
Db 78 YNPISLKRITISIDTSKNQFSLTSSVTAADTAAYVYCARDGG---DDAFDIWGQGTMTV 137
Qy 117 VSSASTKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVL 176



Db 138 VSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPVTYVSNWNGALTSVHTTFAVL 197  
QY 177 QSSGLYSLSSVVTVPSSSLGTYYTCNVDPKPSNTKVDKRVSKYKPPCPSPAPFLGG 236  
Db 198 QSSGLYSLSSVVTVPSSNFGTQYTCNVDPKPSNTKVDKRVSKYKPPCPSPAPFLGG 256  
QY 237 PSVFLPPPKPDKTLMISRTPEVTCVVVDYSDPEVQFNWYVDGVEVHNAKTKPREEQFN 296  
Db 257 PSVFLPPPKPDKTLMISRTPEVTCVVVDYSDPEVQFNWYVDGVEVHNAKTKPREEQFN 316  
QY 297 STYRVVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEE 356  
Db 317 STYRVVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTIKAKGQPREPQVYTLPPSQEE 376  
QY 357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSLRTVDKSRW 416  
Db 377 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSLRTVDKSRW 436  
QY 417 QEGNVFSCVMHEALHNHYTQKSLSLGLK 446  
Db 437 QEGNVFSCVMHEALHNHYTQKSLSLSPGK 466

RESULT 13  
US-10-292-088-70  
; Sequence 70, Application US/10292088  
; Publication No. US20030211100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US  
; CURRENT APPLICATION NUMBER: US/10/292,088  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 70  
; LENGTH: 466  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-292-088-70

Query Match 88.5%; Score 2104.5; DB 4; Length 466;  
Best Local Similarity 89.1%; Pred. No. 6.2e-134;  
Matches 401; Conservative 17; Mismatches 25; Indels 7; Gaps 3;

QY 1 QVOLQESGGLVKPQSTLSLCTCTVSGGSISSGGNWNWIRQHPGKGLWIGIYYSGNTY 60  
Db 20 QVOLQESGGLVKPQSTLSLCTCTVSGGSISSGGNWNWIRQHPGKGLWIGIYYSGNTY 77  
QY 61 YNPGLSKRITISIDTSKQFSLTSLNSVTAADTAATVYCARGG---DDAFDINGQGTMT 116  
Db 78 YNPGLSKRITISIDTSKQFSLTSLNSVTAADTAATVYCARGGGLYGDYGPAPWGQGTMT 137  
QY 117 VSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPVTYVSNWNGALTSVHTTFAVL 176  
Db 138 VSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPVTYVSNWNGALTSVHTTFAVL 197  
QY 177 QSSGLYSLSSVVTVPSSSLGTYYTCNVDPKPSNTKVDKRVSKYKPPCPSPAPFLGG 236  
Db 198 QSSGLYSLSSVVTVPSSNFGTQYTCNVDPKPSNTKVDKRVSKYKPPCPSPAPFLGG 256  
QY 237 PSVFLPPPKPDKTLMISRTPEVTCVVVDYSDPEVQFNWYVDGVEVHNAKTKPREEQFN 296  
Db 257 PSVFLPPPKPDKTLMISRTPEVTCVVVDYSDPEVQFNWYVDGVEVHNAKTKPREEQFN 316  
QY 297 STYRVVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEE 356  
Db 317 STYRVVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTIKAKGQPREPQVYTLPPSQEE 376  
QY 357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSLRTVDKSRW 416  
Db 377 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSLRTVDKSRW 436  
QY 417 QEGNVFSCVMHEALHNHYTQKSLSLGLK 446  
Db 437 QEGNVFSCVMHEALHNHYTQKSLSLSPGK 466

Db 317 STYRVVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTIKAKGQPREPQVYTLPPSQEE 376  
QY 357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSLRTVDKSRW 416  
Db 377 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSLRTVDKSRW 436  
QY 417 QEGNVFSCVMHEALHNHYTQKSLSLGLK 446  
Db 437 QEGNVFSCVMHEALHNHYTQKSLSLSPGK 466

RESULT 14  
US-10-292-088-30  
; Sequence 30, Application US/10292088  
; Publication No. US20030211100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US  
; CURRENT APPLICATION NUMBER: US/10/292,088  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 466  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-292-088-30

Query Match 88.1%; Score 2096.5; DB 4; Length 466;  
Best Local Similarity 88.9%; Pred. No. 2.1e-133;  
Matches 400; Conservative 16; Mismatches 27; Indels 7; Gaps 3;

QY 1 QVOLQESGGLVKPQSTLSLCTCTVSGGSISSGGNWNWIRQHPGKGLWIGIYYSGNTY 60  
Db 20 QVOLQESGGLVKPQSTLSLCTCTVSGGSISSGGNWNWIRQHPGKGLWIGIYYSGNTY 77  
QY 61 YNPGLSKRITISIDTSKQFSLTSLNSVTAADTAATVYCARGG---DGGDDAFDINGQGTMT 116  
Db 78 YNPGLSKRITISIDTSKQFSLTSLNSVTAADTAATVYCARGGGLYGDYGPAPWGQGTMT 137  
QY 117 VSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPVTYVSNWNGALTSVHTTFAVL 176  
Db 138 VSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPVTYVSNWNGALTSVHTTFAVL 197  
QY 177 QSSGLYSLSSVVTVPSSSLGTYYTCNVDPKPSNTKVDKRVSKYKPPCPSPAPFLGG 236  
Db 198 QSSGLYSLSSVVTVPSSNFGTQYTCNVDPKPSNTKVDKRVSKYKPPCPSPAPFLGG 256  
QY 237 PSVFLPPPKPDKTLMISRTPEVTCVVVDYSDPEVQFNWYVDGVEVHNAKTKPREEQFN 296  
Db 257 PSVFLPPPKPDKTLMISRTPEVTCVVVDYSDPEVQFNWYVDGVEVHNAKTKPREEQFN 316  
QY 297 STYRVVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEE 356  
Db 317 STYRVVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTIKAKGQPREPQVYTLPPSQEE 376  
QY 357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSLRTVDKSRW 416  
Db 377 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSLRTVDKSRW 436  
QY 417 QEGNVFSCVMHEALHNHYTQKSLSLGLK 446  
Db 437 QEGNVFSCVMHEALHNHYTQKSLSLSPGK 466

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RESULT 15
US-10-818-068-25
; Sequence 25, Application US/10818068
; Publication No. US20050002930A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: METHODS OF PRODUCTION AND USE OF ANTI-INTEGRIN ANTIBODIES FOR THE
; TITLE OF INVENTION: CONTROL OF TISSUE GRANULATION
; FILE REFERENCE: 05882.0186.NPUS01
; CURRENT APPLICATION NUMBER: US/10/818,068
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-818-068-25

Query Match      87.8%; Score 2088.5; DB 5; Length 451;
Best Local Similarity 87.6%; Pred.No. 7.2e-133;
Matches 397; Conservative 20; Mismatches 27; Indels 9; Gaps 2;

Qy      1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGQNYNNIRQHPGKGLEWIGYIYSGNTY 60
Db      1 QVQLKESGPGLVAPQSLSITCTISGSLTDYGVH--WVRQPPGKGLEWLVVINS DGSST 58
Qy      61 YNPISLKSRITISIDTSKNQFSLTSSVTAADPAVYYCARDG-----GDDAFDIWGQGT 113
Db      59 YNSALKSRMTIRKDNKSKQVFLIMNSLQTDSDAMYCARHGTYTGMTTTGDALDYWGQGT 118
Qy      114 MYTVSSASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 173
Db      119 SVTVSSASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 178
Qy      174 AVLQSSGLYSLSVTVTPSSSLGTITYTCNVDPKPSNTKVDKRVESKYGPPCPCPAPEF 233
Db      179 AVLQSSGLYSLSVTVTPSSSLGTITYTCNVDPKPSNTKVDKRVESKYGPPCPCPAPEF 238
Qy      234 LGGPSVFLFPPPKPDTLMISRTPETCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE 293
Db      239 LGGPSVFLFPPPKPDTLMISRTPETCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE 298
Qy      294 QFNSTYRVVSVLTVLIHQDWLNGKEYCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPS 353
Db      299 QFNSTYRVVSVLTVLIHQDWLNGKEYCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPS 358
Qy      354 QEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDK 413
Db      359 QEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDK 418
Qy      414 SRWQEGNVFSCVMHEALHNHYTQKSLSLCK 446
Db      419 SRWQEGNVFSCVMHEALHNHYTQKSLSLCK 451
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Search completed: December 17, 2005, 01:29:29  
Job time : 148.315 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 17, 2005, 01:18:45 ; Search time 9.46061 Seconds  
(without alignments)  
317.590 Million cell updates/sec

Title: US-10-644-277-62

Perfect score: 2379  
Sequence: 1 QVQLQESGFLVKPQSTLSL.....MHEALHNHYTKSLSLGK 446

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 51470 seqs, 6736768 residues

Total number of hits satisfying chosen parameters: 51470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.New.\*  
1: /cgn2\_6/prodata/1/pubpa/US09\_NEW\_PUB\_PEP.\*  
2: /cgn2\_6/prodata/1/pubpa/US06\_NEW\_PUB\_PEP.\*  
3: /cgn2\_6/prodata/1/pubpa/US07\_NEW\_PUB\_PEP.\*  
4: /cgn2\_6/prodata/1/pubpa/US08\_NEW\_PUB\_PEP.\*  
5: /cgn2\_6/prodata/1/pubpa/PCT\_NEW\_PUB\_PEP.\*  
6: /cgn2\_6/prodata/1/pubpa/US10\_NEW\_PUB\_PEP.\*  
7: /cgn2\_6/prodata/1/pubpa/US11\_NEW\_PUB\_PEP.\*  
8: /cgn2\_6/prodata/1/pubpa/US60\_NEW\_PUB\_PEP.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2044.5	85.9	476	7	US-11-139-499-12
2	1986.5	83.5	476	7	US-11-139-499-4
3	1970.5	82.8	451	6	US-10-923-327-11
4	1967.5	82.7	451	6	US-10-923-327-7
5	1967.5	82.7	451	6	US-10-923-327-9
6	1928.5	81.1	470	7	US-11-144-248-49
7	1920	80.7	477	7	US-11-000-463-395
8	1917	80.6	473	7	US-11-144-248-50
9	1912.5	80.4	470	7	US-11-144-248-45
10	1910	80.3	452	7	US-11-120-338-14
11	1905	80.1	451	7	US-11-120-338-22
12	1901.5	79.9	470	7	US-11-144-248-46
13	1895	79.7	444	7	US-11-172-320-6
14	1895	79.7	444	7	US-11-173-969-6
15	1895	79.7	452	7	US-11-120-338-15
16	1881	79.1	452	7	US-11-120-338-17
17	1876	78.9	451	7	US-11-120-338-25
18	1863	78.3	450	7	US-11-025-712-12
19	1854.5	78.0	478	7	US-11-139-499-8
20	1853.5	77.9	474	7	US-11-000-463-284
21	1842	77.4	579	7	US-11-174-186-41
22	1743	73.3	327	6	US-10-999-866-38
23	1743	73.3	327	7	US-11-061-821-38
24	1611.5	67.7	335	7	US-11-024-251-35
25	1605.5	67.5	326	6	US-10-999-866-36

26	1605.5	67.5	326	7	US-11-144-248-28	Sequence 28, Appl
27	1605.5	67.5	326	7	US-11-061-821-36	Sequence 36, Appl
28	1596.5	67.1	330	7	US-11-022-289-1	Sequence 1, Appl
29	1596.5	67.1	548	7	US-11-022-289-3	Sequence 3, Appl
30	1596.5	67.1	557	7	US-11-022-289-2	Sequence 2, Appl
31	1596.5	67.1	564	7	US-11-022-289-10	Sequence 10, Appl
32	1594.5	67.0	402	7	US-11-024-251-31	Sequence 31, Appl
33	1590.5	66.9	330	7	US-11-022-289-11	Sequence 11, Appl
34	1590.5	66.9	330	7	US-11-075-351-1	Sequence 15, Appl
35	1590.5	66.9	330	7	US-11-165-141-15	Sequence 1, Appl
36	1590.5	66.9	551	7	US-11-022-289-7	Sequence 7, Appl
37	1590.5	66.9	551	7	US-11-022-289-8	Sequence 8, Appl
38	1590.5	66.9	557	7	US-11-022-289-4	Sequence 4, Appl
39	1590.5	66.9	557	7	US-11-022-289-5	Sequence 5, Appl
40	1590.5	66.9	557	7	US-11-022-289-6	Sequence 6, Appl
41	1580	66.4	339	6	US-10-999-866-35	Sequence 35, Appl
42	1580	66.4	339	7	US-11-061-821-35	Sequence 35, Appl
43	1575	66.2	377	6	US-10-999-866-37	Sequence 37, Appl
44	1575	66.2	377	7	US-11-061-821-37	Sequence 37, Appl
45	1251	52.6	917	7	US-11-144-987-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1  
US-11-139-499-12  
; Sequence 12, Application US/11139499  
; Publication No. US20050260205A1  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSON, DARRELL R.  
; APPLICANT: HANNA, NABIL  
; APPLICANT: BRAMS, PETER  
; APPLICANT: HEARD, CHERYL  
; TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2  
; TITLE OF INVENTION: CO-STIMULATORY ANTIGENS  
; FILE REFERENCE: 37003-375681  
; CURRENT APPLICATION NUMBER: US/11/139,499  
; CURRENT FILING DATE: 2005-05-31  
; PRIOR APPLICATION NUMBER: US/09/576,424  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: PCT/US97/19906  
; PRIOR FILING DATE: 1997-10-29  
; PRIOR APPLICATION NUMBER: 08/746,361  
; PRIOR FILING DATE: 1996-11-08  
; PRIOR APPLICATION NUMBER: 08/487,550  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 476  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-139-499-12

Query Match	85.9%	Score	2044.5	DB 7	Length	476			
Best Local Similarity	85.6%	Pred. No.	2.1e-116						
Matches	392	Conservative	21	Mismatches	32	Indels	13	Gaps	4
Qy	1	QVQLQESGFLVKPQSTLSITCTVSGGSISSGGYNNWIRQHPGKLEWIGYTY-YSGNT	59						
Db	20	QVQLQESGFLVKPSETLTSLTCAVSGSI-SGGYGGWIRQHPGKLEWIGSEFVSSGNT	78						
Qy	60	YNNPSLKSRTITSDTSKNQFSLTSSVTAADTAATVYVCARDG-----GDDAFDIWQ	111						
Db	79	YNNPSLKSQVTISTDTSKNQFSLKNSMTAADTAATVYVCRDRLFSVGMVYNNWEDVWGP	138						
Qy	112	GTWTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVWNSGALTSGVHT	171						
Db	139	GLVLTWSSASTKGPSVFPLAPSKSTGGTAALGCLVKDYFPEPTVWNSGALTSGVHT	198						
Qy	172	FPAVLQSSGLYSLSVVTVPSSSLGTITKTYTCNVNDHKPSNTKVDKRVESK---YGPDPSPC	228						

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Db 199 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTCCPC 258
QY 229 PAPEFLGGSPVFLFPKPKDMLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKT 288
Db 259 PAPEFLGGSPVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
QY 289 KPREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPOVY 348
Db 319 KPREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVY 378
QY 349 TLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSR 408
Db 379 TLPPSRDELTKQNVSITCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK 438
QY 409 LTVDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLGLK 446
Db 439 LTVDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLSPGK 476
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## RESULT 2

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US-11-139-499-4
; Sequence 4, Application US/11139499
; Publication No. US200502605A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL R.
; APPLICANT: HANNA, NABIL
; APPLICANT: BRAMS, PETER
; APPLICANT: HEARD, CHERYL
; TITLE OF INVENTION: CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
; TITLE OF INVENTION: CO-STIMULATORY ANTIGENS
; FILE REFERENCE: 37003-275681
; CURRENT APPLICATION NUMBER: US/11/139,499
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: US/09/576,424
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US97/19906
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 08/746,361
; PRIOR FILING DATE: 1996-11-08
; PRIOR APPLICATION NUMBER: 08/487,550
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-139-499-4
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Query Match 83.5%; Score 1986.5; DB 7; Length 476;
Best Local Similarity 83.4%; Pred. No. 6.2e-113;
Matches 382; Conservative 24; Mismatches 39; Indels 13; Gaps 4;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYNWNIROHPGKLEWIGYIYSG-NT 59
Db 20 QVKLQWGESGLLQPSSETLSRTCVSSGGSI-SGYIYTWIRQTPGKLEWIGHIYNGATT 78
QY 60 YNPSSLKRITISIDTSKNQFSLTSSVTAADTAVVYCARDGDDA-----FDIWGO 111
Db 79 NNPSSLKRVTLISKDTSKNQFFELNLSVTDATAVYCARGRPDCTTCYGGWVDWVGP 138
QY 112 GTMTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHT 171
Db 139 GDLVTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHT 198
QY 172 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKRVESK---YGPCCPSC 228
Db 199 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTCCPC 258
QY 229 PAPEFLGGSPVFLFPKPKDMLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKT 288
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Db 259 PAPEFLGGSPVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
QY 289 KPREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPOVY 348
Db 319 KPREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVY 378
QY 349 TLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSR 408
Db 379 TLPPSRDELTKQNVSITCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK 438
QY 409 LTVDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLGLK 446
Db 439 LTVDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLSPGK 476

RESULT 3
US-10-923-327-11
; Sequence 11, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 11
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-923-327-11
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Query Match 82.8%; Score 1970.5; DB 6; Length 451;
Best Local Similarity 83.8%; Pred. No. 5.4e-112;
Matches 379; Conservative 23; Mismatches 43; Indels 7; Gaps 3;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYNWNIROHPGKLEWIGYIYSGNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCLAVSGYSITSGYS-WNIROAPGKLEWVASIKYSGTK 59
QY 61 YNPSSLKRITISIDTSKNQFSLTSSVTAADTAVVYCARDG---GDDAFDIWGGQTMVTV 117
Db 60 YNPVKGRITISLRDSDSKNTFYQWNSLRADTAVYCARSHYFGHHFAVWGQGLTVTV 119
QY 118 SSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ 177
Db 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ 179
QY 178 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKRVESK---YGPCCPSCAPEPL 234
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKRVESKCDKTHTCPPCPAPEPL 239
QY 235 GGPSVFLFPKPKDMLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKT KPREEQ 294
Db 240 GGPSVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQ 299
QY 295 FNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPOVYTLPPSQ 354
Db 300 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 359
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QY 355 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPNNTKTPPVLDSDGSPFLYSLTVDKS 414  
 DB 360 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPNNTKTPPVLDSDGSPFLYSLTVDKS 419

QY 415 RWQEGNVFSCSVMEALHNNHYTKQSLSLGK 446  
 DB 420 RWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 451

RESULT 4  
 US-10-923-327-7  
 ; Sequence 7, Application US/10923327  
 ; Publication No. US20050261208A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ROBINSON, CYNTHIA B.  
 ; APPLICANT: BALL, HOWARD A.  
 ; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR  
 ; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE  
 ; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE  
 ; TITLE OF INVENTION: PULMONARY DISEASE  
 ; FILE REFERENCE: 30775-723.501  
 ; CURRENT APPLICATION NUMBER: US/10/923.327  
 ; CURRENT FILING DATE: 2004-08-20  
 ; PRIOR APPLICATION NUMBER: PCT/US04/25054  
 ; PRIOR FILING DATE: 2004-07-30  
 ; PRIOR FILING DATE: 2003-10-29  
 ; PRIOR FILING DATE: 2003-10-29  
 ; PRIOR FILING DATE: 2003-07-31  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: Patent in Ver. 3.3  
 ; SEQ ID NO 7  
 ; LENGTH: 451  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: construct  
 US-10-923-327-7

Query Match 82.7%; Score 1967.5; DB 6; Length 451;  
 Best Local Similarity 83.6%; Pred. No. 8.1e-112;  
 Matches 378; Conservative 24; Mismatches 43; Indels 7; Gaps 3;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYMNIHQHPGKGLEWIGYISGNTY 60  
 DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYS-WNWIQAQPGKGLEWVASITYDGSN 59

QY 61 YNPGLKSRITISIDTSKNQFSLTSSVTAADTAIVYICARDG---GDDAFDIWGQGTMTV 117  
 DB 60 YNPVSKGRITISRDSSKNTFYLMNSLRADTAIVYICARGSHYFGHWHFAVWGQGLTV 119

QY 118 SSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 177  
 DB 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 179

QY 178 SGLYSLSSVTVTPSSSLGTTKTYTCNVDPKPSNTKVDKRVESK---YGPCCPCPAPEFL 234  
 DB 180 SGLYSLSSVTVTPSSSLGTTQTYICNVNHPKPSNTKVDKRVESKCDKTHTCPPCPAP 239

QY 235 GGPVSVFLPPPKDPTLMISRTPEVTVVDVSDQEDPEVQFNWYDGEVHNNAKTKPREEQ 294  
 DB 240 GGPVSVFLPPPKDPTLMISRTPEVTVVDVSDHEDPEVKFNWYDGEVHNNAKTKPREEQ 299

QY 295 FNSYTRVSVLTVLHODWLNKGEYCKVSNKGLPSSIEKTSKAGQPREPQVYTLPPSQ 354  
 DB 300 YNSTYRVSVLTVLHODWLNKGEYCKVSNKALPAIEKTSKAGQPREPQVYTLPPSR 359

QY 355 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPNNTKTPPVLDSDGSPFLYSLTVDKS 414  
 DB 360 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPNNTKTPPVLDSDGSPFLYSLTVDKS 419

QY 415 RWQEGNVFSCSVMEALHNNHYTKQSLSLGK 446  
 DB 420 RWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 451

RESULT 5  
 US-10-923-327-9  
 ; Sequence 9, Application US/10923327  
 ; Publication No. US20050261208A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ROBINSON, CYNTHIA B.  
 ; APPLICANT: BALL, HOWARD A.  
 ; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR  
 ; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE  
 ; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE  
 ; TITLE OF INVENTION: PULMONARY DISEASE  
 ; FILE REFERENCE: 30775-723.501  
 ; CURRENT APPLICATION NUMBER: US/10/923.327  
 ; CURRENT FILING DATE: 2004-08-20  
 ; PRIOR APPLICATION NUMBER: PCT/US04/25054  
 ; PRIOR FILING DATE: 2004-07-30  
 ; PRIOR FILING DATE: 2003-10-29  
 ; PRIOR FILING DATE: 2003-10-29  
 ; PRIOR FILING DATE: 2003-07-31  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: Patent in Ver. 3.3  
 ; SEQ ID NO 9  
 ; LENGTH: 451  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: construct  
 US-10-923-327-9

Query Match 82.7%; Score 1967.5; DB 6; Length 451;  
 Best Local Similarity 83.6%; Pred. No. 8.1e-112;  
 Matches 378; Conservative 24; Mismatches 43; Indels 7; Gaps 3;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYMNIHQHPGKGLEWIGYISGNTY 60  
 DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYS-WNWIQAQPGKGLEWVASITYDGSN 59

QY 61 YNPGLKSRITISIDTSKNQFSLTSSVTAADTAIVYICARDG---GDDAFDIWGQGTMTV 117  
 DB 60 YNPVSKGRITISRDSSKNTFYLMNSLRADTAIVYICARGSHYFGHWHFAVWGQGLTV 119

QY 118 SSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 177  
 DB 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 179

QY 178 SGLYSLSSVTVTPSSSLGTTKTYTCNVDPKPSNTKVDKRVESK---YGPCCPCPAPEFL 234  
 DB 180 SGLYSLSSVTVTPSSSLGTTQTYICNVNHPKPSNTKVDKRVESKCDKTHTCPPCPAP 239

QY 235 GGPVSVFLPPPKDPTLMISRTPEVTVVDVSDQEDPEVQFNWYDGEVHNNAKTKPREEQ 294  
 DB 240 GGPVSVFLPPPKDPTLMISRTPEVTVVDVSDHEDPEVKFNWYDGEVHNNAKTKPREEQ 299

QY 295 FNSYTRVSVLTVLHODWLNKGEYCKVSNKGLPSSIEKTSKAGQPREPQVYTLPPSQ 354  
 DB 300 YNSTYRVSVLTVLHODWLNKGEYCKVSNKALPAIEKTSKAGQPREPQVYTLPPSR 359

QY 355 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPNNTKTPPVLDSDGSPFLYSLTVDKS 414  
 DB 360 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPNNTKTPPVLDSDGSPFLYSLTVDKS 419

RESULT 6  
US-11-144-248-49  
; Sequence 49, Application US/11144248  
; Publication No. US20050244408A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Bruce D.  
; APPLICANT: Beebe, Jean  
; APPLICANT: Miller, Penelope E.  
; APPLICANT: Moyer, James D.  
; APPLICANT: Corvalan, Jose R.  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
; FILE REFERENCE: ABX-PF2  
; CURRENT APPLICATION NUMBER: US/11/144,248  
; CURRENT FILING DATE: 2005-06-02  
; PRIOR APPLICATION NUMBER: US/10/038,591  
; PRIOR FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: 60/259,927  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 49  
; LENGTH: 470  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-144-248-49

Query Match 81.1%; Score 1928.5; DB 7; Length 470;  
Best Local Similarity 81.7%; Pred. No. 1.8e-109;  
Matches 371; Conservative 23; Mismatches 49; Indels 11; Gaps 4;

QY 1 QVLOESGPGLVKPSQTLSTCTVSGSISGCGNYWNIHQHPGKLEWIGYIYSGNTY 60  
Db 20 QAQLVESGGGLVKPGSRLRLSCAASGFTFSD--YTMWIRQAPGKLEWVSYISSGSTR 77  
QY 61 -YNPSLKSRIITISIDTSKNQFSLTSSVTAADTAVVYCARDGGDAF-----DIWGQ 112  
Db 78 DVADSVKGRFTISRDNKNSLYLQNSLRADTAVVYCRDGVETTFYIYVGMVWGQ 137  
QY 113 TMVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNGALTSGVHVF 172  
Db 138 TTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNGALTSGVHVF 197  
QY 173 PAVLQSSGLYSLSVTVTPSSSLGTYTCNVNDHKPSNTKVDKRVESKVPSPCPAPE 232  
Db 198 PAVLQSSGLYSLSVTVTPSSSLGTYTCNVNDHKPSNTKVDKRVESKVPSPCPAPP 257  
QY 233 FLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSOEDPEVQFNWYVDGVFNHAKTKPRE 292  
Db 258 -VAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVFNHAKTKPRE 316  
QY 293 EQFNSTYRVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKQPREPVYTLPP 352  
Db 317 EQFNSTFRVSVSLTVHODWLNKGEYKCKVSNKGLPAPIEKTISKTKQPREPVYTLPP 376  
QY 353 SQEENTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLRLTVD 412  
Db 377 SREENTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVD 436  
QY 413 KSRWQEGNVFSCVMHEALHNHYTOKSLSLGK 446  
Db 437 KSRWQEGNVFSCVMHEALHNHYTOKSLSLSPGK 470

RESULT 7  
US-11-000-463-395  
; Sequence 395, Application US/11000463  
; Publication No. US20050266423A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Chen, Rui-hong

; APPLICANT: Qian, Xiaohong B.  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Zhang, Jie  
; APPLICANT: Zhou, Ping  
; APPLICANT: Cao, Yi-Cheng  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
; FILE REFERENCE: 785CIP4CN  
; CURRENT APPLICATION NUMBER: US/11/000,463  
; CURRENT FILING DATE: 2004-11-29  
; PRIOR APPLICATION NUMBER: 10/291,265  
; PRIOR FILING DATE: 2002-11-08  
; PRIOR APPLICATION NUMBER: PCT/US01/02623  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 09/922,279  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 09/617,746  
; PRIOR FILING DATE: 2000-07-17  
; PRIOR APPLICATION NUMBER: 09/631,451  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 09/633,870  
; PRIOR FILING DATE: 2000-09-15  
; NUMBER OF SEQ ID NOS: 944  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 395  
; LENGTH: 477  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-000-463-395

Query Match 80.7%; Score 1920; DB 7; Length 477;  
Best Local Similarity 80.4%; Pred. No. 6e-109;  
Matches 370; Conservative 27; Mismatches 47; Indels 16; Gaps 4;

QY 1 QVLOESGPGLVKPSQTLSTCTVSGSISGCGNYWNIHQHPGKLEWIGYIYSG-NT 59  
Db 20 QVQLVESGGGVQVQPSRLRLSCAASGFTFSNYG--MHVVRQAPGKLEWVAAIWYDGSNK 77  
QY 60 YNPSLKSRIITISIDTSKNQFSLTSSVTAADTAVVYCARDGG-----DDAFDIW 109  
Db 78 YVADSVKGRFTISRDNKNSLYLQNSLRADTAVVYCRDGVETTFYIYVGMVWGQ 137  
QY 110 GQGTMTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNGALTSGV 169  
Db 138 GQGTMTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNGALTSGV 197  
QY 170 HTFPAVLQSSGLYSLSVTVTPSSSLGTYTCNVNDHKPSNTKVDKRVESK---YGPPEP 226  
Db 198 HTFPAVLQSSGLYSLSVTVTPSSSLGTYTCNVNDHKPSNTKVDKRVESKCDKTHTCP 257  
QY 227 SCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSOEDPEVQFNWYVDGVFNH 286  
Db 258 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVFNH 317  
QY 287 KTKPREEQFNSTYRVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKQPREPQ 346  
Db 318 KTKPREEQFNSTYRVSVSVLTVLHODWLNKGEYKCKVSNKGLPAPIEKTISKAKQPREPQ 377  
QY 347 VYTLPPSQEENTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY 406  
Db 378 VYTLPPSREENTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY 437  
QY 407 SRLTVDKSRWQEGNVFSCVMHEALHNHYTOKSLSLGK 446  
Db 438 SKLTVDKSRWQEGNVFSCVMHEALHNHYTOKSLSLSPGK 477

RESULT 8  
US-11-144-248-50  
; Sequence 50, Application US/11144248

```
Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 473
TYPE: PRT
ORGANISM: Homo sapiens
US-11-144-248-50

Query Match      80.6%; Score 1917; DB 7; Length 473;
Best Local Similarity 80.7%; Pred. No. 9e-109;
Matches 372; Conservative 22; Mismatches 45; Indels 22; Gaps 5;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYNWIHQHPGKGLWIGIYYSGNT- 59
DB 20 QVQLVESGGGLVQPGGSLRLSCAASGFTFSD--YIMSWIRQAPGKGLWVSISSGSI 77
QY 60 YNPSSLKSRITISIDTSKQFSLTSSVTAADTAATVYICAR-----DGDGDA 105
DB 78 YVADSVKGRFTISRDNKNSLYLQMNSLRAEDTAATVYICARVLEWLYYYG---- 133
QY 106 FDTWGGQMTVTSASATKGSVPFLAPCSRSTSESTAALGCLVKDYFPEPTVYSWNSGAL 165
DB 134 MDVWGQGTITVTSASATKGSVPFLAPCSRSTSESTAALGCLVKDYFPEPTVYSWNSGAL 193
QY 166 TSGVHTPEPAVLQSSGLYSLSSVVPSSSLGTQYTCNVDPKPSNTKVDKRVESKYGPCC 225
DB 194 TSGVHTPEPAVLQSSGLYSLSSVVPSSSLGTQYTCNVDPKPSNTKVDKRVESKYGPCC 253
QY 226 PSCPAPEFLGPGSVFLPPPKDLMISRTPEVTCVVDVSDQEDPEVQFNWYDGVVHN 285
DB 254 PSCPAPE-VAGPSVFLPPPKDLMISRTPEVTCVVDVSDQEDPEVQFNWYDGVVHN 312
QY 286 AKTKPREQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTSKAGQPREP 345
DB 313 AKTKPREEQNSTFRVSVLTVLVHODWLNKGEYKCKVSNKGLPAPIEKTISKTKGQPREP 372
QY 346 QVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 405
DB 373 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 432
QY 406 YSLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLGLK 446
DB 433 YSLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSPGK 473

RESULT 9
US-11-144-248-45
Sequence 45, Application US/11144248
Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR

Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Brunetta, Paul G.
APPLICANT: Grewal, Iqbal S.
APPLICANT: Walicke, Patricia A.
TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
FILE REFERENCE: P2079R2
CURRENT APPLICATION NUMBER: US/11/120,338
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: US 60/568,460
PRIOR FILING DATE: 2004-05-05
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 14
LENGTH: 452
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized

FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 45
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-11-144-248-45

Query Match      80.4%; Score 1912.5; DB 7; Length 470;
Best Local Similarity 81.3%; Pred. No. 1.7e-108;
Matches 369; Conservative 27; Mismatches 47; Indels 11; Gaps 5;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYNWIHQHPGKGLWIGIYYIS-GNT 59
DB 20 EVQLLESGLLVQPGGSLRLSCTASGFTFSYA--NMWVRQAPGKGLWVSAISGSGT 77
QY 60 YNPSSLKSRITISIDTSKQFSLTSSVTAADTAATVYICAR-----DWDGAF 112
DB 78 FYADSVKGRFTISRDNSTRTLYLQMNSLRAEDTAATVYICARLDGWSDSYIYGMVWGOG 137
QY 113 TWVTYSSASTKGPSVPFLAPCSRSTSESTAALGCLVKDYFPEPTVYSWNSGALTSGVHTF 172
DB 138 TTVTYSSASTKGPSVPFLAPCSRSTSESTAALGCLVKDYFPEPTVYSWNSGALTSGVHTF 197
QY 173 PAVLQSSGLYSLSSVVPSSSLGTQYTCNVDPKPSNTKVDKRVESKYGPCCPAPE 232
DB 198 PAVLQSSGLYSLSSVVPSSSLGTQYTCNVDPKPSNTKVDKRVESKYGPCCPAPE 257
QY 233 FLGGPSVFLPPPKDLMISRTPEVTCVVDVSDQEDPEVQFNWYDGVVHNKTKPRE 292
DB 258 -VAGPSVFLPPPKDLMISRTPEVTCVVDVSDQEDPEVQFNWYDGVVHNKTKPRE 316
QY 293 EQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTSKAGQPREPQVYTLPP 352
DB 317 EQNSTYRVVSVLTVLVHODWLNKGEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPP 376
QY 353 SQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLRTVD 412
DB 377 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLRTVD 436
QY 413 KSRWQEGNVFSCSVMEALHNHYTQKSLSLGLK 446
DB 437 KSRWQEGNVFSCSVMEALHNHYTQKSLSLSPGK 470

RESULT 10
US-11-120-338-14
Sequence 14, Application US/11120338
Publication No. US20050271658A1
GENERAL INFORMATION:
APPLICANT: Brunetta, Paul G.
APPLICANT: Grewal, Iqbal S.
APPLICANT: Walicke, Patricia A.
TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
FILE REFERENCE: P2079R2
CURRENT APPLICATION NUMBER: US/11/120,338
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: US 60/568,460
PRIOR FILING DATE: 2004-05-05
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 14
LENGTH: 452
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
```



US-11-120-338-14

Query Match 80.3%; Score 1910; DB 7; Length 452;  
Best Local Similarity 81.1%; Pred. No. 2.3e-108;  
Matches 368; Conservative 27; Mismatches 49; Indels 10; Gaps 4;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIHQHPGKLEWIGVIY-YSNGT 59  
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYN--MHWVRQAPGKLEWVGAIYPGNGDT 58

QY 60 YNPGLSKRITISIDTSKNQFSLTSSVTAADTAVVYCAR----DGGDDAFDIMGQGTWV 115  
DB 59 SYNQFKGRFTISVDKSKNTLYLQWNSLRAEDTAVVYCARVVVYNSYWFYFDVWGQGLV 118

QY 116 TVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175  
DB 119 TVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 178

QY 176 LOSSGLYSLSVVTPVPSSSLGTQYICNVNHKPSNTKVDKRVESK---YGPSPCPSCPAPE 232  
DB 179 LOSSGLYSLSVVTPVPSSSLGTQYICNVNHKPSNTKVDKRVESK---YGPSPCPSCPAPE 238

QY 233 FLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNATKPRE 292  
DB 239 LLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNATKPRE 298

QY 293 EQFNSTYRVVSVLTVLHODWLNKKEYCKVSNKGLPSSIETKISKAKGQPREPQVYTLPP 352  
DB 299 EQYNSTYRVVSVLTVLHODWLNKKEYCKVSNKGLPSSIETKISKAKGQPREPQVYTLPP 358

QY 353 SOEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLTVD 412  
DB 359 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLTVD 418

QY 413 KSRWQGNVFCSCVMHEALHNYTKQSLSLGK 446  
DB 419 KSRWQGNVFCSCVMHEALHNYTKQSLSLSPGK 452

RESULT 11

US-11-120-338-22

; Sequence 22, Application US/11120338

; Publication No. US20050271658A1

; GENERAL INFORMATION:

; APPLICANT: BRUNETTA, PAUL G.

; APPLICANT: GREWAL, IQBAL S.

; APPLICANT: WALICKE, PATRICIA A.

; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE

; FILE REFERENCE: P2079R2

; CURRENT APPLICATION NUMBER: US/11/120,338

; CURRENT FILING DATE: 2003-05-03

; PRIOR APPLICATION NUMBER: US 60/568,460

; NUMBER OF SEQ ID NOS: 25

; SEQ ID NO 22

; LENGTH: 451

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: sequence is synthesized

US-11-120-338-22

Query Match 80.1%; Score 1905; DB 7; Length 451;  
Best Local Similarity 81.0%; Pred. No. 4.5e-108;  
Matches 367; Conservative 27; Mismatches 49; Indels 10; Gaps 4;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIHQHPGKLEWIGVIY-YSNGT 59  
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYN--MHWVRQAPGKLEWVGAIYPGNGDT 58

QY 60 YNPGLSKRITISIDTSKNQFSLTSSVTAADTAVVYCAR----DGGDDAFDIMGQGTWV 115  
DB 59 SYNQFKGRFTISVDKSKNTLYLQWNSLRAEDTAVVYCARVVVYNSYWFYFDVWGQGLV 118

QY 116 TVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175  
DB 119 TVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 178

QY 176 LOSSGLYSLSVVTPVPSSSLGTQYICNVNHKPSNTKVDKRVESK---YGPSPCPSCPAPE 232  
DB 179 LOSSGLYSLSVVTPVPSSSLGTQYICNVNHKPSNTKVDKRVESK---YGPSPCPSCPAPE 238

QY 233 FLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNATKPRE 292  
DB 239 LLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNATKPRE 298

QY 293 EQFNSTYRVVSVLTVLHODWLNKKEYCKVSNKGLPSSIETKISKAKGQPREPQVYTLPP 352  
DB 299 EQYNSTYRVVSVLTVLHODWLNKKEYCKVSNKGLPSSIETKISKAKGQPREPQVYTLPP 358

QY 353 SOEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLTVD 412  
DB 359 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLTVD 418

QY 413 KSRWQGNVFCSCVMHEALHNYTKQSLSLG 445  
DB 419 KSRWQGNVFCSCVMHEALHNYTKQSLSLSPG 451

RESULT 12

US-11-144-248-46

; Sequence 46, Application US/11144248

; Publication No. US20050244408A1

; GENERAL INFORMATION:

; APPLICANT: Cohen, Bruce D.

; APPLICANT: Beebe, Jean

; APPLICANT: Miller, Penelope E.

; APPLICANT: Moyer, James D.

; APPLICANT: Corvalan, Jose R.

; APPLICANT: Gallo, Michael

; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR

; FILE REFERENCE: ABX-PF2

; CURRENT APPLICATION NUMBER: US/11/144,248

; CURRENT FILING DATE: 2005-06-02

; PRIOR APPLICATION NUMBER: US/10/038,591

; PRIOR FILING DATE: 2002-01-04

; PRIOR APPLICATION NUMBER: 60/259,927

; PRIOR FILING DATE: 2001-01-05

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 46

; LENGTH: 470

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-144-248-46

Query Match 79.9%; Score 1901.5; DB 7; Length 470;  
Best Local Similarity 80.8%; Pred. No. 7.6e-108;  
Matches 367; Conservative 25; Mismatches 51; Indels 11; Gaps 4;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIHQHPGKLEWIGVIYYS-GNT 59  
DB 20 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYA--MSWVRQAPGKLEWVAISGGSGT 77

QY 60 YNPGLSKRITISIDTSKNQFSLTSSVTAADTAVVYCARDDGDD-----APDIMGQ 112  
DB 78 YYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVVYCAKGYSGWYIYVYGMVWGQ 137

QY 113 TMWTVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 172  
DB 138 TWTVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 197

QY 173 PAVLQSSGLYSLSVVTPVPSSSLGTQYICNVNHKPSNTKVDKRVESKYGPPSPCPSCPAPE 232  
DB 198 PAVLQSSGLYSLSVVTPVPSNFGTQYTCNVHDKPSNTKVDKTVRERCCVCEPCPAPP 257



QY 233 FLGGPSVFLPPKPKDMLSRTEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPRE 292  
Db 258 -VAGPSVFLPPKPKDMLSRTEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPRE 316  
QY 293 EGFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPRPQVYVTLPP 352  
Db 317 EGFNSTYRVSVLTVVHQDNLNGKEYKCKVSNKGLPAPIEKTISKTKGQPRPQVYVTLPP 376  
QY 353 SQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLTVD 412  
Db 377 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLTVD 436  
QY 413 KSRWQGNVFCSCVMHEALHNNHYTQKLSLSLKG 446  
Db 437 KSRWQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 470  
RESULT 13  
US-11-172-320-6  
; Sequence 6, Application US/11172320  
; Publication No. US2005024413A1  
; GENERAL INFORMATION:  
; APPLICANT: Adolf, Guenther  
; APPLICANT: Baum, Anke  
; APPLICANT: Heider, Karl-Heinz  
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using  
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and  
; TITLE OF INVENTION: Chemotherapeutic Agents  
; FILE REFERENCE: 1/1383  
; CURRENT APPLICATION NUMBER: US/11/172,320  
; CURRENT FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: US/10/645,215  
; PRIOR FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: EP 02 018 686.2  
; PRIOR FILING DATE: August 21, 2002  
; PRIOR APPLICATION NUMBER: US 60/405,956  
; PRIOR FILING DATE: August 26, 2002  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain  
US-11-172-320-6  
Query Match 79.7%; Score 1895; DB 7; Length 444;  
Best Local Similarity 81.2%; Pred. No. 1.8e-107;  
Matches 366; Conservative 27; Mismatches 46; Indels 12; Gaps 5;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGNY-WNIRQHPGKLEWIGYIYSGN- 58  
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFS---YDMSWVRQAPGKLEWVSTISSGGY 57  
QY 59 TYNPSLKSRIITSDTSKNQFSLTLSVTAADTAVYICARDGDDAFDIWGQGTMTVYS 118  
Db 58 TYILDSTIKGRFTISRDNKNSLYLQMSLRAEDTAVYICARQ-----LDYWGRTLVTS 113  
QY 119 SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 178  
Db 114 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 173  
QY 179 SGLYSLSVTVTPSSSLGTTKTYTCNVDPKPKNTKVDKRVESK---YGPCCPSCAPEFLG 235  
Db 174 SGLYSLSVTVTPSSSLGTTQYICNVNHPKNTKVDKRVESKCDKTHTCPCPAPELLG 233  
QY 236 GPSVFLFPKPKDMLSRTEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQF 295  
Db 234 GPSVFLFPKPKDMLSRTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 293  
QY 296 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPRPQVYVTLPPSQE 355  
Db 179 SGLYSLSVTVTPSSSLGTTKTYTCNVDPKPKNTKVDKRVESK---YGPCCPSCAPEFLG 235  
Db 174 SGLYSLSVTVTPSSSLGTTQYICNVNHPKNTKVDKRVESKCDKTHTCPCPAPELLG 233  
QY 236 GPSVFLFPKPKDMLSRTEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQF 295  
Db 234 GPSVFLFPKPKDMLSRTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 293  
QY 296 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPRPQVYVTLPPSQE 355

Db 294 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAKGQPRPQVYVTLPPSRD 353  
QY 356 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLTVDKSR 415  
Db 354 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLTVDKSR 413  
QY 416 WQGNVFCSCVMHEALHNNHYTQKLSLSLKG 446  
Db 414 WQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 444  
RESULT 14  
US-11-173-969-6  
; Sequence 6, Application US/11173969  
; Publication No. US20050271672A1  
; GENERAL INFORMATION:  
; APPLICANT: Adolf, G. et al.  
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates  
; FILE REFERENCE: 1/1211  
; CURRENT APPLICATION NUMBER: US/11/173,969  
; CURRENT FILING DATE: 2005-07-01  
; PRIOR APPLICATION NUMBER: US/10/150,475  
; PRIOR FILING DATE: 2002-05-17  
; PRIOR APPLICATION NUMBER: US 60/307,451  
; PRIOR FILING DATE: 2001-07-24  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Humanised  
; OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO: 6  
US-11-173-969-6  
Query Match 79.7%; Score 1895; DB 7; Length 444;  
Best Local Similarity 81.2%; Pred. No. 1.8e-107;  
Matches 366; Conservative 27; Mismatches 46; Indels 12; Gaps 5;  
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGNY-WNIRQHPGKLEWIGYIYSGN- 58  
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFS---YDMSWVRQAPGKLEWVSTISSGGY 57  
QY 59 TYNPSLKSRIITSDTSKNQFSLTLSVTAADTAVYICARDGDDAFDIWGQGTMTVYS 118  
Db 58 TYILDSTIKGRFTISRDNKNSLYLQMSLRAEDTAVYICARQ-----LDYWGRTLVTS 113  
QY 119 SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 178  
Db 114 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 173  
QY 179 SGLYSLSVTVTPSSSLGTTKTYTCNVDPKPKNTKVDKRVESK---YGPCCPSCAPEFLG 235  
Db 174 SGLYSLSVTVTPSSSLGTTQYICNVNHPKNTKVDKRVESKCDKTHTCPCPAPELLG 233  
QY 236 GPSVFLFPKPKDMLSRTEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQF 295  
Db 234 GPSVFLFPKPKDMLSRTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 293  
QY 296 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPRPQVYVTLPPSQE 355  
Db 294 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAKGQPRPQVYVTLPPSRD 353  
QY 356 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLTVDKSR 415  
Db 354 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLTVDKSR 413  
QY 416 WQGNVFCSCVMHEALHNNHYTQKLSLSLKG 446  
Db 414 WQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 444

```
RESULT 15
US-11-120-338-15
; Sequence 15, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IOBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 15
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-15

Query Match          79.7%; Score 1895; DB 7; Length 452;
Best Local Similarity 80.4%; Pred No. 1.8e-107;
Matches 365; Conservative 28; Mismatches 51; Indels 10; Gaps 4;

QY 1 QVQLQESGFLVKPSQTLTCTVSGSGSISSGGNYNMWIRQHPGKLEWIGYIY-YSQGT 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYN--MHVVRQAPGKLEWVGAIYPGNGDT 58
QY 60 YNPSLKSRITISITSKNQPSLTLSSTVAADTAIVYCAR----DGGDDAFDIWGQGTMV 115
Db 59 SYNQKFKGRFTISVDKSKNTLYLQNSLRAEDTAIVYCARVVVYSNSYWFYDVMGQGTLV 118
QY 116 TVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 175
Db 119 TVSSASTKGPSVFPLAPSKSTSGTAAAGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 178
QY 176 LQSSGLYSLSSVTVFPSSSLGTQTYTCNVDHKPSNTKVDKRVESK---YGPSPCSCPAPE 232
Db 179 LQSSGLYSLSSVTVFPSSSLGTQTYTCNVNHHKPSNTKVDKVEPKSCDKTHTCPPCPAPE 238
QY 233 FLGGPSVFLFPPPKKOTLMI SRTPEVTCVVVDVSDPEDEVQPNWYVDGVEVHNAKTKPRE 292
Db 239 LLGGPSVFLFPPPKKOTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 298
QY 293 EGFNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIISKAGQPREPOVYITLPP 352
Db 299 EQYNATYRVSVLTVLHODWLNKGYCKVSNKALPAPIATISKAGQPREPOVYITLPP 358
QY 353 SQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPLVDSGSPFLYSRLTVD 412
Db 359 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPLVDSGSPFLYSKLTVD 418
QY 413 KSRWQEGNVFSCSVNMEALHNHYTOKLSLSLCK 446
Db 419 KSRWQQGNVFSCSVNMEALHNHYTOKLSLSLSPGK 452
```

Search completed: December 17, 2005, 01:29:49  
Job time : 10.4606 secs

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OM protein - protein search, using sw model

Run on: December 17, 2005, 01:09:23 ; Search time 84.9515 Seconds  
(without alignments)  
1106.832 Million cell updates/sec

Title: US-10-644-277-64  
Perfect score: 1115  
Sequence: 1 DQMTQSPSSLSASVGRVT.....EVTHQGLSPVTKSFNRGRC 214

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1115	100.0	*214	8 ADK52358	Adk52358 Human ant
2	1060	95.1	238	9 AEB45883	Aeb45883 Human mon
3	1051	94.3	236	7 ADD93785	Add93785 Monoclonal
4	1045	93.7	502	8 ADN97515	Adn97515 Artificia
5	1039	93.2	367	3 AAY55078	Aay55078 Single ch
6	1039	93.2	626	3 AAY55081	Aay55081 Single ch
7	1037	93.0	237	8 ADQ90721	Adq90721 Anti-VEGF
8	1034	92.7	214	7 ADC26154	Adc26154 Parent an
9	1034	92.7	237	2 AAW70703	Aaw70703 Protein e
10	1034	92.7	237	5 ABB81107	Abb81107 Anti-VEGF
11	1034	92.7	237	5 ABP51952	Abp51952 Plasmid p
12	1034	92.7	237	8 ADO14128	Ado14128 Plasmid p
13	1034	92.7	237	8 ADO14131	Ado14131 Plasmid p
14	1034	92.7	237	8 ADQ90703	Adq90703 Anti-VEGF
15	1034	92.7	237	8 ADQ90701	Adq90701 Anti-VEGF
16	1034	92.7	237	8 ADQ90705	Adq90705 Anti-VEGF
17	1034	92.7	237	8 ADQ90709	Adq90709 Anti-VEGF
18	1034	92.7	237	8 ADQ90723	Adq90723 Anti-VEGF
19	1034	92.7	237	8 ADQ90707	Adq90707 Anti-VEGF
20	1034	92.7	260	5 ABP41164	Abp41164 Human ova
21	1034	92.7	650	5 ABP61241	Abp61241 Phage-dis
22	1027	92.1	214	2 AAW34504	Aaw34504 Light cha
23	1027	92.1	214	2 AAW34506	Aaw34506 Light cha
24	1027	92.1	214	2 AAW95615	Aaw95615 Humanized

25	1027	92.1	214	2 AAW30632	Aaw30632 Recombina
26	1027	92.1	214	2 AAY08754	Aay08754 Human ant
27	1027	92.1	214	4 AAB66777	Aab66777 rhuMab CD
28	1027	92.1	214	5 ABG31889	Abg31889 Humanised
29	1027	92.1	214	8 ADK18342	Adk18342 Amino aci
30	1027	92.1	214	8 ADQ17122	Adq17122 Humanised
31	1027	92.1	214	9 AEB27968	Aeb27968 Humanized
32	1027	92.1	233	2 AAR30777	Aar30777 pH52-9.0
33	1027	92.1	237	2 AAW95622	Aaw95622 PS1130 ex
34	1027	92.1	237	2 AAW30634	Aaw30634 Recombina
35	1027	92.1	237	4 AAB66784	Aab66784 Protein e
36	1027	92.1	237	6 ABP72745	Abp72745 Anti-CD18
37	1027	92.1	237	9 AEB27976	Aeb27976 E. coli S
38	1027	92.1	245	2 AAR98943	Aar98943 Humanised
39	1027	92.1	537	3 AAB03664	Aab03664 Anti-CD18
40	1026	92.0	233	2 AAR22754	Aar22754 Reshaped
41	1026	92.0	272	5 AAU97611	Aau97611 Protein #
42	1026	92.0	275	5 AAU97608	Aau97608 Protein e
43	1026	92.0	288	5 AAU97609	Aau97609 Protein e
44	1026	92.0	288	5 AAU97609	Aau97609 Protein e
45	1025.5	92.0	213	8 ADP88495	Adp88495 Humanised

ALIGNMENTS

RESULT 1	
ADK52358	
ID	ADK52358 standard; protein; 214 AA.
XX	XX
AC	ADK52358;
XX	XX
DT	20-MAY-2004 (first entry)
XX	XX
DE	Human anti-MCP-1 variable region light chain #16.
XX	XX
KW	monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW	Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;
KW	Vasotropic; Immunosuppressive; Neuroprotective; Neoplastic;
KW	Inflammatory condition; cancer; arthritis; multiple sclerosis;
KW	anti-MCP-1; heavy chain; light chain.
XX	XX
OS	Homo sapiens.
XX	XX
PN	WQ2004016769-A2.
XX	XX
PD	26-FEB-2004.
XX	XX
PF	19-AUG-2003; 2003WO-US026232.
XX	XX
PR	19-AUG-2002; 2002US-0404802P.
PA	(ABGE-) ABGENIX INC.
XX	XX
PI	Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI	Bhakta S;
XX	XX
DR	WPI; 2004-203794/19.
DR	N-PSDB; ADK52357.
XX	XX
PT	New human monoclonal antibody that binds to monocyte chemo-attractant
PT	protein-1 and is immobilized on an insoluble matrix, useful for
PT	diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT	rheumatoid arthritis or psoriasis.
XX	XX
PS	Claim 2; SEQ ID NO 64; 154pp; English.
XX	XX
CC	The present invention relates to a human monoclonal antibody that binds
CC	to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC	for the preparation of a medicament useful for treating neoplastic or
CC	inflammatory conditions. The neoplastic disease is selected from breast
CC	cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC	stomach cancer, endometrial cancer, kidney cancer, colon cancer,

CC pancreatic cancer or prostrate cancer. The inflammatory condition is  
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,  
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The  
CC antibodies are also useful for diagnosing the above diseases. It is also  
CC useful for the determining the level of MCP-1 and MCP-1 family members in  
CC patient samples. The present sequence represents a human anti-MCP-1  
CC variable region light chain sequence.  
XX  
SQ Sequence 214 AA;  
  
Query Match 100.0%; Score 1115; DB 8; Length 214;  
Best Local Similarity 100.0%; Pred. No. 2e-55; 0; Indels 0; Gaps 0;  
Matches 214; Conservative 0; Mismatches 0;  
  
QY 1 DIQMTQSPSSLSASVGRVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 60  
DB |||||  
1 DIQMTQSPSSLSASVGRVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 60  
  
QY 61 RFSGSGSGTDFTTINSLOPEDIAITYCOEYNNLPYSFGQGTKLIRKTVAAPSVFIFPP 120  
DB |||||  
61 RFSGSGSGTDFTTINSLOPEDIAITYCOEYNNLPYSFGQGTKLIRKTVAAPSVFIFPP 120  
  
QY 121 SDEQLKSGTASVVCLLNNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLT 180  
DB |||||  
121 SDEQLKSGTASVVCLLNNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLT 180  
  
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214  
DB |||||  
181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214  
  
RESULT 2  
AEB45883  
ID AEB45883 standard; protein; 238 AA.  
AC AEB45883;  
XX  
DT 06-OCT-2005 (first entry)  
XX  
DE Human monoclonal anti-MadCAM antibody #24.  
XX  
KW Monoclonal antibody; mucosal addressin cell adhesion molecule; MadCAM;  
KW inflammation; inflammatory bowel disease; Crohn's disease;  
KW ulcerative colitis; diverticular disease; gastritis; liver disease;  
KW primary biliary cirrhosis; primary sclerosing cholangitis;  
KW insulin dependent diabetes; graft versus host disease; antiinflammatory;  
KW gastrointestinal-gen.; antidiabetic; hepatotropic; antidiabetic;  
KW immunosuppressive; antibody.  
XX  
OS Homo sapiens.  
XX  
PN WO2005067620-A2.  
XX  
PD 28-JUL-2005.  
XX  
PF 07-JAN-2005; 2005WO-US000370.  
XX  
PR 09-JAN-2004; 2004US-0535490P.  
XX  
PA (PFIZ ) PFIZER INC.  
PA (ABGE-) ABGENIX INC.  
PA (PFIZ ) PFIZER LTD.  
XX  
PI Pullien N, Molloy E, Kellermann S, Green LL, Haak-Frendscho M;  
XX  
DR WPI: 2005-554958/56.  
DR N-PSDB; AEB45882.  
XX  
PT New antibody to Mucosal Adressin Cell Adhesion Molecule, useful for  
PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel  
PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or  
PT graft versus host disease.  
XX

PS Claim 8; SEQ ID NO 48; 167pp; English.  
XX  
CC The invention relates to a human monoclonal antibody or its antigen-  
CC binding portion that specifically binds to mucosal addressin cell  
CC adhesion molecule (MADCAM). The invention also relates to a hybridoma  
CC cell line that produces the human monoclonal antibody, a pharmaceutical  
CC composition comprising an amount of the monoclonal antibody or its  
CC antigen-binding portion and a pharmaceutical carrier, a method of  
CC treating inflammatory disease in a subject, an isolated cell line that  
CC produces the monoclonal antibody or its antigen-binding portion or the  
CC heavy chain or light chain of the antibody or of its portion, an isolated  
CC nucleic acid molecule comprising a nucleotide sequence encoding the heavy  
CC chain or its antigen-binding portion or the light chain or its antigen-  
CC binding portion of an antibody described above, a vector comprising the  
CC nucleic acid molecule, where the vector optionally comprises an  
CC expression control sequence operably linked to the nucleic acid molecule,  
CC a host cell comprising the vector or the nucleic acid molecule above, a  
CC method of producing a human monoclonal antibody or its antigen-binding  
CC portion that specifically binds MadCAM, a method of isolating an antibody  
CC or its antigen-binding portion that specifically binds to MadCAM, a  
CC method of treating a subject in need of a human antibody or its antigen-  
CC binding portion that specifically binds to MadCAM and inhibits binding to  
CC alpha4beta7, a method of inhibiting alpha4beta7 binding to cells  
CC expressing human MadCAM, a method of inhibiting MadCAM-mediated leukocyte  
CC -endothelial cell adhesion, migration and infiltration into tissues, a  
CC method of inhibiting alpha4beta7/MadCAM-dependent cellular adhesion,  
CC inhibiting the MadCAM-mediated recruitment of lymphocytes to  
CC gastrointestinal lymphoid tissue, a method of diagnosing a disorder  
CC characterized by circulating soluble human MadCAM and detecting  
CC inflammation in a subject. The antibody, composition and methods are  
CC useful for diagnosing and treating inflammatory disease, e.g.  
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
CC diverticular disease, gastritis, liver disease, primary biliary  
CC cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and  
CC graft versus host disease. This sequence represents a human monoclonal  
CC anti-MadCAM antibody of the invention.  
XX  
SQ Sequence 238 AA;

Query Match 95.1%; Score 1060; DB 9; Length 238;  
Best Local Similarity 95.8%; Pred. No. 2.8e-52;  
Matches 205; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 DIQMTQSPSSLSASVGRVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 60  
DB |||||  
25 DIQMTQSPSSLSASVGRVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 84  
  
QY 61 RFSGSGSGTDFTTINSLOPEDIAITYCOEYNNLPYSFGQGTKLIRKTVAAPSVFIFPP 120  
DB |||||  
85 RFSGSGSGTDFTTINSLOPEDIAITYCOEYNNLPYSFGQGTKLIRKTVAAPSVFIFPP 144  
  
QY 121 SDEQLKSGTASVVCLLNNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLT 180  
DB |||||  
145 SDEQLKSGTASVVCLLNNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLT 204  
  
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214  
DB |||||  
205 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238

RESULT 3  
ADD93785  
ID ADD93785 standard; protein; 236 AA.  
XX  
AC ADD93785;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Monoclonal antibody 20.13.3 light chain.  
XX  
KW Monoclonal antibody; antibody; antiasthmatic; antiallergic;  
KW antiinflammatory; immunosuppressive; dermatological;  
KW gastrointestinal-gen.; antihelminthic; cytostatic; ophthalmological;  
KW

bronchodilator; interleukin-5; human; gene therapy.  
Homo sapiens.  
Key Location/Qualifiers  
Peptide 1..22 /note= "Signal peptide"  
Protein 23..236 /note= "light chain"  
Misc-difference 23..130 /note= "Region specifically described in Claim 2"  
Misc-difference 46..119 /note= "Region specifically described in Claim 2"  
Region 46..56 /note= "CDR1"  
Region 72..78 /note= "CDR2"  
Region 111..119 /note= "CDR3"

WO2003085089-A2.  
16-OCT-2003.  
27-MAR-2003; 2003WO-US009260.  
29-MAR-2002; 2002US-0369044P.  
(SCHE ) SCHERING CORP.  
(ABGE-) ABGENIX INC.  
Greenfeder S, Corvalan J;  
WPI; 2003-804302/75.  
N-PSDB; ADD93784.  
New antibody or its antigen-binding fragment that specifically binds interleukin-5, useful for diagnosing, treating or preventing a condition associated with undesired interleukin-5 activity, e.g. asthma or allergic rhinitis.

Claim 2; Page 26; 75pp; English.  
The present sequence is the protein sequence of the light chain of anti-human interleukin-5 (IL-5) human monoclonal antibody (Mab) 20.13.3. To obtain this IgG4 Mab, Xenomice (TM) were immunised with human IL-5. Spleen and/or lymph nodes were then fused with myeloma P3-X63-Ag8.653 or myeloma NSO-bcl2 cells, and hybridomas were screened by ELISA for the presence of human IgG/kappa specific for IL-5. Nucleotides comprising the present sequence, or nucleotides 1-707, 1102-1137, 1256-1505, 1683-2002, 58-709, and 148-381 of it, are claimed and used in methods of the invention. The invention relates to antibodies or their antigen-binding fragments that specifically bind IL-5. Human anti-IL-5 antibodies are provided, including chimeric, bispecific, derivatised, single chain antibodies or portions of fusion proteins, and methods of making anti-IL-5 antibodies, pharmaceutical compositions comprising these antibodies and methods of using the antibodies and compositions for diagnosis and treatment. The invention also provides gene therapy methods using nucleic acids encoding the heavy and/or light chain molecules that comprise the human anti-IL-5 antibodies, and transgenic animals. The antibodies can be used to prevent or inhibit a condition or disorder characterised by undesired IL-5 activity, including asthma, asthma exacerbations, asthma worsening episodes, chronic pneumonia, allergic rhinitis, perennul allergic rhinitis, allergic bronchopulmonary aspergillosis, hyperesinophilia, Churg-Strauss syndrome, atopic dermatitis, onchocercal dermatitis, episodic angioedema, eosinophilic myalgia syndrome, coeliac disease, eosinophilic gastroenteritis, helminth infections, Hodgkin's disease, nasal polyps, Loeffler's syndrome, urticaria, hypereosinophilic bronchitis, arteritis nodosa, sinusitis, chronic sinusitis, eosinophilic oesophagitis, allergic eosinophilic oesophagitis, or allergic conjunctivitis, by decreasing or inhibiting the infiltration of eosinophils into affected tissue. The antibodies are also useful for preventing or inhibiting an IL-5 mediated allergic response in a subject

CC or an IL-5 mediated event, such as eosinophil proliferation, maturation, survival, activation, migration into the bloodstream, adhesion to CC endothelium, infiltration into tissues, pulmonary oedema, CC bronchoconstriction, airway hyperresponsiveness, pulmonary eosinophilia CC or neutrophilia, cutaneous eosinophilia, or airway epithelial damage (all CC claimed).  
XX  
SQ Sequence 236 AA;  
Query Match 94.3%; Score 1051; DB 7; Length 236;  
Best Local Similarity 94.4%; Pred No. 8.9e-52;  
Matches 202; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGDRVTITCOASQDISNYLNWYQKPGKAPKLLIYDASNLETVGPS 60  
Db 23 DIQMTQSPSSLSASVGDRVTITCOASQDIINLNWYQKPGKAPKLLIYDASNLETVGPS 82  
QY 61 RFSGSGSGTDFTTINSLOPEDIAIYCOEYNNLPYSGQGTKEIKRTVAAPSVFIFPP 120  
Db 83 RFSGSGSGTDFTTISLQPEDIAIYCOQYDNHPLTFGGGTVKVEIRRTVAAPSVFIFPP 142  
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYLSLT 180  
Db 143 SDEQLKSGTASVVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYLSLT 202  
QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214  
Db 203 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 236  
RESULT 4  
ADN97515  
ID ADN97515 standard; protein; 502 AA.  
XX AC ADN97515;  
XX DT 01-JUL-2004 (first entry)  
XX DE Artificial protein construction protein #16.  
XX KW artificial proprotein; propeptide; protein engineering; antibody.  
XX OS Unidentified.  
XX PN WO2004031362-A2.  
XX PD 15-APR-2004.  
XX PF 03-OCT-2003; 2003WO-US031420.  
XX PR 03-OCT-2002; 2002US-0415940P.  
XX PA (LARG-) LARGE SCALE BIOLOGY CORP.  
XX PI Reini SJ, Edwards P;  
XX DR WPI; 2004-330170/30.  
XX N-PSDB; ADN97514.  
XX New artificial proprotein comprises three peptide sequences, useful for PT artificial multimeric protein engineering in eukaryotes.  
XX PS Example 2; SEQ ID NO 88; 244pp; English.  
XX The invention relates to an artificial proprotein comprising three CC peptide sequences: a first peptide sequence of interest, a propeptide CC sequence attached to the C-terminus of the first peptide sequence of CC interest, and a second peptide of interest attached to the C-terminus of CC the propeptide sequence. The artificial proprotein and polynucleotides CC are useful for artificial multimeric protein engineering, e.g. antibodies CC and antibody fragments in eukaryotes. This sequence corresponds to a CC protein used in the generation of the protein of the invention.  
XX

SQ Sequence 502 AA;

Query Match 93.7%; Score 1045; DB 8; Length 502;  
Best Local Similarity 93.5%; Pred. No. 3.8e-51;  
Matches 200; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDISNYLNWYQOKPGKAPKLLIYDASNLTGVPS 60  
DB 23 DIQMTQSPSSLSASVGRVTITTCQASQDISNYLNWYQOKPGKAPKLLIYDASNLTGVPS 82  
QY 61 RFGSGSGTDFTTINSLOPEDIAITYCOEYNNLPYSFGQGTKEIKRTVAAPSFIIPP 120  
DB 83 RFGSGSGTDFTTINSLOPEDIAITYCOYDNLPLTFGGGKVEIKRTVAAPSFIIPP 142  
QY 121 SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 180  
DB 143 SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 202  
QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214  
DB 203 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 5  
AAV55078  
ID AAY55078 standard; protein; 367 AA.  
AC AAY55078;  
DT 25-FEB-2000 (first entry)  
DE Single chain Fv protein sequence shPMI-Kappa.  
KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
KW antigen-binding cell; secretabie functional protein; antigenic protein;  
KW protein isolation; diagnosis; ScFv.  
OS Synthetic.  
XX WO9960113-A1.  
XX 25-NOV-1999.  
XX 30-APR-1999; 99WO-JP002341.  
XX 20-MAY-1998; 98JP-00138652.  
XX 01-OCT-1998; 98JP-00279876.  
XX (CHUS ) CHUGAI SEIYAKU KK.  
XX Tsuchiya M, Saito M, Ohtomo T;  
XX WPI; 2000-039382/03.  
XX N-PSDB; AA240308.  
XX Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
XX production of drugs treating abnormal functions of the protein.  
XX Example 7; Page 86-89; 120pp; Japanese.  
XX This sequence represents a single chain Fv (ScFv) sequence. The invention  
XX relates to a method for isolating a gene encoding a membrane-bound  
XX protein, comprising introducing a vector into a cell, contacting an  
XX antigen with the cell expressing the fused protein encoded by the vector  
XX on its surface to select an antigen-binding cell, and isolating the cDNA.  
XX The vector contains DNA encoding a secretabie functional protein with  
XX antigenicity and binding affinity, and a cDNA ligated to DNA downstream  
XX of the 3' end of the coding sequence. The method can be used to isolate a  
XX membrane-bound protein for diagnosis and study. It can also be used for  
XX producing drugs treating abnormal functions of the protein. Such a  
XX technique is efficient and selective, which is different from the prior-  
XX art transmembrane trap (TMT) method wherein an epitope recognised by an

CC antibody is carried in a fused protein  
XX  
SQ Sequence 367 AA;

Query Match 93.2%; Score 1039; DB 3; Length 367;  
Best Local Similarity 93.9%; Pred. No. 6.2e-51;  
Matches 200; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDISNYLNWYQOKPGKAPKLLIYDASNLTGVPS 60  
DB 154 DIQMTQSPSSLSASVGRVTITTCRASQDISNYLNWYQOKPGKAPKLLIYYSRLHSGVPS 213  
QY 61 RFGSGSGTDFTTINSLOPEDIAITYCOEYNNLPYSFGQGTKEIKRTVAAPSFIIPP 120  
DB 214 RFGSGSGTDFTTINSLOPEDIAITYCOQGNLTLPYTFGQGTKEIKRTVAAPSFIIPP 273  
QY 121 SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 180  
DB 274 SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 333  
QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGE 213  
DB 334 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGE 366

RESULT 6  
AAV55081  
ID AAY55081 standard; protein; 626 AA.  
AC AAY55081;  
DT 25-FEB-2000 (first entry)  
DE Single chain Fv protein sequence shPM1-kappa-BvGS3.  
KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
KW antigen-binding cell; secretabie functional protein; antigenic protein;  
KW protein isolation; diagnosis; ScFv.  
OS Synthetic.  
XX WO9960113-A1.  
XX 25-NOV-1999.  
XX 30-APR-1999; 99WO-JP002341.  
XX 20-MAY-1998; 98JP-00138652.  
XX 01-OCT-1998; 98JP-00279876.  
XX (CHUS ) CHUGAI SEIYAKU KK.  
XX Tsuchiya M, Saito M, Ohtomo T;  
XX WPI; 2000-039382/03.  
XX N-PSDB; AA240316.  
XX Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
XX production of drugs treating abnormal functions of the protein.  
XX Example 7; Page 103-109; 120pp; Japanese.  
XX This sequence represents a single chain Fv (ScFv) sequence. The invention  
XX relates to a method for isolating a gene encoding a membrane-bound  
XX protein, comprising introducing a vector into a cell, contacting an  
XX antigen with the cell expressing the fused protein encoded by the vector  
XX on its surface to select an antigen-binding cell, and isolating the cDNA.  
XX The vector contains DNA encoding a secretabie functional protein with  
XX antigenicity and binding affinity, and a cDNA ligated to DNA downstream  
XX of the 3' end of the coding sequence. The method can be used to isolate a  
XX membrane-bound protein for diagnosis and study. It can also be used for  
XX producing drugs treating abnormal functions of the protein. Such a

CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
CC antibody is carried in a fused protein  
XX  
SQ Sequence 626 AA;

Query Match 93.2%; Score 1039; DB 3; Length 626;  
Best Local Similarity 93.3%; Pred. No. 1e-50; 6; Indels 0; Gaps 0;  
Matches 200; Conservative 7; Mismatches 7;

QY 1 DIQMTQSPSSLSASVGRVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGVS 60  
DB 413 DIQMTQSPSSLSASVGRVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGVS 472  
QY 61 RFGSGSGTDFTTINSLOPEDIATYTCQSYNNLPYFGQGTKEIKRTVAAPSVFIFPP 120  
DB 473 RFGSGSGTDFTTINSLOPEDIATYTCQSYNNLPYFGQGTKEIKRTVAAPSVFIFPP 532  
QY 121 SDEQLKSGTASVCLLNFPYQKQVDNALQSGNSQESVTEQDSKDSSTLSLT 180  
DB 533 SDEQLKSGTASVCLLNFPYQKQVDNALQSGNSQESVTEQDSKDSSTLSLT 592  
QY 181 LSKADYEKHKVYACEVTHQGLSPVTKSFNRGE 213  
DB 593 LSKADYEKHKVYACEVTHQGLSPVTKSFNRGE 625

RESULT 7  
ID ADQ90721 standard; protein; 237 AA.  
XX ADQ90721;  
XX 21-OCT-2004 (first entry)  
XX Anti-VEGF antibody light chain protein SEQ ID NO:25.  
DE antibody; antigen binding fragment; cell culture; variable domain;  
XX modified framework region; hypervariable region; cystostatic;  
KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;  
KW tumour; inflammatory disorder; angiogenic disorder;  
KW immunological disorder; anti-VEGF antibody;  
KW anti vascular endothelial cell growth factor antibody; light chain.  
XX  
OS Homo sapiens.  
OS Synthetic.  
OS W02004065417-A2.  
XX 05-AUG-2004.  
XX 23-JAN-2004; 2004WO-US001844.  
XX 23-JAN-2003; 2003US-0442484P.  
XX (GETH ) GENENTECH INC.  
XX Simmons L;  
XX WPI; 2004-562149/54.  
XX N-PSDB; ADQ90720.  
XX Producing an antibody or antigen binding fragment in high yield in a cell  
XX culture, comprises expressing a variable domain with a modified framework  
XX region in a host cell.  
XX Example 6; SEQ ID NO 25; 161pp; English.  
XX The present invention describes a method for producing an antibody or  
XX antigen binding fragment in high yield in a cell culture. The method  
XX comprises expressing a variable domain of the antibody or antigen binding  
XX fragment comprising a modified framework region (FR) in a host cell, and  
XX recovering the antibody or antigen binding fragment variable domain

CC comprising the modified framework from the host cell. The modified PR in  
CC the method described above has a substitution of at least one amino acid  
CC position with a different amino acid, where the different amino acid is  
CC the amino acid found at the corresponding PR position of a human subgroup  
CC variable domain consensus sequence that has a hypervariable region 1  
CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity  
CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.  
CC The antibody or antigen binding fragment variable domain comprises the  
CC modified PR that has improved yield in cell culture compared to an  
CC unmodified antibody or antigen-binding fragment. The antibody and antigen  
CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and  
CC immunomodulatory activities, and can be used in antibody therapy. The  
CC methods and compositions of the present invention are useful for  
CC producing antibodies or antigen binding fragments in cell culture, in  
CC particular for improving the yield of recombinant antibodies or antigen  
CC binding fragments in cell culture. The antibodies of the invention can be  
CC used to diagnose, treat, inhibit or prevent e.g. tumours and  
CC inflammatory, angiogenic and immunological disorders. The present  
CC sequence represents the light chain of an anti-VEGF (vascular endothelial  
CC cell growth factor) antibody, which is used in the exemplification of the  
XX present invention.  
XX SQ Sequence 237 AA;

Query Match 93.0%; Score 1037; DB 8; Length 237;  
Best Local Similarity 92.1%; Pred. No. 5.5e-51;  
Matches 197; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGVS 60  
DB 24 DIQMTQSPSSLSASVGRVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGVS 83  
QY 61 RFGSGSGTDFTTINSLOPEDIATYTCQSYNNLPYFGQGTKEIKRTVAAPSVFIFPP 120  
DB 84 RFGSGSGTDFTTINSLOPEDIATYTCQSYNNLPYFGQGTKEIKRTVAAPSVFIFPP 143  
QY 121 SDEQLKSGTASVCLLNFPYQKQVDNALQSGNSQESVTEQDSKDSSTLSLT 180  
DB 144 SDEQLKSGTASVCLLNFPYQKQVDNALQSGNSQESVTEQDSKDSSTLSLT 203  
QY 181 LSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 214  
DB 204 LSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 237

RESULT 8  
ADC26154  
ID ADC26154 standard; protein; 214 AA.  
XX ADC26154;  
XX 18-DEC-2003 (first entry)  
DE Parent anti-VEGF Y0101 antibody wild-type light chain protein.  
XX antibody variant; cytostatic; cancer; parent; anti-VEGF;  
KW vascular endothelial growth factor; Y0101; light chain; wild-type.  
XX Unidentified.  
XX WO2003068801-A2.  
XX 21-AUG-2003.  
XX 11-FEB-2003; 2003WO-US004184.  
XX 11-FEB-2002; 2002US-0355895P.  
XX 10-SEP-2002; 2002US-0409685P.  
XX (GETH ) GENENTECH INC.  
XX Lowman HB, Marvin JS;  
XX



DR WPI; 2003-697521/66.  
XX Making an antibody variant of a parent antibody specific to an antigen by  
PT identifying a target amino acid residue within the variable domain of the  
PT parent antibody and substituting the target residue with a different  
PT amino acid residue.  
XX Example 1; SEQ ID NO 1; 81pp; English.  
XX The invention relates to a novel method for making an antibody variant of  
CC a parent antibody specific to an antigen. This is achieved via  
CC identifying a target amino acid residue within the variable domain of the  
CC parent antibody and substituting the target residue with a different  
CC replacement amino acid residue such that the charge complementarity  
CC between the antibody and antigen is increased. The antibody variant of  
CC the invention demonstrates cytostatic activity whilst the method may be  
CC useful for treating cancer. The current sequence is that of the parent  
CC anti-VEGF (vascular endothelial growth factor) Y0101 antibody wild-type  
CC light chain protein of the invention.  
XX  
SQ Sequence 214 AA;

Query Match 92.7%; Score 1034; DB 7; Length 214;  
Best Local Similarity 91.6%; Pred. No. 7.4e-51;  
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGRDVTITCSASQDISNYLNWYQKPKAPKLLIYDASNLETGVPS 60  
DB 1 DIQLTQSPSSLSASVGRDVTITCSASQDISNYLNWYQKPKAPKLLIYFTSSLHSGVPS 60  
QY 61 RFGSGSGTDFTTINSLOPEDIATYCYQENYNNLPYSGQGKLEIKRTVAAPSVFIFPP 120  
DB 61 RFGSGSGTDFTTISSLQPEDFATYCYQYSTVPWTFGGTKVEIKRTVAAPSVFIFPP 120  
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTLSLT 180  
DB 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTLSLT 180  
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214  
DB 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 9  
AAW70703  
ID AAW70703 standard; protein; 237 AA.  
AC AAW70703;  
XX  
DT 27-JAN-1999 (first entry)  
XX  
DE Protein encoded by Fab-display antibody vector phMB4-19-1.6.  
XX  
KW Murine; humanised antibody; VEGF-induced angiogenesis; tumour;  
KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;  
KW retinal disorder; age-related macular degeneration; diabetic retinopathy;  
KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..23  
FT Protein /note= "STII signal sequence TIR-1"  
FT Protein 24..237  
FT /note= "anti-VEGF light chain"  
XX  
PN WO9845331-A2.  
PD 15-OCT-1998.  
PF 03-APR-1998; 98WO-US006604.  
XX  
XX 07-APR-1997; 97US-00833504.  
PR 06-AUG-1997; 97US-00908469.  
XX  
XX (GETH ) GENENTECH INC.  
XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;  
PI

DR WPI; 1998-568337/48.  
DR N-PSDB; AAV63493.  
XX New humanised antibody with affinity for vascular endothelial growth  
PT factor - for treatment of tumours, retinal disease and other angiogenic  
PT states, also related nucleic acid, vectors and transformed cells.  
XX Example 3; Fig 8A-E; 100pp; English.  
XX The present sequence is encoded by the Fab-display antibody vector phMB4-  
CC 19-1.6, which is used in the course of the invention. The specification  
CC describes humanised murine anti-vascular endothelial growth factor (anti-  
CC VEGF) antibodies. The humanised antibodies are used to inhibit VEGF-  
CC induced angiogenesis, particularly for treating or preventing tumours (of  
CC any type) and retinal disorders (e.g. age-related macular degeneration  
CC or diabetic retinopathy). They can also be used to treat other conditions  
CC that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,  
CC atherosclerosis, Grave's disease, etc  
XX  
SQ Sequence 237 AA;

Query Match 92.7%; Score 1034; DB 2; Length 237;  
Best Local Similarity 91.6%; Pred. No. 8.1e-51;  
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGRDVTITCSASQDISNYLNWYQKPKAPKLLIYDASNLETGVPS 60  
DB 24 DIQLTQSPSSLSASVGRDVTITCSASQDISNYLNWYQKPKAPKLLIYFTSSLHSGVPS 83  
QY 61 RFGSGSGTDFTTINSLOPEDIATYCYQENYNNLPYSGQGKLEIKRTVAAPSVFIFPP 120  
DB 84 RFGSGSGTDFTTISSLQPEDFATYCYQYSTVPWTFGGTKVEIKRTVAAPSVFIFPP 143  
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTLSLT 180  
DB 144 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTLSLT 203  
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214  
DB 204 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 10  
ABB81107  
ID ABB81107 standard; protein; 237 AA.  
AC ABB81107;  
XX  
DT 05-NOV-2002 (first entry)  
XX  
DE Anti-VEGF light chain fragment.  
XX  
KW Immunoglobulin; promoter; cytostatic; antiinflammatory; immunomodulator;  
KW neuroprotective; CD11; tissue factor; vascular endothelial growth factor;  
KW VEGF.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..23  
FT Protein /note= "STII signal sequence TIR-1"  
FT Protein 24..237  
FT /note= "anti-VEGF light chain"  
XX  
PN WO200261090-A2.  
XX  
XX 08-AUG-2002.  
XX  
XX 13-DEC-2001; 2001WO-US048691.  
XX  
XX 14-DEC-2000; 2000US-0256164P.  
XX  
XX (GETH ) GENENTECH INC.

XX Simmons LC, Klimowski L, Reilly DE, Yansura DG;  
XX WPI; 2002-619253/66.  
XX N-PSDB; ABN86646.  
XX New polynucleotide comprising first and second promoter-cistron pairs,  
XX useful for diagnosing, treating or preventing diseases associated with  
XX abnormal expression and/or activity of antigens such as inflammatory  
XX disorders.  
XX Disclosure; Fig 21A-C; 104pp; English.  
XX The invention provides a polynucleotide, which encodes an immunoglobulin  
XX (Ig), comprising a first or second promoter-cistron pair consisting of a  
XX first or second promoter and cistron, respectively. The first cistron of  
XX the first promoter-cistron pair comprises a first translational  
XX initiation region (TIR-L) operably linked to a nucleic acid sequence  
XX encoding an Ig light chain and the second cistron of the second promoter-  
XX cistron pair comprises a second translational initiation region (TIR-H)  
XX operably linked to a nucleic acid sequence encoding an Ig heavy chain.  
XX Upon expression of the polynucleotide in a prokaryotic host cell, light  
XX and heavy chains are folded and assembled to form a biologically active  
XX Ig. The antibody of the invention is useful for diagnosing, treating or  
XX preventing diseases or conditions associated with abnormal expression and  
XX /or activity of one or more antigen molecules e.g. lymphoid malignancies,  
XX inflammatory, angiogenic, immunologic, neuronal, glial, astrocytic,  
XX hypothalamic or other glandular disorders. The present sequence  
XX represents the amino acid sequence of an anti-vascular endothelial growth  
XX factor (VEGF) light chain fragment of the cistron vector pXVG2AP11  
XX Sequence 237 AA;  
Query Match 92.7%; Score 1034; DB 5; Length 237;  
Best Local Similarity 91.6%; Pred. No. 8.1e-51;  
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 DIQQTSPSSLSASVGDRTVITTCASQDISNYLNWYQKPGKAPKLLIYDASNLGVPS 60  
Db 24 DIQQTSPSSLSASVGDRTVITTCASQDISNYLNWYQKPGKAPKLLIYDASNLGVPS 83  
Qy 61 RFGSGSGTDFTTINSLOPEDATYTCQYNNLPYSFGQGTKEIKRTVAAPSVFIIPP 120  
Db 84 RFGSGSGTDFTTINSLOPEDATYTCQYNNLPYSFGQGTKEIKRTVAAPSVFIIPP 143  
Qy 121 SDEQLKSGTASVVCLLNNFPYPRKQVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 180  
Db 144 SDEQLKSGTASVVCLLNNFPYPRKQVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 203  
Qy 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214  
Db 204 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 11  
ABP51952  
ID ABP51952 standard; protein; 237 AA.  
XX AC ABP51952;  
XX DT 09-OCT-2002 (first entry)  
XX XX Plasmid pY0317 anti-VEGF Fab amino acid sequence SEQ ID NO:2 #1.  
XX Bacterial host; protease; degp; prc; spr; anti-VEGF antibody; anti-CD20;  
XX humanized; Apo2 ligand; anti-CD18; anti-tissue factor; 2C4; anti-CD20;  
XX anti-vascular endothelial growth factor; anti-Her-2; anti-CD40; Fab;  
XX anti-CD11a; Fab; Fab'; Fab'; Fab'; Fab'; Fab'; Fab'; Fab'; Fab'; Fab';  
XX Mus sp.  
XX OS Escherichia coli.  
XX OS Synthetic.

XX FH Key Location/Qualifiers  
XX FT Peptide 1..23  
XX FT Protein /label= signal  
XX FT 24..237  
XX FT /label= anti-VEGF\_Fab  
XX WO200248376-A2.  
XX 20-JUN-2002.  
XX 07-DEC-2001; 2001WO-US047581.  
XX 14-DEC-2000; 2000US-02561622p.  
XX (GETH ) GENENTECH INC.  
XX Chen CY;  
XX WPI; 2002-583522/62.  
XX N-PSDB; ABQ73919.  
XX Novel Escherichia coli strain useful for producing polypeptide, deficient  
XX in degp and prc encoding protease, and harboring mutant spr gene, product  
XX of gene suppresses growth phenotypes of strains harboring prc mutants.  
XX Example 1; Fig 1A-C; 63pp; English.  
XX The present invention describes an Escherichia coli strain (I) deficient  
XX in chromosomal degp and prc encoding protease Degp and Prc, respectively,  
XX and harbouring a mutant spr gene, the product of mutant spr gene  
XX suppresses growth phenotypes exhibited by strains harbouring prc mutants.  
XX (I) is useful for producing a polypeptide, by culturing (I) comprising  
XX nucleic acid encoding the polypeptide, which is heterologous to the  
XX strain, such that the nucleic acid is expressed, and recovering the  
XX heterologous polypeptide from the strain. The heterologous polypeptide is  
XX proteolytically sensitive. Culturing of (I) is performed in a fermentor  
XX under conditions of high- or low-cell density fermentation. The  
XX polypeptide is recovered from the periplasm or culture medium of the  
XX strain. The polypeptide is an antibody (humanised or full-length  
XX antibody) or Apo2 ligand. The antibody is an anti-CD18, anti-vascular  
XX endothelial growth factor (VEGF), anti-tissue factor, 2C4, anti-Her-2,  
XX anti-CD20, anti-CD40, or anti-CD11a antibody. The antibody is also an  
XX antibody fragment having a light chain (kappa light chain). The antibody  
XX fragment is a Fab, Fab', Fab'2 or Fab'2-leucine zipper fusion, anti-CD18  
XX Fab'2-leucine zipper fusion, anti-tissue factor Fab'2-leucine zipper  
XX fusion or anti-VEGF Fab, with or without a histidine or lysine tag, anti-  
XX tissue factor Fab'2-leucine zipper fusion with a 6-histidine tag, or anti-  
XX -CD18 Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-CD18  
XX Fab'2-leucine zipper fusion with a 6-lysine tag. The present sequence  
XX represents an anti-VEGF Fab amino acid sequence from the present  
XX invention  
XX Sequence 237 AA;

Query Match 92.7%; Score 1034; DB 5; Length 237;  
Best Local Similarity 91.6%; Pred. No. 8.1e-51;  
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 DIQQTSPSSLSASVGDRTVITTCASQDISNYLNWYQKPGKAPKLLIYDASNLGVPS 60  
Db 24 DIQQTSPSSLSASVGDRTVITTCASQDISNYLNWYQKPGKAPKLLIYDASNLGVPS 83  
Qy 61 RFGSGSGTDFTTINSLOPEDATYTCQYNNLPYSFGQGTKEIKRTVAAPSVFIIPP 120  
Db 84 RFGSGSGTDFTTINSLOPEDATYTCQYNNLPYSFGQGTKEIKRTVAAPSVFIIPP 143  
Qy 121 SDEQLKSGTASVVCLLNNFPYPRKQVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 180  
Db 144 SDEQLKSGTASVVCLLNNFPYPRKQVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 203  
Qy 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214  
Db 204 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 12  
 ADO14128  
 ID ADO14128 standard; protein; 237 AA.  
 AC ADO14128;  
 XX  
 DT 12-AUG-2004 (first entry)  
 DE Plasmid pxVG2AP11 expression cassette light chain protein SEQ ID NO:8.  
 KW antibody; variant heavy chain hinge region; immunoconjugate; cytostatic;  
 KW immunosuppressive; immunotherapy; tumour; cancer; immune disorder;  
 KW expression cassette; plasmid pxVG2AP11; anti-VEGF light chain.  
 XX  
 OS Synthetic.  
 PN WO2004042017-A2.  
 XX  
 PD 21-MAY-2004.  
 XX  
 PF 30-OCT-2003; 2003WO-US034610.  
 XX  
 PR 31-OCT-2002; 2002US-0422952P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PI Reilly D, Yansura DG;  
 DR WPI; 2004-390607/36.  
 DR N-PSDB; ADO14127.  
 XX  
 PT New antibody comprising a variant heavy chain hinge region incapable of  
 PT inter-heavy chain disulfide linkage, useful for treating, preventing,  
 PT diagnosing, delaying or preventing a disease, e.g. tumor, cancer or  
 PT immune disorder.  
 XX  
 PS Example 1; SEQ ID NO 8; 124pp; English.  
 XX  
 CC The present invention describes an antibody comprising a variant heavy  
 CC chain hinge region incapable of inter-heavy chain disulfide linkage. Also  
 CC described: (1) an antibody lacking inter-heavy chain disulfide linkage;  
 CC (2) an immunoconjugate comprising the antibody conjugated with a  
 CC heterologous moiety; (3) a composition comprising the antibody or  
 CC immunoconjugate, and carrier; (4) an article of manufacture comprising  
 CC the composition in a container; (5) a polynucleotide encoding the  
 CC antibody or immunoconjugate, or a variant immunoglobulin heavy chain  
 CC incapable of inter-heavy chain disulfide linkage; (6) a recombinant  
 CC vector for expressing the antibody or immunoconjugate; (7) a host cell  
 CC comprising the recombinant vector; (8) expressing in a host cell an  
 CC antibody of interest in which at least one inter-heavy chain disulfide  
 CC linkage is eliminated, and recovering the antibody from the host cell;  
 CC (9) an aglycosylated antibody produced by the method; and (10) treating,  
 CC preventing, diagnosing, delaying or preventing a disease in a subject,  
 CC The antibody has cytostatic and immunosuppressive activities, and can be  
 CC used in immunotherapy. The antibody, immunoconjugate and methods are  
 CC useful for treating, preventing, diagnosing, delaying or preventing a  
 CC disease, e.g. tumour, cancer or immune disorder. The present sequence  
 CC represents the anti-VEGF light chain from the expression cassette of  
 CC plasmid pxVG2AP11, which is used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 237 AA;  
 Query Match 92.7%; Score 1034; DB 8; Length 237;  
 Best Local Similarity 91.6%; Pred. No. 8 1e-51;  
 Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNYYQKPKGAPKLLIYDASNLTGVP 60  
 DB 24 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNYYQKPKGAPKVLIIYFTSSLSHGVPS 83

QY 61 RFGSGSGTDFTFITNSLPEDIAITYYCOEYNNLPYSPFGQGTKEIKRTVAAPSVFIFPP 120  
 DB 84 RFGSGSGTDFTLTISSLPEDFATYYCQQISTVPWTFGQGTKEIKRTVAAPSVFIFPP 143  
 QY 121 SDEQLKSGTASVWCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLSTLT 180  
 DB 144 SDEQLKSGTASVWCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLSTLT 203  
 QY 181 LSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 214  
 DB 204 LSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 237  
 RESULT 13  
 ADO14131  
 ID ADO14131 standard; protein; 237 AA.  
 AC ADO14131;  
 XX  
 DT 12-AUG-2004 (first entry)  
 DE Plasmid pxVG11VNERK expression cassette light chain protein SEQ ID NO:11.  
 KW antibody; variant heavy chain hinge region; immunoconjugate; cytostatic;  
 KW immunosuppressive; immunotherapy; tumour; cancer; immune disorder;  
 KW expression cassette; plasmid pxVG11VNERK; anti-VEGF light chain.  
 XX  
 OS Synthetic.  
 PN WO2004042017-A2.  
 XX  
 PD 21-MAY-2004.  
 XX  
 PF 30-OCT-2003; 2003WO-US034610.  
 XX  
 PR 31-OCT-2002; 2002US-0422952P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PI Reilly D, Yansura DG;  
 DR WPI; 2004-390607/36.  
 DR N-PSDB; ADO14130.  
 XX  
 PT New antibody comprising a variant heavy chain hinge region incapable of  
 PT inter-heavy chain disulfide linkage, useful for treating, preventing,  
 PT diagnosing, delaying or preventing a disease, e.g. tumor, cancer or  
 PT immune disorder.  
 XX  
 PS Example 1; SEQ ID NO 11; 124pp; English.  
 XX  
 CC The present invention describes an antibody comprising a variant heavy  
 CC chain hinge region incapable of inter-heavy chain disulfide linkage. Also  
 CC described: (1) an antibody lacking inter-heavy chain disulfide linkage;  
 CC (2) an immunoconjugate comprising the antibody conjugated with a  
 CC heterologous moiety; (3) a composition comprising the antibody or  
 CC immunoconjugate, and carrier; (4) an article of manufacture comprising  
 CC the composition in a container; (5) a polynucleotide encoding the  
 CC antibody or immunoconjugate, or a variant immunoglobulin heavy chain  
 CC incapable of inter-heavy chain disulfide linkage; (6) a recombinant  
 CC vector for expressing the antibody or immunoconjugate; (7) a host cell  
 CC comprising the recombinant vector; (8) expressing in a host cell an  
 CC antibody of interest in which at least one inter-heavy chain disulfide  
 CC linkage is eliminated, and recovering the antibody from the host cell;  
 CC (9) an aglycosylated antibody produced by the method; and (10) treating,  
 CC preventing, diagnosing, delaying or preventing a disease in a subject.  
 CC The antibody has cytostatic and immunosuppressive activities, and can be  
 CC used in immunotherapy. The antibody, immunoconjugate and methods are  
 CC useful for treating, preventing, diagnosing, delaying or preventing a  
 CC disease, e.g. tumour, cancer or immune disorder. The present sequence  
 CC represents the anti-VEGF light chain from the expression cassette of  
 CC plasmid pxVG11VNERK, which is used in the exemplification of the present  
 CC invention.

```
XX Sequence 237 AA;
SQ
Query Match 92.7%; Score 1034; DB 8; Length 237;
Best Local Similarity 91.6%; Pred. No. 8.1e-51;
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
DB 24 DIQLTQSPSSLSASVGDRTITTCASQDISNYLNWYQKPGKAPKLVLIYFTSSLHSGVPS 83
QY 61 RFGSGSGTDFTTINSLQPEDIATYYCOEYNNLPYSFGQGTKEIKRTVAAPSFIIPP 120
DB 84 RFGSGSGTDFTTISLSQPEDFATYYCOQYSTVPWTFQGTKEIKRTVAAPSFIIPP 143
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTLSLT 180
DB 144 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTLSLT 203
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 204 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 14
ADQ90703
ID ADQ90703 standard; protein; 237 AA.
XX
AC ADQ90703;
XX
XX 21-OCT-2004 (first entry)
XX
DE Anti-VEGF antibody Y0317 light chain protein SEQ ID NO:7.
XX
XX antibody; antigen binding fragment; cell culture; variable domain;
KW modified framework region; hypervariable region; cytostatic;
KW antinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
KW tumour; inflammatory disorder; angiogenic disorder;
KW immunological disorder; anti-VEGF antibody;
KW anti vascular endothelial cell growth factor antibody; light chain.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO2004065417-A2.
XX
XX 05-AUG-2004.
XX
XX 23-JAN-2004; 2004WO-US001844.
XX
XX 23-JAN-2003; 2003US-0442484P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Simmons L;
XX
XX WPI; 2004-562149/54.
XX
XX N-PSDB; ADQ90702.
XX
XX Producing an antibody or antigen binding fragment in high yield in a cell
XX culture, comprises expressing a variable domain with a modified framework
XX region in a host cell.
XX
XX Example 2; SEQ ID NO 7; 161pp; English.
XX
XX The present invention describes a method for producing an antibody or
XX antigen binding fragment in high yield in a cell culture. The method
XX comprises expressing a variable domain of the antibody or antigen binding
XX fragment comprising a modified framework region (FR) in a host cell, and
XX recovering the antibody or antigen binding fragment variable domain
XX comprising the modified framework from the host cell. The modified FR in
XX the method described above has a substitution of at least one amino acid
XX position with a different amino acid, where the different amino acid is
```

```
CC the amino acid found at the corresponding FR position of a human subgroup
CC variable domain consensus sequence that has a hypervariable region 1
CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
CC The antibody or antigen binding fragment variable domain comprises the
CC modified FR that has improved yield in cell culture compared to an
CC unmodified antibody or antigen-binding fragment. The antibody and antigen
CC binding fragment have cytostatic, antinflammatory, antiangiogenic and
CC immunomodulatory activities, and can be used in antibody therapy. The
CC methods and compositions of the present invention are useful for
CC producing antibodies or antigen binding fragments in cell culture, in
CC particular for improving the yield of recombinant antibodies or antigen
CC binding fragments in cell culture. The antibodies of the invention can be
CC used to diagnose, treat, inhibit or prevent e.g. tumours and
CC inflammatory, angiogenic and immunological disorders. The present
CC sequence represents the light chain of an anti-VEGF (vascular endothelial
CC cell growth factor) antibody, which is used in the exemplification of the
XX present invention.
XX
SQ Sequence 237 AA;
```

```
Query Match 92.7%; Score 1034; DB 8; Length 237;
Best Local Similarity 91.6%; Pred. No. 8.1e-51;
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 1 DIQMTQSPSSLSASVGDRTITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
DB 24 DIQLTQSPSSLSASVGDRTITTCASQDISNYLNWYQKPGKAPKLVLIYFTSSLHSGVPS 83
QY 61 RFGSGSGTDFTTINSLQPEDIATYYCOEYNNLPYSFGQGTKEIKRTVAAPSFIIPP 120
DB 84 RFGSGSGTDFTTISLSQPEDFATYYCOQYSTVPWTFQGTKEIKRTVAAPSFIIPP 143
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTLSLT 180
DB 144 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTLSLT 203
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 204 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237
```

```
RESULT 15
ADQ90701
ID ADQ90701 standard; protein; 237 AA.
XX
AC ADQ90701;
XX
XX 21-OCT-2004 (first entry)
XX
DE Anti-VEGF antibody VNERK light chain protein SEQ ID NO:5.
XX
XX antibody; antigen binding fragment; cell culture; variable domain;
KW modified framework region; hypervariable region; cytostatic;
KW antinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
KW tumour; inflammatory disorder; angiogenic disorder;
KW immunological disorder; anti-VEGF antibody;
KW anti vascular endothelial cell growth factor antibody; light chain.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO2004065417-A2.
XX
XX 05-AUG-2004.
XX
XX 23-JAN-2004; 2004WO-US001844.
XX
XX 23-JAN-2003; 2003US-0442484P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Simmons L;
XX
```

XX WPI: 2004-562149/54.  
DR N-PSDB; ADQ90700.  
XX  
PT Producing an antibody or antigen binding fragment in high yield in a cell  
PT culture, comprises expressing a variable domain with a modified framework  
PT region in a host cell.  
XX  
PS Example 2; SEQ ID NO 5; 161pp; English.  
XX  
CC The present invention describes a method for producing an antibody or  
CC antigen binding fragment in high yield in a cell culture. The method  
CC comprises expressing a variable domain of the antibody or antigen binding  
CC fragment comprising a modified framework region (FR) in a host cell, and  
CC recovering the antibody or antigen binding fragment variable domain  
CC comprising the modified framework from the host cell. The modified FR in  
CC the method described above has a substitution of at least one amino acid  
CC position with a different amino acid, where the different amino acid is  
CC the amino acid found at the corresponding FR position of a human subgroup  
CC variable domain consensus sequence that has a hypervariable region 1  
CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity  
CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.  
CC The antibody or antigen binding fragment variable domain comprises the  
CC modified FR that has improved yield in cell culture compared to an  
CC unmodified antibody or antigen-binding fragment. The antibody and antigen  
CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and  
CC immunomodulatory activities, and can be used in antibody therapy. The  
CC methods and compositions of the present invention are useful for  
CC producing antibodies or antigen binding fragments in cell culture, in  
CC particular for improving the yield of recombinant antibodies or antigen  
CC binding fragments in cell culture. The antibodies of the invention can be  
CC used to diagnose, treat, inhibit or prevent e.g. tumours and  
CC inflammatory, angiogenic and immunological disorders. The present  
CC sequence represents the light chain of an anti-VEGF (vascular endothelial  
CC cell growth factor) antibody, which is used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 237 AA;

Query Match 92.7%; Score 1034; DB 8; Length 237;  
Best Local Similarity 91.6%; Pred. No. 8.1e-51;  
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQKPKAPKLLIYDASNLETGYPS 60  
DB 24 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQKPKAPKLLIYFTSSLHSGVPS 83  
QY 61 RFGSGSGTDFTTINSLQPEDIATYYCOEYNNLPYFGQGTKLRIKRTVAAPSVFIFPP 120  
DB 84 RFGSGSGTDFTTLISSLPEDFAIYYCQQYSTVPWTFGQGTKEIKRTVAAPSVFIFPP 143  
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT 180  
DB 144 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT 203  
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214  
DB 204 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237

Search completed: December 17, 2005, 01:18:33  
Job time : 86.9515 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 17, 2005, 01:10:58 ; Search time 16,2121 Seconds  
(without alignments)  
1270.061 Million cell updates/sec

Title: US-10-644-277-64  
Perfect score: 1115  
Sequence: 1 DIQMTPSSLSASVGDVRT.....EVTHQGLSPVTKSFNRGEC 214

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	943.5	84.6	215	2 JE0242	Ig kappa chain NIG
2	913.5	81.9	215	2 JE0244	Ig kappa chain NIG
3	897.5	80.5	215	2 JE0243	Ig kappa chain NIG
4	882.5	79.1	215	2 A23746	Ig kappa chain V-I
5	868	77.8	216	2 JE0241	Ig kappa chain Am3
6	745	66.8	230	2 S33161	Ig kappa chain - s
7	742	66.5	234	2 S14237	Ig kappa chain pre
8	741	66.5	240	2 S06084	Ig kappa chain pre
9	721	64.7	234	2 S01320	Ig kappa chain V r
10	716	64.2	218	2 S68241	Ig kappa chain V r
11	714	64.0	218	2 JC5810	monoclonal antibod
12	712	63.9	220	2 A31790	Ig kappa chain V r
13	708.5	63.5	225	2 S37484	Ig kappa chain - m
14	696	62.4	214	2 S68212	Ig kappa chain (Ma
15	688.5	61.7	219	2 S38865	Ig kappa chain - m
16	683.5	61.3	235	2 S25058	Ig kappa chain - m
17	683	61.3	210	2 A56159	Ig kappa chain V r
18	682.5	61.2	217	2 S42772	Ig kappa chain - m
19	681.5	61.1	219	2 PC4203	Ig kappa chain (mo
20	678.5	60.9	219	2 S52038	Ig kappa chain - m
21	670.5	60.1	219	2 S16112	Ig kappa chain V r
22	661.5	59.3	225	2 J10029	Ig kappa chain pre
23	602	54.0	178	2 P70219	Ig kappa chain V-C
24	601.5	53.9	135	2 S52059	JC-kappa protein -
25	571.5	51.3	229	2 A20969	Ig kappa chain pre
26	551	49.4	139	2 S40365	Ig kappa chain - h
27	548	49.1	106	1 K3HU	Ig kappa chain C r
28	546.5	49.0	238	2 A49633	Ig lambda-like cha
29	516.5	46.3	197	2 S29593	Ig kappa chain (WM

30	514	46.1	110	2 S44118	Ig kappa chain V-J
31	513	46.0	99	2 A37927	Ig kappa chain C r
32	510	45.7	108	1 K1HU4U	Ig kappa chain V-I
33	507	45.5	99	2 S26653	Ig kappa chain C r
34	504	45.2	129	2 S52789	Ig kappa chain V r
35	503	45.1	108	1 K1HURE	Ig kappa chain V-I
36	501	44.9	108	1 K1HU4G	Ig kappa chain V-I
37	501	44.9	108	2 I39154	Ig kappa chain (BR
38	497.5	44.6	135	2 S24320	Ig kappa chain pre
39	495	44.4	108	1 K1HURY	Ig kappa chain V-I
40	491	44.0	127	2 S40367	Ig kappa chain V-J
41	488	43.8	141	2 A49134	Ig kappa chain V r
42	487	43.7	117	2 S42263	Ig kappa chain V r
43	487	43.7	117	2 S43528	Ig kappa chain V r
44	487	43.7	144	2 PLO106	Ig kappa chain pre
45	484	43.4	108	1 K1HULY	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

JE0242  
Ig kappa chain NIG26 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0242  
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T  
submitted to JIPID, November 1998  
A:Description: Structure relationship of kappatype light chains with AL amyloidosis: Mult  
A:Reference number: JE0241  
A:Accession: JE0242  
A:Molecule type: protein

A:Residues: 1-215 <ALI>  
A:Cross-references: UNIPARC:UPI0000176983  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-91/Domain: immunoglobulin homology <1MW>

Query Match 84.6%; Score 943.5; DB 2; Length 215;  
Best Local Similarity 82.8%; Pred. No. 1.2e-55;  
Matches 178; Conservative 18; Mismatches 18; Indels 1; Gaps 1;

QY	1	DIQMTPSSLSASVGDVRTITTCQASQDIS-NYLNWYQKPKGKAPKLLIYDASNLETGVP	59
DB	1	EIVLTQSPGTLISLSPGERATLSCRASQSVSNVYQKPGQAPSLIYDASSRATGIP	60
QY	60	SRFSGSGSTDFFTINSIQPDIAIYQCOEYNNLPYSFGQTKLEIKRTVAAPSVFIFP	119
DB	61	DRPFGSGSGTDFITITISGLEPEDFAVYQCQYDRPPTFGQTKVEIKRTVAAPSVFIFP	120
QY	120	PSDEQLKSGTASVVCILNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSTYSLSSTL	179
DB	121	PSDEQLKSGTASVVCILNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSTYSLSSTL	180
QY	180	TLISKADYEKKHVACVETHQGLSSPVTKSFNRGEC	214
DB	181	TLISKADYEKKHVACVETHQGLSSPVTKSFNRGEC	215

RESULT 2

JE0244  
Ig kappa chain NIG2 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0244  
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T  
submitted to JIPID, November 1998  
A:Description: A new subgroup of k type light chains (Vk) identified in cases of AL amy  
A:Reference number: JE0243  
A:Accession: JE0244  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
A:Cross-references: UNIPARC:UPI0000176982







```
QY 121 SDEQLKSGTASVYVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLSSTLT 180
Db 141 SSELQTSFGASVVCFLNNFYPKDINVKWKIDGSRQGVNLNSWTDDSKDSTYSMSSTLT 200
QY 181 LSKADYEKKHKYACEVTHQGLSSPVTKSFNRGEC 214
Db 201 LTKDEYERHNSYTCEATHKTSPIVKSFNRRNEC 234

RESULT 10
S68241
Ig kappa chain V region (Mab13-1) - mouse (fragment)
N:Alternate names: immunoglobulin light chain
C:Species: Mus musculus (house mouse)
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S68241; S68214
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
submitted to the EMBL Data Library, March 1994
A:Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrin
A:Reference number: S68241
A:Accession: S68241
A:Molecule type: mRNA
A:Residues: 1-218 <TAK>
A:Cross-references: UNIPARC:UPI000011B263; EMBL:D29670; NID:9473962; PIDN:BAA06141.1; PI
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68211; MUID:96085223; PMID:7498516
A:Accession: S68214
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 'NI', 3-212 <TAW>
A:Cross-references: UNIPARC:UPI0000176980; EMBL:D29670
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 64.2%; Score 716; DB 2; Length 218;
Best Local Similarity 60.6%; Pred. No. 1.3e-40;
Matches 132; Conservative 37; Mismatches 45; Indels 4; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVITTCQASQDISN----YLNWYQOKPGKAPKLLIYDASNLET 56
Db 1 ELVLTQSPASLAVSLGQRATISCRASKSVASGYIMHWYQOKPGPPKLLISLATNLES 60
QY 57 GVPFRFSGSGGTDTFTTINSLOPEDIATYYCQENYNNLPYSGQGTQKLEIKRTVAAPSVF 116
Db 61 GVPARFSGSGGTDTFTLNHPVEEDVATYYCQHSRELPLTFGAGTKLELRADAAPTVS 120
QY 117 IPPPSDEQLKSGTASVYVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 176
Db 121 IPPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQGVNLNSWTDDSKDSTYSMS 180
QY 177 STLTLSKADYEKKHKYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 STLTUTKDEYERHNSYTCEATHKTSPIVKSFNRRNEC 218

RESULT 11
JC5810
monoclonal antibody 13-1 light chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: JC5810
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
A:Reference number: JC5810; MUID:98063277; PMID:9398605
A:Accession: JC5810
A:Molecule type: protein
A:Residues: 1-218 <AKA>
A:Cross-references: UNIPARC:UPI0000176988
A:Comment: This catalytic antibody has peroxidase oxidase. It is directed against a porp
```

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 64.0%; Score 714; DB 2; Length 218;  
Best Local Similarity 61.0%; Pred. No. 1.8e-40;  
Matches 133; Conservative 35; Mismatches 46; Indels 4; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVITTCQASQDISN----YLNWYQOKPGKAPKLLIYDASNLET 56  
Db 1 NIVLTQSPASLAVSLGQRATISCRASKSVASGYIMHWYQOKPGPPKLLISLATNLES 60

QY 57 GVPFRFSGSGGTDTFTTINSLOPEDIATYYCQENYNNLPYSGQGTQKLEIKRTVAAPSVF 116  
Db 61 GVPARFSGSGGTDTFTLNHPVEEDVATYYCQHSRELPLTFGAGTKLELRADAAPTVS 120

QY 117 IPPPSDEQLKSGTASVYVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 176  
Db 121 IPPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQGVNLNSWTDDSKDSTYSMS 180

QY 177 STLTLSKADYEKKHKYACEVTHQGLSSPVTKSFNRGEC 214  
Db 181 STLTUTKDEYERHNSYTCEATHKTSPIVKSFNRRNEC 218

RESULT 12

A31790

Ig kappa chain V region (17/9) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 21-Jan-2000

C:Accession: A31790

R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.

J. Biol. Chem. 263, 17100-17105, 1988

A:Title: Preliminary crystallographic data, primary sequence, and binding data for an ant

A:Reference number: A92886; MUID:89034213; PMID:3182835

A:Accession: A31790

A:Molecule type: mRNA

A:Residues: 1-220 <SCH>

A:Cross-references: UNIPARC:UPI0000114E12; GB:M23626; GB:J04061; NID:9533234; PIDN:AAA391

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 63.9%; Score 712; DB 2; Length 220;  
Best Local Similarity 61.1%; Pred. No. 2.5e-40;  
Matches 135; Conservative 34; Mismatches 44; Indels 8; Gaps 3;

QY 1 DIQMTQSPSSLSASVGRVITTCQASQDI-----SNYLNWYQOKPGKAPKLLIYDASN 54  
Db 1 DIVMTQSPSLTIVTAGEKVTMSTSSQSLFNSGKQKYLTYQOKPGQPPKVLIVWASTR 60

QY 55 ETGVPSRFSGSGGTDTFTTINSLOPEDIATYYCQ-EYNNLPYSGQGTQKLEIKRTVAAP 113  
Db 61 ESGVPSDRFTSGSGGTDTFTLTSSVQAEDLAVYYCQDYSN-PLTFGGGTQKLELRADAAP 119

QY 114 SVETFPSPDEQLKSGTASVYVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSY 173  
Db 120 TVSIFFPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQGVNLNSWTDDSKDSY 179

QY 174 SLSSTLTLSKADYEKKHKYACEVTHQGLSSPVTKSFNRGEC 214  
Db 180 SMSSTLTLTKDEYERHNSYTCEATHKTSPIVKSFNRRNEC 220

RESULT 13

S37484

Ig kappa chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 11-Jan-2000

C:Accession: S37484

R:Ducancel, F.F.D.

submitted to the EMBL Data Library, February 1993

A:Reference number: S37483

A:Accession: S37484

A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-225 <DUC>  
A:Cross-references: UNIPARC:UPI0000116118; EMBL:X70424; NID:G406254; PIDN:CAA49869.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 63.5%; Score 708.5; DB 2; Length 225;  
Best Local Similarity 63.1%; Pred. No. 4.3e-40;  
Matches 135; Conservative 32; Mismatches 44; Indels 3; Gaps 2;

QY 2 IQMTQSPSSLSASVGDRTITCOASQDIISNYLNWYQKPKAPKLLIYDASNLETVGPR 61  
DB 14 IVMQTQSPSSLSASVGDRTITCOASQDIISNYLNWYQKPKAPKLLIYDASNLETVGPR 73

QY 62 FSGSGSGTDTFTINSLOPEDIATYCYQYNNLPYSFGOGTKLEIKRTVAAPSVFI 120  
DB 74 FTGSGYGTDTFTISTVQAEADLAVYFCQDYSS--YTFGGGTKEIKRADAAPT 131

QY 121 SDQLKSGTASVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYSLSTLT 180  
DB 132 SSFQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLNSWTDQDSKDYSLSTLT 191

QY 181 LSKADYEKKHYACEVTHOGLSSPVTKSFNREGC 214  
DB 192 LTKDEYERHNSYTCEATHTKTSTSPIVKSFNRNEC 225

RESULT 14  
S68212  
Ig kappa chain (Mab03-1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 29-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 11-Jan-2000  
C:Accession: S68212  
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.  
PEBS Lett. 375, 273-276, 1995  
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin  
A:Reference number: S68211; MUID:96085223; PMID:7498516  
A:Accession: S68212  
A>Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-214 <TAK>  
A:Cross-references: UNIPARC:UPI00017697E; EMBL:D29668  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 62.4%; Score 696; DB 2; Length 214;  
Best Local Similarity 60.7%; Pred. No. 2.7e-39;  
Matches 130; Conservative 35; Mismatches 43; Indels 6; Gaps 1;

QY 1 DIQMTQSPSSLSASVGDRTITCOASQDI-----SNYLNWYQKPKAPKLLIYDASN 54  
DB 1 DIVMTQSPSSLSASVGDRTITCOASQDI-----SNYLNWYQKPKAPKLLIYDASN 60

QY 55 ETGVPSRFSGSGGTDTFTINSLOPEDIATYCYQYNNLPYSFGOGTKLEIKRTVAAPS 114  
DB 61 ESGVPSRFSGSGGTDTFTINSLOPEDIATYCYQYNNLPYSFGOGTKLEIKRTVAAPS 120

QY 115 VFIPPPSDEQLKSGTASVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYSL 174  
DB 121 VSIFPPSDEQLTSGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLNSWTDQDSKDYSL 180

QY 175 LSSTLTLSKADYEKKHYACEVTHOGLSSPVTKS 208  
DB 181 MSSTLTLTQDEYERHNSYTCEATHTKTSTSPIVKS 214

RESULT 15  
S38865  
Ig kappa chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 15-Jun-2001  
C:Accession: S38865  
R:Klipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993  
A:Description: Combination of a defined specificity and desired isotype by cloning of an  
A:Reference number: S38864  
A:Accession: S38865  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-219 <KIP>  
A:Cross-references: UNIPARC:UPI0000116538; EMBL:Z27396; NID:G416538; PIDN:CAA81787.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 61.7%; Score 688.5; DB 2; Length 219;  
Best Local Similarity 58.0%; Pred. No. 8.7e-39;  
Matches 127; Conservative 38; Mismatches 49; Indels 5; Gaps 1;

QY 1 DIQMTQSPSSLSASVGDRTITCOASQDI-----SNYLNWYQKPKAPKLLIYDASN 55

DB 1 ELVMTQSPSSLSASVGDRTITCOASQDI-----SNYLNWYQKPKAPKLLIYDASN 60

QY 56 TGVPSRFSGSGGTDTFTINSLOPEDIATYCYQYNNLPYSFGOGTKLEIKRTVAAPSV 115

DB 61 SGVPSRFSGSGGTDTFTINSLOPEDIATYCYQYNNLPYSFGOGTKLEIKRTVAAPSV 120

QY 116 FIFPPSDEQLKSGTASVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYSL 175

DB 121 SIFPPSDEQLTSGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLNSWTDQDSKDYSL 180

QY 176 SSTLTLSKADYEKKHYACEVTHOGLSSPVTKSFNREGC 214

DB 181 SSTLTLTQDEYERHNSYTCEATHTKTSTSPIVKSFNRGEC 219

Search completed: December 17, 2005, 01:24:34  
Job time : 17.2121 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2005, 01:10:08 ; Search time 97,9212 Seconds  
(without alignments)  
1541.883 Million cell updates/sec

Title: US-10-644-277-64  
Perfect score: 1115  
Sequence: 1 DQMTQSPSLASVGDRT.....EVTHQGLSPVTKSFNRGSC 214

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1012	90.8	236	Q7Z3Y4_HUMAN	Q7Z3Y4 homo sapien
2	1004	90.0	236	Q502W4_HUMAN	Q502W4 homo sapien
3	1003	90.0	236	Q6GMX8_HUMAN	Q6GMX8 homo sapien
4	1003	90.0	236	Q6GMW1_HUMAN	Q6GMW1 homo sapien
5	1001	89.8	236	Q6GMX0_HUMAN	Q6GMX0 homo sapien
6	992	89.0	236	Q6PIH4_HUMAN	Q6PIH4 homo sapien
7	992	89.0	236	Q6PIH7_HUMAN	Q6PIH7 homo sapien
8	986	88.4	236	Q6GMX9_HUMAN	Q6GMX9 homo sapien
9	985	88.3	236	Q6PIT5_HUMAN	Q6PIT5 homo sapien
10	984	88.3	234	Q5EFP6_HUMAN	Q5EFP6 homo sapien
11	974	87.4	234	Q7Z473_HUMAN	Q7Z473 homo sapien
12	935.5	81.9	235	Q6GMW0_HUMAN	Q6GMW0 homo sapien
13	914	82.0	236	Q6PII8_HUMAN	Q6PII8 homo sapien
14	905.5	81.2	235	Q6PJF2_HUMAN	Q6PJF2 homo sapien
15	901.5	80.9	235	Q6GMV9_HUMAN	Q6GMV9 homo sapien
16	900	80.7	236	Q6P5S8_HUMAN	Q6P5S8 homo sapien
17	894	78.4	240	Q6PIH6_HUMAN	Q6PIH6 homo sapien
18	872.5	78.3	239	Q8TCD0_HUMAN	Q8TCD0 homo sapien
19	871	78.1	234	Q56919_HUMAN	Q56919 homo sapien
20	868.5	77.9	239	Q8NEK0_HUMAN	Q8NEK0 homo sapien
21	849.5	76.2	239	Q6P491_HUMAN	Q6P491 homo sapien
22	770	69.1	234	Q4KM66_RAT	Q4KM66 rattus norv
23	750	67.3	189	Q56917_HUMAN	Q56917 homo sapien
24	742	66.5	236	Q7TS98_MOUSE	Q7TS98 mus musculu
25	735	65.9	234	Q5M838_RAT	Q5M838 rattus norv
26	725	65.0	240	Q52L64_MOUSE	Q52L64 mus musculu
27	723	64.8	238	Q58EU4_MOUSE	Q58EU4 mus musculu
28	716	64.2	238	Q66J87_MOUSE	Q66J87 mus musculu
29	715	64.1	236	Q52L95_MOUSE	Q52L95 mus musculu
30	687.5	61.7	235	Q58EV6_MOUSE	Q58EV6 mus musculu
31	682.5	61.2	219	Q65ZC0_MOUSE	Q65ZC0 mus musculu

32	682.5	61.2	237	2	Q569Y8_MOUSE	Q569Y8 mus musculu
33	674.5	60.5	235	2	Q5XFY8_MOUSE	Q5XFY8 mus musculu
34	670.5	60.1	239	2	Q58EU8_MOUSE	Q58EU8 mus musculu
35	653.5	58.6	234	2	Q5XKG4_MOUSE	Q5XKG4 mus musculu
36	631	56.6	241	2	Q63ZX4_MOUSE	Q63ZX4 mus musculu
37	599	53.7	120	2	Q6P5R5_HUMAN	Q6P5R5 homo sapien
38	555.5	49.8	243	2	Q6NTU5_XENLA	Q6NTU5 xenopus lae
39	549	49.2	237	2	Q7SZ36_XENLA	Q7SZ36 homo sapien
40	548	49.1	106	1	KAC_HUMAN	P01834 homo sapien
41	518.5	46.5	239	2	Q5HZC6_XENTR	Q5HZC6 xenopus tro
42	510	45.7	108	1	KVIB_HUMAN	P01594 homo sapien
43	503	45.1	108	1	KVIO_HUMAN	P01607 homo sapien
44	501	44.9	108	1	KVIA_HUMAN	P01593 homo sapien
45	495	44.4	108	1	KVIP_HUMAN	P01608 homo sapien

ALIGNMENTS

RESULT 1  
Q7Z3Y4\_HUMAN  
ID Q7Z3Y4\_HUMAN PRELIMINARY; PRT; 236 AA.  
AC Q7Z3Y4;  
DT 01-OCT-2003 (Tremblrel. 25, Created)  
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Skeletal Muscle;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Skeletal Muscle;  
RA Strausberg R.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR ENBL; BC005332; AAH05332.1; -; mRNA.  
DR HSP; P01834; IHEZ.  
DR Ensembl; ENSG00000163245; Homo sapiens.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
KW Hypothetical protein; Immunoglobulin domain.

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SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;
Query Match 90.8%; Score 1012; DB 2; Length 236;
Best Local Similarity 90.7%; Pred. No. 1.8e-74;
Matches 194; Conservative 10; Mismatches 10; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRDVTITTCASQDSISNVLNNYQOKPGKAPKLLIYDASNLETGVPS 60
DB 23 DIQMTQSPSSLSASVGRDVTITTCASQDSISNVLNNYQOKPGKAPKLLIYDASNLETGVPS 82
QY 61 RFGSGSGTDFTTINSLOPEDIAIYCOEYNNLPYSFGQGTKEIKRTVAAPSFIIPP 120
DB 83 KFGSGSGTDFLTITSSLOPEDFATYCCQYKSPVTFQGTKEIKRTVAAPSFIIPP 142
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLT 180
DB 143 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLT 202
QY 181 LSKADYEHKHVYACEVTHQGLSSPVTKSFNRGEC 214
DB 203 LSKADYEHKHVYACEVTHQGLSSPVTKSFNRGEC 236
RESULT 2
Q502W4 HUMAN
ID Q502W4_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q502W4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL BC095489; AHA95489.1; -; mRNA.
DR SMR; Q502W4; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
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DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25936 MW; E2DF79AC18756AA9 CRC64;
Query Match 90.0%; Score 1004; DB 2; Length 236;
Best Local Similarity 90.2%; Pred. No. 8e-74;
Matches 193; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRDVTITTCASQDSISNVLNNYQOKPGKAPKLLIYDASNLETGVPS 60
DB 23 DIQMTQSPSSLSASVGRDVTITTCASQDSISNVLNNYQOKPGKAPKLLIYDASNLETGVPS 82
QY 61 RFGSGSGTDFTTINSLOPEDIAIYCOEYNNLPYSFGQGTKEIKRTVAAPSFIIPP 120
DB 83 RFGSGSGTDFLTITSSLOPEDFATYCCQYKSPVTFQGTKEIKRTVAAPSFIIPP 142
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLT 180
DB 143 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLT 202
QY 181 LSKADYEHKHVYACEVTHQGLSSPVTKSFNRGEC 214
DB 203 LSKADYEHKHVYACEVTHQGLSSPVTKSFNRGEC 236
RESULT 3
Q6GMX8 HUMAN
ID Q6GMX8_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMX8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
```

RA SCHMERCH A., SCHEIN J.E., JONES S.J.M., MALLA M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human



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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073775; AAH3775.1; -; mRNA.
DR SMR; Q6GMX0; 23-236.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7B92BF8F CRC64;

Query Match 89.8%; Score 1001; DB 2; Length 236;
Best Local Similarity 89.3%; Pred. No. 1.4e-73;
Matches 191; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

OY 1 DIQMTQSPSSLSASVGRVTITTCQASQDISNYLNWYQKPKAPKLLIYDASNLGTGVP 60
DB 23 DIQMTQSPSSLSASVGRVTITTCRASQINNYLNWYQLKPKAPNLLIYAASSLSQSGVP 82

OY 61 RFGSGSGTDFTTINSIQPEDIATYYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIFPP 120
DB 83 RFGSGSGTDFLTITSSRLRPDDFATYYCQSYNIPLETFGGTNVIRKRTVAAPSVFIFPP 142

OY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
DB 143 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 202

OY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 203 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 6
Q6PIH4 HUMAN
ID Q6PIH4 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6PIH4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034146; AAH34146.1; -; mRNA.
DR HSSP; P01607; 1AR2.
DR SMR; Q6PIH4; 23-236.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25871 MW; BE01A28CD06BEE26 CRC64;

Query Match 89.0%; Score 992; DB 2; Length 236;
Best Local Similarity 89.3%; Pred. No. 7.6e-73;
Matches 191; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

OY 1 DIQMTQSPSSLSASVGRVTITTCQASQDISNYLNWYQKPKAPKLLIYDASNLGTGVP 60
DB 23 DIQMTQSPSTLSASVGRVTIACRASQWISDLAWYQKPKAPKLLIYDASRLSGLSVP 82

OY 61 RFGSGSGTDFTTINSIQPEDIATYYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIFPP 120
DB 83 RFGSGSGTDFLTITSSRLRPDDFATYYCQSYNIPLETFGGTNVIRKRTVAAPSVFIFPP 142

OY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
DB 143 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 202

OY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 203 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 7
Q6PIH7 HUMAN
ID Q6PIH7 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6PIH7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
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DE	IGKC protein.	DE	IGKC protein.
GN	Name=IGKC;	GN	Name=IGKC;
OS	Homo sapiens (Human)	OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;	OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC	Homo.	OC	Homo.
OX	NCBI_TaxID=9606;	OX	NCBI_TaxID=9606;
RN	[1]	RN	[1]
RP	NUCLEOTIDE SEQUENCE.	RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Primary B-Cells;	RC	TISSUE=Primary B-Cells;
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,	RA	Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,	RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,	RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT	"Generation and initial analysis of more than 15,000 full-length human	RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences."	RT	and mouse cDNA sequences."
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN	[2]	RN	[2]
RP	NUCLEOTIDE SEQUENCE.	RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Primary B-Cells;	RC	TISSUE=Primary B-Cells;
RG	NIH MGC Project;	RG	NIH MGC Project;
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC034141; AAH34141.1; -; mRNA.	DR	EMBL; BC034141; AAH34141.1; -; mRNA.
DR	HSSP; P01607; 1A2.	DR	HSSP; P01607; 1A2.
DR	SMR; Q6PIH7; 23-236.	DR	SMR; Q6PIH7; 23-236.
DR	Ensembl; ENSG00000163245; Homo sapiens.	DR	Ensembl; ENSG00000163245; Homo sapiens.
DR	InterPro; IPR003599; Ig.	DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR007110; Ig-like.	DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig cl.	DR	InterPro; IPR003597; Ig cl.
DR	InterPro; IPR003006; Ig_MHC.	DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig v.	DR	InterPro; IPR003596; Ig v.
DR	Pfam; PF07654; Cl-set; 1.	DR	Pfam; PF07654; Cl-set; 1.
DR	SMART; SM00409; IGV; 1.	DR	SMART; SM00409; IGV; 1.
DR	SMART; SM00407; IGV; 1.	DR	SMART; SM00407; IGV; 1.
DR	PROSITE; PS00835; IG LIKE; 2.	DR	PROSITE; PS00835; IG LIKE; 2.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN 1.	DR	PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ	SEQUENCE 236 AA; 25603 MW; 8BC561106861213P CRC64;	SQ	SEQUENCE 236 AA; 25603 MW; 8BC561106861213P CRC64;
Query Match 89.0%; Score 992; DB 2; Length 236;		Query Match 88.4%; Score 986; DB 2; Length 236;	
Best Local Similarity 89.3%; Pred. No. 7.6e-73;		Best Local Similarity 88.3%; Pred. No. 2.3e-72;	
Matches 191; Conservative 11; Mismatches 12; Indels 0; Gaps 0;		Matches 189; Conservative 11; Mismatches 14; Indels 0; Gaps 0;	
Qy	1 DIQMTQSPSLASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60	Qy	1 DIQMTQSPSLASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
Db	23 DIQLTQSPSLASVGDRTVITTCRASQGISYLAWYQKPGKAPNLLIYAASLTQSGVPS 82	Db	23 DIQMTQSPSLASVGDRTVITTCRASQNSVRSLAWYQORPEKAPKLLIYATSSLHSGVPS 82
Qy	61 RFGSGSGTDFTTINSLOPEDATYYCOEYNLPYSFGOGTKLEIKRTVAAPSVFIIPP 120	Qy	61 RFGSGSGTDFTTINSLOPEDATYYCOEYNLPYSFGOGTKLEIKRTVAAPSVFIIPP 120
Db	83 RFGSGSGTDFTTINSLOPEDATYYCQYNTYPLTFGGTKVEIKRTVAAPSVFIIPP 142	Db	83 RFGSGSGTDFTTINSLOPEDATYYCQYNTYPLTFGGTKVEIKRTVAAPSVFIIPP 142
Qy	121 SDEQLKSGTASVVCLLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDSSTLSSTLT 180	Qy	121 SDEQLKSGTASVVCLLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDSSTLSSTLT 180
Db	143 SDEQLKSGTASVVCLLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDSSTLSSTLT 202	Db	143 SDEQLKSGTASVVCLLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDSSTLSSTLT 202
Qy	181 LSKADYEKKHYACEVTHQGLSSPVTKSNRREC 214	Qy	181 LSKADYEKKHYACEVTHQGLSSPVTKSNRREC 214
Db	203 LSKADYEKKHYACEVTHQGLSSPVTKSNRREC 236	Db	203 LSKADYEKKHYACEVTHQGLSSPVTKSNRREC 236
RESULT 8		RESULT 8	
ID	Q6GMX9 HUMAN PRELIMINARY; PRT; 236 AA.	ID	Q6GMX9 HUMAN PRELIMINARY; PRT; 236 AA.
AC	O6GMX9;	AC	O6GMX9;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)	DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

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RESULT 9
OSPIITS HUMAN
ID Q6PIT5_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6PIT5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko M., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029444; AAH29444.1; -; mRNA.
DR HSSP; P01607; 1A22.
DR SMR; Q6PIT5; 26-236.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25741 MW; BD50AF071FEE351 CRC64;
Query Match 88.3%; Score 985; DB 2; Length 236;
Best Local Similarity 88.7%; Pred. No. 2,8e-72;
Matches 189; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 2 IQMTQSPSSLSASVGRVTITCOASQDISNVLNYYQKPGKAPKLLIYDASNLETGVPSR 61
DB 24 IQLTQSPSSLSASVGERVTITCRASQGISALLAWYQKPGKPLLIYDASTMESGVPSR 83
QY 62 FSGSGSGTDFTTINSIQLPEDIATYYCQYNNLPYSFGQGTGLEIKRTVAAPSVFIFPPS 121
DB 84 FSGSGSGTFTLTINSIQLPEDFATYYCQYNNLPYSFGQGTGLEIKRTVAAPSVFIFPPS 143
QY 122 DEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYISLSSTLT 181
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25741 MW; BD50AF071FEE351 CRC64;
Query Match 88.3%; Score 985; DB 2; Length 236;
Best Local Similarity 88.7%; Pred. No. 2,8e-72;
Matches 189; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 2 IQMTQSPSSLSASVGRVTITCOASQDISNVLNYYQKPGKAPKLLIYDASNLETGVPSR 61
DB 22 IRMTQSPSSFSASTGDRVTITCRASQDIRNVAVYQKSGKAPKFLIYASTLQSGVPSR 81
QY 62 FSGSGSGTDFTTINSIQLPEDIATYYCQYNNLPYSFGQGTGLEIKRTVAAPSVFIFPPS 121
DB 82 FSGSGSGTFTLTINSIQLQSEDFATYYCQYNNSPPTFGQGTREITRTVAAPSVFIFPPS 141
QY 122 DEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYISLSSTLT 181
DB 142 DEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYISLSSTLT 201
QY 182 SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 202 SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
RESULT 11
Q7Z473 HUMAN
ID Q7Z473_HUMAN PRELIMINARY; PRT; 234 AA.
AC Q7Z473;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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DB 144 DEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYISLSSTLT 203
QY 182 SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 204 SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236
RESULT 10
QSEPF6 HUMAN
ID QSEPF6_HUMAN PRELIMINARY; PRT; 234 AA.
AC QSEPF6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Anti-RHD monoclonal T125 kappa light chain precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RT "Sequence determination of the recombinant human anti-RHD monoclonal
antibody T125."
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY894991; AA82027.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 234 anti-RHD monoclonal T125 kappa light
chain.
FT SEQUENCE 234 AA; 25698 MW; 866DCD1E4FD7D5EA CRC64;
Query Match 88.3%; Score 984; DB 2; Length 234;
Best Local Similarity 88.7%; Pred. No. 3,4e-72;
Matches 189; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 2 IQMTQSPSSLSASVGRVTITCOASQDISNVLNYYQKPGKAPKLLIYDASNLETGVPSR 61
DB 22 IRMTQSPSSFSASTGDRVTITCRASQDIRNVAVYQKSGKAPKFLIYASTLQSGVPSR 81
QY 62 FSGSGSGTDFTTINSIQLPEDIATYYCQYNNLPYSFGQGTGLEIKRTVAAPSVFIFPPS 121
DB 82 FSGSGSGTFTLTINSIQLQSEDFATYYCQYNNSPPTFGQGTREITRTVAAPSVFIFPPS 141
QY 122 DEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYISLSSTLT 181
DB 142 DEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYISLSSTLT 201
QY 182 SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 202 SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
RESULT 11
Q7Z473 HUMAN
ID Q7Z473_HUMAN PRELIMINARY; PRT; 234 AA.
AC Q7Z473;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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## RESULT 12

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QY 180 TLISKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 214
Db 201 TLISKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 235

RESULT 13
Q6PIL8 HUMAN
ID Q6PIL8_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6PIL8;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Soares M.B., Bernaldo M.F., Casavant T.L., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032451; AAH32451.1; -; mRNA.
DR HSP; P01837; 1KCU.
DR SMR; Q6PIL8; 21-236.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_M.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;

Query Match 82.0%; Score 914; DB 2; Length 236;
Best Local Similarity 81.7%; Pred. No. 1.8e-66;
Matches 174; Conservative 19; Mismatches 18; Indels 2; Gaps 2;

QY 4 MTQSPSSLSASVGRVTTTQASQDI-SNYLNWYQKPGKAPKLLIYDASNLETGVPSRF 62
Db 24 LTQSPGTLSPGERATLSCRAQSLSYLAWYQKPGQAPRLLIYGVSSRATGIPDRF 83

RESULT 14
Q6PJF2 HUMAN
ID Q6PJF2_HUMAN PRELIMINARY; PRT; 235 AA.
AC Q6PJF2;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Soares M.B., Bernaldo M.F., Casavant T.L., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016380; AAH16380.1; -; mRNA.
DR HSP; P01837; 1KCU.
DR SMR; Q6PJF2; 21-235.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_M.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

Query Match 81.2%; Score 905.5; DB 2; Length 235;
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Search completed: December 17, 2005, 01:23:40  
Job time : 98.9212 secs

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Db      141 PSDEQLKSGTASVVCILNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSSIL 200
Qy      180 TLSKADYERKHVVACEVTHOGLSSPVTKSFNRGEC 214
Db      201 TLSKADYERKHVVACEVTHOGLSSPVTKSFNRGEC 235

Search completed: December 17, 2005, 01:23:40
Job time : 98.9212 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2005, 01:13:49 ; Search time 21.4 Seconds  
(without alignments)  
826.757 Million cell updates/sec

Title: US-10-644-277-64  
Perfect score: 1115  
Sequence: 1 DIQMTQSPSSLSASVGRVT.....EVTHQGLSPVTKSFNRGEC 214

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Issued Patents AA.\*
- 1: /cgn2\_6/prodata/1/iaa/5 COMB.pep.\*
  - 2: /cgn2\_6/prodata/1/iaa/6 COMB.pep.\*
  - 3: /cgn2\_6/prodata/1/iaa/H COMB.pep.\*
  - 4: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep.\*
  - 5: /cgn2\_6/prodata/1/iaa/RE COMB.pep.\*
  - 6: /cgn2\_6/prodata/1/iaa/baCkfilea1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1034	92.7	237	2	US-08-908-469-100
2	1034	92.7	491	2	US-10-011-125A-2
3	1032	92.6	214	1	US-07-934-373C-39
4	1032	92.6	214	2	US-08-437-642B-39
5	1032	92.6	214	4	PCT-US93-07832-39
6	1027	92.1	214	1	US-07-934-373C-40
7	1027	92.1	214	1	US-08-788-800-11
8	1027	92.1	214	2	US-08-437-642B-40
9	1027	92.1	214	2	US-09-037-309-2
10	1027	92.1	214	2	US-09-097-171A-2
11	1027	92.1	214	2	US-09-460-587-2
12	1027	92.1	214	2	US-09-940-166A-2
13	1027	92.1	214	4	PCT-US93-07832-40
14	1027	92.1	233	1	US-07-934-373C-25
15	1027	92.1	233	2	US-08-437-642B-25
16	1027	92.1	233	2	US-08-146-206C-25
17	1027	92.1	233	2	US-09-705-686-25
18	1027	92.1	233	2	US-09-705-392A-25
19	1027	92.1	233	2	US-09-705-398-25
20	1027	92.1	233	4	PCT-US93-07832-25
21	1027	92.1	237	2	US-09-037-309-6
22	1027	92.1	237	2	US-09-097-171A-10
23	1027	92.1	237	2	US-09-422-712B-2
24	1027	92.1	237	2	US-09-607-756-2
25	1027	92.1	237	2	US-09-460-587-6
26	1027	92.1	237	2	US-09-940-166A-6
27	1025	91.9	233	2	US-08-030-175-43

28	1020	91.5	214	2	US-09-472-087-71	Sequence 71, Appl
29	1016	90.1	218	4	PCT-US96-13152-2	Sequence 2, Appl1
30	1014	90.1	214	1	US-08-458-516-12	Sequence 12, Appl
31	1013	90.9	212	2	US-10-011-125A-5	Sequence 5, Appl1
32	1011	90.7	236	2	US-09-853-053-30	Sequence 30, Appl
33	1010	90.6	234	2	US-09-800-729-150	Sequence 150, Appl
34	1006	90.2	218	1	US-08-887-352B-13	Sequence 13, Appl
35	1006	90.2	218	2	US-08-466-151-9	Sequence 9, Appl1
36	1006	90.2	218	2	US-09-109-207C-13	Sequence 13, Appl
37	1006	90.2	218	2	US-09-296-005-13	Sequence 13, Appl
38	1006	90.2	218	2	US-08-466-163B-9	Sequence 9, Appl1
39	1006	90.2	218	2	US-09-920-171-13	Sequence 13, Appl
40	1006	90.2	218	2	US-09-802-096-9	Sequence 9, Appl1
41	1006	90.2	218	2	US-09-802-077-9	Sequence 9, Appl1
42	1006	90.2	218	2	US-09-716-028-13	Sequence 13, Appl
43	1006	90.2	218	2	US-10-113-996-13	Sequence 13, Appl
44	1006	90.2	218	2	US-09-925-179-9	Sequence 9, Appl1
45	1004.5	90.1	235	2	US-09-910-059-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1  
US-08-908-469-100  
; Sequence 100, Application US/08908469  
; Patent No. 6884879  
; GENERAL INFORMATION:  
; APPLICANT: Baca, Manuel  
; Wells, James A.  
; Presta, Leonard G.  
; Lowman, Henry B.  
; Chen, Yvonne M.  
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
NUMBER OF SEQUENCES: 131  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/908,469  
FILING DATE: 21-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/833,504  
FILING DATE: 07-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Cui, Steven X.  
REGISTRATION NUMBER: 44,637  
REFERENCE/DOCKET NUMBER: P1093P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 100:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 237 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 100:  
US-08-908-469-100

Query Match 92.7%; Score 1034; DB 2; Length 237;  
Best Local Similarity 91.6%; Pred. No. 1.4e-78;  
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;



QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINSYLNWYQKPGKAPKLLIYDASNLETGVP 60  
DB 24 DIQLTQSPSSLSASVGDRTVITTCQASQDINSYLNWYQKPGKAPKLLIYFTSSLSHGVP 83  
QY 61 RFGSGSGTDTFTTINSLOPEDIAITYCOEYNNLPYSFGQGTKEIKRTVAAPSFIIPP 120  
DB 84 RFGSGSGTDTFTTINSLOPEDFAITYCOQYSTVPWTGQGTKEIKRTVAAPSFIIPP 143  
QY 121 SDEQLKSGTASVCLNNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 180  
DB 144 SDEQLKSGTASVCLNNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 203  
QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNREGC 214  
DB 204 LSKADYERKHVYACEVTHQGLSSPVTKSFNREGC 237

## RESULT 2

US-10-011-125A-2  
; Sequence 2, Application US/10011125A  
; Patent No. 6828121  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Christina Yu-Ching  
; TITLE OF INVENTION: BACTERIAL HOST STRAINS  
; FILE REFERENCE: P1804R1  
; CURRENT APPLICATION NUMBER: US/10/011,125A  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: US 60/256,162  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 12  
; SEQ ID NO 2  
; LENGTH: 491  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence is synthesized.  
; Patent No. 6828121  
US-10-011-125A-2

Query Match 92.7%; Score 1034; DB 2; Length 491;

Best Local Similarity 91.6%; Pred. No. 3.3e-78;

Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINSYLNWYQKPGKAPKLLIYDASNLETGVP 60  
DB 24 DIQLTQSPSSLSASVGDRTVITTCQASQDINSYLNWYQKPGKAPKLLIYFTSSLSHGVP 83  
QY 61 RFGSGSGTDTFTTINSLOPEDIAITYCOEYNNLPYSFGQGTKEIKRTVAAPSFIIPP 120  
DB 84 RFGSGSGTDTFTTINSLOPEDFAITYCOQYSTVPWTGQGTKEIKRTVAAPSFIIPP 143  
QY 121 SDEQLKSGTASVCLNNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 180  
DB 144 SDEQLKSGTASVCLNNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 203  
QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNREGC 214  
DB 204 LSKADYERKHVYACEVTHQGLSSPVTKSFNREGC 237

## RESULT 3

US-07-934-373C-39  
; Sequence 39, Application US/07934373C  
; Patent No. 5821337  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco

; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/934,373C  
; FILING DATE: 21-Aug-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 214 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-07-934-373C-39

Query Match 92.6%; Score 1032; DB 1; Length 214;

Best Local Similarity 92.5%; Pred. No. 1.8e-78;

Matches 198; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINSYLNWYQKPGKAPKLLIYDASNLETGVP 60  
DB 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINSYLNWYQKPGKAPKLLIYFTSSLSHGVP 60  
QY 61 RFGSGSGTDTFTTINSLOPEDIAITYCOEYNNLPYSFGQGTKEIKRTVAAPSFIIPP 120  
DB 61 RFGSGSGTDTFTTINSLOPEDFAITYCOQGTLPPTFGQGTKEIKRTVAAPSFIIPP 120  
QY 121 SDEQLKSGTASVCLNNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 180  
DB 121 SDEQLKSGTASVCLNNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 180  
QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNREGC 214  
DB 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNREGC 214

## RESULT 4

US-08-437-642B-39  
; Sequence 39, Application US/08437642B  
; Patent No. 6054297  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/437,642B  
FILING DATE: 09-May-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 214 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-437-642B-39

Query Match 92.6%; Score 1032; DB 2; Length 214;  
Best Local Similarity 92.5%; Pred. No. 1.8e-78;  
Matches 198; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60  
DB 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYVTSLESGVPS 60  
QY 61 RFGSGSGTDFTTINSLOPEDATYYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIAPP 120  
DB 61 RFGSGSGTDYTLTISSLQPEDFATYYCQCGNTLPPTFGQGTKEIKRTVAAPSVFIAPP 120  
QY 121 SDQLKSGTASVCLNNFYPRAKQVQVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT 180  
DB 121 SDEQLKSGTASVCLNNFYPRAKQVQVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT 180  
QY 181 LSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 214  
DB 181 LSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 214

RESULT 5  
PCT-US93-07832-39  
Sequence 39, Application PC/TUS9307832  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07832

FILING DATE: 19930820  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME:  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 709P2PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/952-9881  
TELEFAX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 214 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US93-07832-39

Query Match 92.6%; Score 1032; DB 4; Length 214;  
Best Local Similarity 92.5%; Pred. No. 1.8e-78;  
Matches 198; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60  
DB 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYVTSLESGVPS 60  
QY 61 RFGSGSGTDFTTINSLOPEDATYYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIAPP 120  
DB 61 RFGSGSGTDYTLTISSLQPEDFATYYCQCGNTLPPTFGQGTKEIKRTVAAPSVFIAPP 120  
QY 121 SDEQLKSGTASVCLNNFYPRAKQVQVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT 180  
DB 121 SDEQLKSGTASVCLNNFYPRAKQVQVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT 180  
QY 181 LSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 214  
DB 181 LSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 214

RESULT 6  
US-07-934-373C-40  
Sequence 40, Application US/07934373C  
Patent No. 5821337  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
APPLICANT: Leonard G. Presta  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,373C  
FILING DATE: 21-Aug-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-40

Query Match          92.1%; Score 1027; DB 1; Length 214;
Best Local Similarity 92.1%; Pred. No. 4.7e-78;
Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINSYLNWYQOKPGKAPKLLIYDASNLETGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQDINNLYNLYQOKPGKAPKLLIYYTSTLHSGVPS 60
QY 61 RFGSGSGTDFTTINSIQLQPEDIATYYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIFPP 120
Db 61 RFGSGSGTDYTLTISSQLQPEDFATYYCQGNLTLPPTFGQGTKEIKRTVAAPSVFIFPP 120
QY 121 SDEQLKSGTASVVCLLNFPYEPKAVQWKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
Db 121 SDEQLKSGTASVVCLLNFPYEPKAVQWKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
QY 181 LSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 LSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 7
US-08-788-800-11
; Sequence 11, Application US/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
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; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-788-800-11

Query Match          92.1%; Score 1027; DB 1; Length 214;
Best Local Similarity 92.1%; Pred. No. 4.7e-78;
Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINSYLNWYQOKPGKAPKLLIYDASNLETGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQDINNLYNLYQOKPGKAPKLLIYYTSTLHSGVPS 60
QY 61 RFGSGSGTDFTTINSIQLQPEDIATYYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIFPP 120
Db 61 RFGSGSGTDYTLTISSQLQPEDFATYYCQGNLTLPPTFGQGTKEIKRTVAAPSVFIFPP 120
QY 121 SDEQLKSGTASVVCLLNFPYEPKAVQWKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
Db 121 SDEQLKSGTASVVCLLNFPYEPKAVQWKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
QY 181 LSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 LSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 8
US-08-437-642B-40
; Sequence 40, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
```

Matches	197;	Conservative	8;	Mismatches	9;	Indels	0;	Gaps	0;
QY	1	DIQMTQSPSSLSASVGDRTVITTCQASQDINSYLNWYQKPKGKAPKLLIYDASNLETGVPS	60						
DB	1	DIQMTQSPSSLSASVGDRTVITTCQASQDINSYLNWYQKPKGKAPKLLIYDASNLETGVPS	60						
QY	61	RFSGSGSGTDFTTINSIQPEDFATYYCQEQNTLPPFTGGQTKVEIKRTVAAPSVFI	120						
DB	61	RFSGSGSGTDFTTINSIQPEDFATYYCQEQNTLPPFTGGQTKVEIKRTVAAPSVFI	120						
QY	121	SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYLSSTLT	180						
DB	121	SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYLSSTLT	180						
QY	181	LSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC	214						
DB	181	LSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC	214						
<p>Query Match 92.1%; Score 1027; DB 2; Length 214;            Best Local Similarity 92.1%; Pred. No. 4.7e-78;            Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;</p>									
QY	1	DIQMTQSPSSLSASVGDRTVITTCQASQDINSYLNWYQKPKGKAPKLLIYDASNLETGVPS	60						
DB	1	DIQMTQSPSSLSASVGDRTVITTCQASQDINSYLNWYQKPKGKAPKLLIYDASNLETGVPS	60						
QY	61	RFSGSGSGTDFTTINSIQPEDFATYYCQEQNTLPPFTGGQTKVEIKRTVAAPSVFI	120						
DB	61	RFSGSGSGTDFTTINSIQPEDFATYYCQEQNTLPPFTGGQTKVEIKRTVAAPSVFI	120						
QY	121	SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYLSSTLT	180						
DB	121	SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYLSSTLT	180						
QY	181	LSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC	214						
DB	181	LSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC	214						
<p>Query Match 92.1%; Score 1027; DB 2; Length 214;            Best Local Similarity 92.1%; Pred. No. 4.7e-78;            Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;</p>									
QY	1	DIQMTQSPSSLSASVGDRTVITTCQASQDINSYLNWYQKPKGKAPKLLIYDASNLETGVPS	60						
DB	1	DIQMTQSPSSLSASVGDRTVITTCQASQDINSYLNWYQKPKGKAPKLLIYDASNLETGVPS	60						
QY	61	RFSGSGSGTDFTTINSIQPEDFATYYCQEQNTLPPFTGGQTKVEIKRTVAAPSVFI	120						
DB	61	RFSGSGSGTDFTTINSIQPEDFATYYCQEQNTLPPFTGGQTKVEIKRTVAAPSVFI	120						
QY	121	SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYLSSTLT	180						
DB	121	SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYLSSTLT	180						
QY	181	LSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC	214						
DB	181	LSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC	214						
<p>Query Match 92.1%; Score 1027; DB 2; Length 214;            Best Local Similarity 92.1%; Pred. No. 4.7e-78;            Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;</p>									
QY	1	DIQMTQSPSSLSASVGDRTVITTCQASQDINSYLNWYQKPKGKAPKLLIYDASNLETGVPS	60						
DB	1	DIQMTQSPSSLSASVGDRTVITTCQASQDINSYLNWYQKPKGKAPKLLIYDASNLETGVPS	60						
QY	61	RFSGSGSGTDFTTINSIQPEDFATYYCQEQNTLPPFTGGQTKVEIKRTVAAPSVFI	120						
DB	61	RFSGSGSGTDFTTINSIQPEDFATYYCQEQNTLPPFTGGQTKVEIKRTVAAPSVFI	120						
QY	121	SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYLSSTLT	180						
DB	121	SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYLSSTLT	180						
QY	181	LSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC	214						
DB	181	LSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC	214						
<p>Query Match 92.1%; Score 1027; DB 2; Length 214;            Best Local Similarity 92.1%; Pred. No. 4.7e-78;            Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;</p>									
QY	1	DIQMTQSPSSLSASVGDRTVITTCQASQDINSYLNWYQKPKGKAPKLLIYDASNLETGVPS	60						
DB	1	DIQMTQSPSSLSASVGDRTVITTCQASQDINSYLNWYQKPKGKAPKLLIYDASNLETGVPS	60						
QY	61	RFSGSGSGTDFTTINSIQPEDFATYYCQEQNTLPPFTGGQTKVEIKRTVAAPSVFI	120						
DB	61	RFSGSGSGTDFTTINSIQPEDFATYYCQEQNTLPPFTGGQTKVEIKRTVAAPSVFI	120						
QY	121	SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDS							

QY 61 RFGSGSGTDTFTTINSLOPEDIATYCOEYNNLPYSFGQGTKLBIKRTVAAPSFIIPP 120  
Db 61 RFGSGSGTDTFTTINSLOPEDIATYCOEYNNLPYSFGQGTKLBIKRTVAAPSFIIPP 120  
QY 121 SDEQLKSGTASVVCLLNNFPYKQVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180  
Db 121 SDEQLKSGTASVVCLLNNFPYKQVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180  
QY 181 LSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 214  
Db 181 LSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 214

## RESULT 11

US-09-460-587-2  
; Sequence 2, Application US/09460587  
; Patent No. 6322997  
; GENERAL INFORMATION:  
; APPLICANT: Blank, Gregory S.  
; APPLICANT: Narindray, Daljit S.  
; APPLICANT: Zapata, Gerardo A.  
; TITLE OF INVENTION: Protein Recovery  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/460,587  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/097,309  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schwartz, Timothy R.  
; REGISTRATION NUMBER: 32171  
; REFERENCE/DOCKET NUMBER: P1105R1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-7467  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 214 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-09-460-587-2

Query Match 92.1%; Score 1027; DB 2; Length 214;  
Best Local Similarity 92.1%; Pred. No. 4.7e-78;  
Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGRVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 60  
Db 1 DIQMTQSPSSLSASVGRVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 60  
QY 61 RFGSGSGTDTFTTINSLOPEDIATYCOEYNNLPYSFGQGTKLBIKRTVAAPSFIIPP 120  
Db 61 RFGSGSGTDTFTTINSLOPEDIATYCOEYNNLPYSFGQGTKLBIKRTVAAPSFIIPP 120  
QY 121 SDEQLKSGTASVVCLLNNFPYKQVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180  
Db 121 SDEQLKSGTASVVCLLNNFPYKQVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180

QY 181 LSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 214  
Db 181 LSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 214  
RESULT 12  
US-09-940-166A-2  
; Sequence 2, Application US/09940166A  
; Patent No. 6716598  
; GENERAL INFORMATION:  
; APPLICANT: Blank, Gregory S.  
; APPLICANT: Narindray, Daljit S.  
; APPLICANT: Zapata, Gerardo A.  
; TITLE OF INVENTION: Protein Recovery  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/940.166A  
; FILING DATE: 27-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/097,309  
; FILING DATE: 13-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schwartz, Timothy R.  
; REGISTRATION NUMBER: 32171  
; REFERENCE/DOCKET NUMBER: P1105R1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-7467  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 214 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-940-166A-2

Query Match 92.1%; Score 1027; DB 2; Length 214;  
Best Local Similarity 92.1%; Pred. No. 4.7e-78;  
Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGRVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 60  
Db 1 DIQMTQSPSSLSASVGRVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 60  
QY 61 RFGSGSGTDTFTTINSLOPEDIATYCOEYNNLPYSFGQGTKLBIKRTVAAPSFIIPP 120  
Db 61 RFGSGSGTDTFTTINSLOPEDIATYCOEYNNLPYSFGQGTKLBIKRTVAAPSFIIPP 120  
QY 121 SDEQLKSGTASVVCLLNNFPYKQVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180  
Db 121 SDEQLKSGTASVVCLLNNFPYKQVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180  
QY 181 LSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 214  
Db 181 LSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 214  
RESULT 13  
PCT-US93-07832-40  
; Sequence 40, Application PC/TUS9307832

GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,373C  
FILING DATE: 21-Aug-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 233 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-07-934-373C-25

Query Match 92.1%; Score 1027; DB 1; Length 233;  
Best Local Similarity 92.1%; Pred. No. 5.2e-78;  
Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCOASQDISNYLNWYQKPKAPKLLIYDASNLTGVPS 60  
Db 20 DIQMTQSPSSLSASVGRVTITCRASQDINNLYNWYQKPKAPKLLIYDASNLTGVPS 79

Qy 61 RFSGSGSGTDFTTINSLOPEDATYYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIFPP 120  
Db 80 RFSGSGSGTDYTLTISLSQPEDFATYYCOQGNLTLPPTFGQGTKEIKRTVAAPSVFIFPP 139

Qy 121 SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTLSLT 180  
Db 140 SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTLSLT 199

Qy 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214  
Db 200 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 233

RESULT 15  
US-08-437-642B-25  
Sequence 25, Application US/08437642B  
Patent No. 6054297  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESS: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA

GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07832  
FILING DATE: 19930820  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME:  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 709P2PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE:  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 214 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US93-07832-40

Query Match 92.1%; Score 1027; DB 4; Length 214;  
Best Local Similarity 92.1%; Pred. No. 4.7e-78;  
Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCOASQDISNYLNWYQKPKAPKLLIYDASNLTGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASQDINNLYNWYQKPKAPKLLIYDASNLTGVPS 60

Qy 61 RFSGSGSGTDFTTINSLOPEDATYYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIFPP 120  
Db 61 RFSGSGSGTDYTLTISLSQPEDFATYYCOQGNLTLPPTFGQGTKEIKRTVAAPSVFIFPP 120

Qy 121 SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTLSLT 180  
Db 121 SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTLSLT 180

Qy 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214  
Db 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 14  
US-07-934-373C-25  
Sequence 25, Application US/07934373C  
Patent No. 5821337  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
TITLE OF INVENTION: Immunoglobulin Variants

ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/437,642B  
FILING DATE: 09-May-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 233 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-437-642B-25

Query Match 92.1%; Score 1027; DB 2; Length 233;  
Best Local Similarity 92.1%; Pred. No. 5.2e-78;  
Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGDRVTITCRASQDINSYLNWYQKPKKLLIYDASNLETGVP 60  
DB 20 DIQMTQSPSSLSASVGDRVTITCRASQDINSYLNWYQKPKKLLIYDASNLETGVP 79  
QY 61 RPSGSGGTDTFTTINSLOPEDIAFYCOEYNNLPYFSGQGTKEIKETVAAPSVEIIPP 120  
DB 80 RPSGSGGTDTFTTINSLOPEDIAFYCOEYNNLPYFSGQGTKEIKETVAAPSVEIIPP 139  
QY 121 SPEQLKSGTASVVCILNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTLT 180  
DB 140 SPEQLKSGTASVVCILNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTLT 199  
QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214  
DB 200 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 233

Search completed: December 17, 2005, 01:25:46  
Job time : 22.4 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2005, 01:14:05 ; Search time 70.6849 Seconds  
(without alignments)  
1264.988 Million cell updates/sec

Title: US-10-644-277-64  
Perfect score: 1115  
Sequence: 1 DIQMTQSPSSLSASVGDVRT.....EVTHQGLSPVTKSFNRGEC 214

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pap:  
2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pap:  
3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pap:  
4: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pap:  
5: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pap:  
6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1115	100.0	214	5	US-10-644-277-64
2	1060	95.1	238	6	US-11-031-485-48
3	1051	94.3	236	4	US-10-401-344-4
4	1045	93.7	502	4	US-10-679-820-88
5	1045	93.7	502	6	US-11-132-143-88
6	1043	93.5	236	6	US-11-131-648-20
7	1043	93.5	236	6	US-11-131-648-49
8	1037	93.0	667	5	US-10-764-428-25
9	1034	92.7	214	4	US-10-364-953-1
10	1034	92.7	237	3	US-09-056-1608-100
11	1034	92.7	237	4	US-10-020-786-10
12	1034	92.7	237	4	US-10-234-671-100
13	1034	92.7	237	5	US-10-697-995-8
14	1034	92.7	237	5	US-10-697-995-11
15	1034	92.7	237	5	US-10-974-591-100
16	1034	92.7	237	6	US-11-071-291-10
17	1034	92.7	260	4	US-10-264-049-2296
18	1034	92.7	491	4	US-10-011-125-2
19	1034	92.7	667	5	US-10-764-428-7
20	1034	92.7	667	5	US-10-764-428-13
21	1034	92.7	670	5	US-10-764-428-5
22	1034	92.7	670	5	US-10-764-428-9
23	1034	92.7	670	5	US-10-764-428-11
24	1034	92.7	670	5	US-10-764-428-27
25	1027	92.1	214	3	US-09-940-166A-2
26	1027	92.1	214	3	US-09-811-384-11
27	1027	92.1	214	4	US-10-404-286-11

28	1027	92.1	214	4	US-10-762-967-2	Sequence 2, Appli
29	1027	92.1	214	5	US-10-745-775-17	Sequence 17, Appli
30	1027	92.1	214	6	US-11-077-717-2	Sequence 2, Appli
31	1027	92.1	233	5	US-10-835-641-25	Sequence 25, Appli
32	1027	92.1	237	3	US-09-940-166A-6	Sequence 6, Appli
33	1027	92.1	237	4	US-10-227-694-1	Sequence 1, Appli
34	1027	92.1	237	4	US-10-762-967-6	Sequence 6, Appli
35	1027	92.1	237	5	US-10-754-212-2	Sequence 2, Appli
36	1027	92.1	237	6	US-11-077-717-10	Sequence 10, Appli
37	1027	92.1	245	3	US-09-797-941A-6	Sequence 6, Appli
38	1027	92.1	245	5	US-10-965-585-6	Sequence 6, Appli
39	1026	92.0	259	3	US-09-979-948C-4	Sequence 6, Appli
40	1026	92.0	259	3	US-09-979-948C-6	Sequence 6, Appli
41	1025	91.9	213	4	US-10-379-392-135	Sequence 135, App
42	1023	91.7	213	4	US-10-379-392-153	Sequence 153, App
43	1023	91.7	233	4	US-10-404-724-68	Sequence 68, Appli
44	1022	91.7	212	4	US-10-320-231A-77	Sequence 77, Appli
45	1022	91.7	212	5	US-10-867-506-77	Sequence 77, Appli

ALIGNMENTS

RESULT 1  
US-10-644-277-64  
; Sequence 64, Application US/10644277  
; Publication No. US20050058639A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudae, Jean M.  
; APPLICANT: Haak-Frendescho, Mary  
; APPLICANT: Foord, Orit  
; APPLICANT: Liang, Meina L.  
; APPLICANT: Ahluwalia, Kiran  
; APPLICANT: Bhakta, Sunil  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE  
; TITLE OF INVENTION: CHEMO-ATTRACTANT PROTEIN-1 (MCP-1) AND USES THEREOF  
; FILE REFERENCE: ABGENIX.091A  
; CURRENT APPLICATION NUMBER: US/10/644,277  
; CURRENT FILING DATE: 2003-08-19  
; PRIOR APPLICATION NUMBER: 60/404,802  
; PRIOR FILING DATE: 2002-08-19  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 64  
; LENGTH: 214  
; TYPE: PRT  
; ORGANISM: Homosapien  
US-10-644-277-64

Query Match 100.0%; Score 1115; DB 5; Length 214;  
Best Local Similarity 100.0%; Pred. No. 1.1e-57;  
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DIQMTQSPSSLSASVGDVRTITTCQASQDLSNVLNWTQKPGKAPKLLIYDASNLETGVPS	60
DB	1	DIQMTQSPSSLSASVGDVRTITTCQASQDLSNVLNWTQKPGKAPKLLIYDASNLETGVPS	60
QY	61	RFSGSGSGTDFTTINSLPEDIAITYCOEYNNLPVSFGGKTLEIKRTVAAPSVFIFPP	120
DB	61	RFSGSGSGTDFTTINSLPEDIAITYCOEYNNLPVSFGGKTLEIKRTVAAPSVFIFPP	120
QY	121	SDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT	180
DB	121	SDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT	180
QY	181	LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	214
DB	181	LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	214

RESULT 2  
US-11-031-485-48  
; Sequence 48, Application US/11031485



Publication No. US20050232917A1  
GENERAL INFORMATION:  
APPLICANT: MULLEN, NICHOLAS  
APPLICANT: MOLLOY, ELIZABETH  
APPLICANT: KELLERMANN, SIRID-AIMEE  
APPLICANT: GREEN, LARRY L.  
APPLICANT: HAAK-FRENDSCHO, MARY  
TITLE OF INVENTION: ANTIBODIES TO MADCAM  
FILE REFERENCE: ABX-PF6  
CURRENT APPLICATION NUMBER: US/11/031,485  
CURRENT FILING DATE: 2005-01-07  
PRIOR APPLICATION NUMBER: 60/535,490  
PRIOR FILING DATE: 2004-01-09  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: Patentin ver. 3.3  
SEQ ID NO 48  
LENGTH: 238  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-031-485-48

Query Match 95.1%; Score 1060; DB 6; Length 238;  
Best Local Similarity 95.8%; Pred. No. 1.9e-54;  
Matches 205; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTTTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60  
DB 25 DIQMTQSPSSLSASVGDRTTTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 84  
QY 61 RFGSGSGTDFTTINSLOPEDIAITYCYQEVNNLPYSGQGTKEIKRTVAAPSFIIPP 120  
DB 85 RFGSGSGTDFTTISSLOPEDIAITYSCOHSDNLNLTITGGQTRLEIKRTVAAPSFIIPP 144  
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSLSTLT 180  
DB 145 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSLSTLT 204  
QY 181 LSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 214  
DB 205 LSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 238

RESULT 3  
US-10-401-344-4  
Sequence 4, Application US/10401344  
Publication No. US20030194404A1  
GENERAL INFORMATION:  
APPLICANT: Schering Corporation and Abgenix, Inc.  
APPLICANT: Corvalan, Jose  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO INTERLEUKIN-5 AND METHODS AND COME  
FILE REFERENCE: LI01564WI  
CURRENT APPLICATION NUMBER: US/10/401,344  
CURRENT FILING DATE: 2003-03-27  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 4  
LENGTH: 236  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: Signal Peptide  
LOCATION: (1)..(22)  
OTHER INFORMATION:  
US-10-401-344-4

Query Match 94.3%; Score 1051; DB 4; Length 236;  
Best Local Similarity 94.4%; Pred. No. 6.3e-54;  
Matches 202; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTTTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60  
|||

DB 23 DIQMTQSPSSLSASVGDRTTTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 82  
QY 61 RFGSGSGTDFTTINSLOPEDIAITYCYQEVNNLPYSGQGTKEIKRTVAAPSFIIPP 120  
DB 83 RFGSGSGTDFTTISSLOPEDIAITYCYQEVNNLPYSGQGTKEIKRTVAAPSFIIPP 142  
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSLSTLT 180  
DB 143 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSLSTLT 202  
QY 181 LSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 214  
DB 203 LSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 236

RESULT 4  
US-10-679-620-88  
Sequence 88, Application US/10679620  
Publication No. US20040110930A1  
GENERAL INFORMATION:  
APPLICANT: Large Scale Biology  
APPLICANT: Reini, Stephen J.  
APPLICANT: Edwards, Patricia C.  
TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING  
FILE REFERENCE: 34150-004A  
CURRENT APPLICATION NUMBER: US/10/679,620  
CURRENT FILING DATE: 2003-10-03  
PRIOR APPLICATION NUMBER: 60/415,940  
PRIOR FILING DATE: 2002-10-03  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 88  
LENGTH: 502  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Hufab H2 , see Example 2  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (232)..(232)  
OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
US-10-679-620-88

Query Match 93.7%; Score 1045; DB 4; Length 502;  
Best Local Similarity 93.5%; Pred. No. 2.7e-53;  
Matches 200; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTTTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60  
DB 23 DIQMTQSPSSLSASVGDRTTTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 82  
QY 61 RFGSGSGTDFTTINSLOPEDIAITYCYQEVNNLPYSGQGTKEIKRTVAAPSFIIPP 120  
DB 83 RFGSGSGTDFTTISSLOPEDIAITYCYQEVNNLPYSGQGTKEIKRTVAAPSFIIPP 142  
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSLSTLT 180  
DB 143 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSLSTLT 202  
QY 181 LSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 214  
DB 203 LSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 236

RESULT 5  
US-11-132-143-88  
Sequence 88, Application US/11132143  
Publication No. US20050207977A1  
GENERAL INFORMATION:  
APPLICANT: Large Scale Biology  
APPLICANT: Reini, Stephen J.  
APPLICANT: Edwards, Patricia C.  
TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING

```

; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/11/132,143
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 88
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hufab H2 , see Example 2
; NAME/KEY: misc feature
; LOCATION: (232)..(232)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; US-11-132-143-88

Query Match          93.7%; Score 1045; DB 6; Length 502;
Best Local Similarity 93.5%; Pred. No. 2.7e-53;
Matches 200; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGPS 60
DB 23 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGPS 82

QY 61 RFGSGSGTDFTTINSLOPEDIATYYCOEYNNLPYSFGQGTKEIKRTVAAPSFIFFPP 120
DB 83 RFGSGSGTDFTTINSLOPEDIATYYCOQYDNLPTFGGTVKVEIKRTVAAPSFIFFPP 142

QY 121 SDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 180
DB 143 SDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 202

QY 181 LSKADYEKKVKYACEVTHQGLSSPVTKSFNRGEC 214
DB 203 LSKADYEKKVKYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 6
US-11-131-648-20
; Sequence 20, Application US/11/131648
; Publication No. US20050221400A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Jakobovits, Aya
; APPLICANT: Xiao-Chi, Jia
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Shao, Hui
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT BIND TO PSCA PROTEINS
; FILE REFERENCE: 51158-20088.20
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/616,381
; PRIOR FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: 60/617,881
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/621,310
; PRIOR FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: 60/633,077
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: 10/857,484
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/475,064
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-131-648-49

Query Match          93.5%; Score 1043; DB 6; Length 236;
Best Local Similarity 93.0%; Pred. No. 1.9e-53;
Matches 199; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGPS 60
DB 23 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGPS 82

QY 61 RFGSGSGTDFTTINSLOPEDIATYYCOEYNNLPYSFGQGTKEIKRTVAAPSFIFFPP 120
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 20
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-131-648-20

Query Match          93.5%; Score 1043; DB 6; Length 236;
Best Local Similarity 93.0%; Pred. No. 1.9e-53;
Matches 199; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGPS 60
DB 23 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGPS 82

QY 61 RFGSGSGTDFTTINSLOPEDIATYYCOEYNNLPYSFGQGTKEIKRTVAAPSFIFFPP 120
DB 83 RFGSGSGTDFTTINSLOPEDIATYYCCQYDNLPTFGGTVKVDIKRTVAAPSFIFFPP 142

QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 180
DB 143 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 202

QY 181 LSKADYEKKVKYACEVTHQGLSSPVTKSFNRGEC 214
DB 203 LSKADYEKKVKYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 7
US-11-131-648-49
; Sequence 49, Application US/11/131648
; Publication No. US20050221400A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Jakobovits, Aya
; APPLICANT: Xiao-Chi, Jia
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Shao, Hui
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT BIND TO PSCA PROTEINS
; FILE REFERENCE: 51158-20088.20
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/616,381
; PRIOR FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: 60/617,881
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/621,310
; PRIOR FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: 60/633,077
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: 10/857,484
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/475,064
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-131-648-49

Query Match          93.5%; Score 1043; DB 6; Length 236;
Best Local Similarity 93.0%; Pred. No. 1.9e-53;
Matches 199; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGPS 60
DB 23 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGPS 82

QY 61 RFGSGSGTDFTTINSLOPEDIATYYCOEYNNLPYSFGQGTKEIKRTVAAPSFIFFPP 120
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; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-056-160B-100

Query Match          92.7%; Score 1034; DB 3; Length 237;
Best Local Similarity 91.6%; Pred. No. 6.2e-53;
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLASASVGDRVTITCOASQDISNYLNWYQOKPGKAPKLLIYDASNLETGVPS 60
Db 24 DIQLTQSPSSLASASVGDRVTITCSASQDISNYLNWYQOKPGKAPKLLIYFTSSLHSGVPS 83
QY 61 RFGSGSGTDFTTINSIQPEDIATYYCQEVNNLPYSFGQGTKLEIKRTVAAPSVFIPPP 120
Db 84 RFGSGSGTDYTLTIISSLOPEDFATYYCQYSTVPWTFGQGTKEIKRTVAAPSVFIPPP 143
QY 121 SDQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLSTLT 180
Db 144 SDQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLSTLT 203
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 204 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 11
US-10-020-786-10
; Sequence 10, Application US/10020786
; Publication No. US20030073164A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Laura C.
; APPLICANT: Klimowski, Laura
; APPLICANT: Reilly, Dorothea
; APPLICANT: Yansura, Daniel G.
; TITLE OF INVENTION: PROXAROTICALLY PRODUCED ANTIBODIES AND USES THEREOF
; FILE REFERENCE: P1793K1
; CURRENT APPLICATION NUMBER: US/10/020,786
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/256,164
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 10
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: anti-VEGF light chain
US-10-020-786-10

Query Match          92.7%; Score 1034; DB 4; Length 237;
Best Local Similarity 91.6%; Pred. No. 6.2e-53;
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLASASVGDRVTITCOASQDISNYLNWYQOKPGKAPKLLIYDASNLETGVPS 60
Db 24 DIQLTQSPSSLASASVGDRVTITCSASQDISNYLNWYQOKPGKAPKLLIYFTSSLHSGVPS 83
QY 61 RFGSGSGTDFTTINSIQPEDIATYYCQEVNNLPYSFGQGTKLEIKRTVAAPSVFIPPP 120
Db 84 RFGSGSGTDFTLTIISSLOPEDFATYYCQYSTVPWTFGQGTKEIKRTVAAPSVFIPPP 143
QY 121 SDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLSTLT 180
Db 144 SDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLSTLT 203
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 204 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 12
US-10-234-671-100
; Sequence 100, Application US/10234671

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Search completed: December 17, 2005, 01:29:31  
Job time : 72.6849 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 17, 2005, 01:18:45 ; Search time 4.53939 Seconds  
(without alignments)  
317.590 Million cell updates/sec

Title: US-10-644-277-64

Perfect score: 1115  
Sequence: 1 DQMTQSPSSLSASVGRVT.....EVTHQGLSPVTKFNRGRC 214

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 51470 seqs, 6736768 residues

Total number of hits satisfying chosen parameters: 51470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA New:
- 1: /cgn2\_6/ptodata/1/pubpaa/US09 NEW PUB pep.\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/US06 NEW PUB pep.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US07 NEW PUB pep.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US08 NEW PUB pep.\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/PCT NEW PUB pep.\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/US10 NEW PUB pep.\*
  - 7: /cgn2\_6/ptodata/1/pubpaa/US11 NEW PUB pep.\*
  - 8: /cgn2\_6/ptodata/1/pubpaa/US60 NEW PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1027	92.1	214	7 US-11-025-712-11	Sequence 11, Appl
2	1010	90.6	236	7 US-11-144-248-48	Sequence 48, Appl
3	1006	90.2	218	7 US-11-084-554-11	Sequence 11, Appl
4	1003	90.0	218	6 US-10-923-327-12	Sequence 12, Appl
5	1003	90.0	218	6 US-10-923-327-17	Sequence 17, Appl
6	1002	89.9	236	7 US-11-144-248-52	Sequence 52, Appl
7	1001	89.8	218	6 US-10-923-327-8	Sequence 8, Appl
8	1001	89.8	218	6 US-10-923-327-10	Sequence 10, Appl
9	1001	89.8	363	7 US-11-000-463-335	Sequence 335, App
10	998	89.5	218	6 US-10-923-327-6	Sequence 6, Appl
11	997	89.4	367	7 US-11-000-463-899	Sequence 899, App
12	993	89.1	236	7 US-11-144-248-47	Sequence 47, Appl
13	989	88.7	214	7 US-11-094-625-9	Sequence 9, Appl
14	987	88.5	236	7 US-11-144-248-51	Sequence 51, Appl
15	985.5	88.4	213	7 US-11-120-338-13	Sequence 13, Appl
16	984.5	88.3	213	7 US-11-120-338-16	Sequence 16, Appl
17	957	85.8	237	7 US-11-054-669-109	Sequence 109, App
18	949	85.1	214	7 US-11-173-564-1	Sequence 1, Appl
19	932.5	83.6	384	7 US-11-000-463-804	Sequence 804, App
20	932.5	83.6	384	7 US-11-000-463-805	Sequence 805, App
21	932.5	83.6	384	7 US-11-000-463-806	Sequence 806, App
22	932.5	83.6	384	7 US-11-000-463-807	Sequence 807, App
23	919.5	82.5	213	7 US-11-172-320-4	Sequence 4, Appl
24	919.5	82.5	213	7 US-11-173-969-4	Sequence 4, Appl
25	909.5	81.6	213	7 US-11-173-969-8	Sequence 8, Appl

26	909.5	81.6	213	7 US-11-173-969-8	Sequence 8, Appl
27	895.5	80.3	213	7 US-11-174-186-42	Sequence 42, Appl
28	858.5	77.0	239	7 US-11-139-499-6	Sequence 6, Appl
29	622.5	55.8	307	7 US-11-000-463-332	Sequence 332, App
30	622.5	55.8	312	7 US-11-000-463-334	Sequence 334, App
31	592	53.1	136	7 US-11-144-248-2	Sequence 2, Appl
32	572.5	51.3	411	7 US-11-075-351-47	Sequence 47, Appl
33	569.5	51.1	374	7 US-11-075-351-42	Sequence 42, Appl
34	558	50.0	366	7 US-11-075-351-38	Sequence 38, Appl
35	554	49.7	110	7 US-11-024-251-27	Sequence 27, Appl
36	553	49.6	107	6 US-10-999-866-40	Sequence 40, Appl
37	553	49.6	107	7 US-11-025-712-5	Sequence 5, Appl
38	553	49.6	107	7 US-11-075-351-61	Sequence 61, Appl
39	553	49.6	107	7 US-11-061-821-40	Sequence 40, Appl
40	548	49.1	106	7 US-11-144-248-26	Sequence 26, Appl
41	548	49.1	106	7 US-11-024-251-29	Sequence 29, Appl
42	548	49.1	106	7 US-11-165-141-17	Sequence 17, Appl
43	498	44.7	108	7 US-11-120-338-3	Sequence 3, Appl
44	498	44.7	110	6 US-10-648-816-1	Sequence 1, Appl
45	495	44.4	110	6 US-10-648-816-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1  
US-11-025-712-11  
; Sequence 11, Application US/11025712  
; Publication No. US20050255108A1  
; GENERAL INFORMATION:  
; APPLICANT: Bednar, Martin M.  
; Thomas, G. Roger  
; Gross, Cordell E.  
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/11/025,712  
; FILING DATE: 28-Dec-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/10/404,286  
; FILING DATE: 31-Mar-2003  
; APPLICATION NUMBER: 09/811384  
; FILING DATE: 20-DEC-2000  
; APPLICATION NUMBER: 09/251652  
; FILING DATE: 17-FEB-2000  
; APPLICATION NUMBER: 08/788800  
; FILING DATE: 22-JAN-1997  
; APPLICATION NUMBER: 60/093038  
; FILING DATE: 23-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Evans, David W.  
; REGISTRATION NUMBER: NONE  
; REFERENCE/DOCKET NUMBER: P1729C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1739  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 214 amino acids  
; TYPE: Amino Acid



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;
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-11-025-712-11

Query Match      92.1%; Score 1027; DB 7; Length 214;
Best Local Similarity 92.1%; Pred. No. 2.1e-48;
Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLGTGVP 60
Db 1 DIQMTQSPSSLSASVGRVTITTCRASQDINNVLNNYQKPGKAPKLLIYTTSTLHSGVPS 60
QY 61 RSGSGSGDTFTTINSLOPEDIAITYCOEYNLPSYFCQGTKEIKRTVAAPSVFIIPP 120
Db 61 RFGSGSGDTFTLTSSLOPEFATYCCQGNLTPTFGGKVEIKRTVAAPSVFIIPP 120
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
Db 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
QY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
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RESULT 2
US-11-144-248-48
; Sequence 48, Application US/11144248
; Publication No. US2005024408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR FILING DATE: 2002-01-04
; PRIOR FILING DATE: 2002-01-04
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-48
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Query Match      90.6%; Score 1010; DB 7; Length 236;
Best Local Similarity 90.7%; Pred. No. 1.7e-47;
Matches 194; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLGTGVP 60
Db 23 DIQMTQSPSSLSASVGRVTITTCRASQGIKNDLWYQKPGKAPKRLIYAASLSQGVPS 82
QY 61 RSGSGSGDTFTTINSLOPEDIAITYCOEYNLPSYFCQGTKEIKRTVAAPSVFIIPP 120
Db 83 RFGSGSGDTFTLTSSLOPEFATYCCLOHNSPYTFGGKVEIKRTVAAPSVFIIPP 142
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
Db 143 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLT 202
QY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 203 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236
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```
RESULT 3
US-11-084-554-11
; Sequence 11, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korvet, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-11
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Query Match      90.2%; Score 1006; DB 7; Length 218;
Best Local Similarity 89.0%; Pred. No. 2.6e-47;
Matches 194; Conservative 11; Mismatches 9; Indels 4; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDI-----SNYLNWYQKPGKAPKLLIYDASNL 56
Db 1 DIQMTQSPSSLSASVGRVTITTCRASQSDVDGSDSYNNWYQKPGKAPKLLIYAASYLE 60
QY 57 GVPFRFSGSGSGDTFTTINSLOPEDIAITYCYQEYNNLPYSFGQGTKEIKRTVAAPSV 116
Db 61 GVPFRFSGSGSGDTFTLTSSLOPEFATYCYCQSHEDPYTFGGTKVEIKRTVAAPSV 120
QY 117 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 176
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
QY 177 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
```

```
RESULT 4
US-10-923-327-12
; Sequence 12, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; FILE REFERENCE: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 12
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: construct  
US-10-923-327-12

Query Match 90.0%; Score 1003; DB 6; Length 218;  
Best Local Similarity 89.0%; Pred. No. 3.8e-47;  
Matches 194; Conservative 11; Mismatches 9; Indels 4; Gaps 1;  
QY 1 DIQMTQSPSSLSASVGRVTITTCASQDI-----SNLYNNYQOKPGKAPKLLIYDASNLET 56  
DB 1 DIQMTQSPSSLSASVGRVTITTCASQDI-----SNLYNNYQOKPGKAPKLLIYDASNLET 60  
QY 57 GVPSSRFGSGSGGDTFTTINSLOPEDATYVCOYNNLPYSFGQGTKEIKRTVAAPSVP 116  
DB 61 GVPSSRFGSGSGGDTFTTINSLOPEDATYVCOYNNLPYSFGQGTKEIKRTVAAPSVP 120  
QY 117 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 176  
DB 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180  
QY 177 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214  
DB 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 5

US-10-923-327-17  
Sequence 17, Application US/10923327  
Publication No. US20050261208A1  
GENERAL INFORMATION:  
APPLICANT: ROBINSON, CYNTHIA B.  
APPLICANT: BALL, HOWARD A.  
TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR  
TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE  
TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE  
TITLE OF INVENTION: PULMONARY DISEASE  
FILE REFERENCE: 30775-723.501  
CURRENT APPLICATION NUMBER: US/10/923,327  
CURRENT FILING DATE: 2004-08-20  
PRIOR APPLICATION NUMBER: PCT/US04/25054  
PRIOR FILING DATE: 2004-07-30  
PRIOR APPLICATION NUMBER: 10/698,073  
PRIOR FILING DATE: 2003-10-29  
PRIOR APPLICATION NUMBER: 60/492,231  
PRIOR FILING DATE: 2003-07-31  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 17  
LENGTH: 218  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: construct  
US-10-923-327-17

Query Match 90.0%; Score 1003; DB 6; Length 218;  
Best Local Similarity 89.0%; Pred. No. 3.8e-47;  
Matches 194; Conservative 11; Mismatches 9; Indels 4; Gaps 1;  
QY 1 DIQMTQSPSSLSASVGRVTITTCASQDI-----SNLYNNYQOKPGKAPKLLIYDASNLET 56  
DB 1 DIQMTQSPSSLSASVGRVTITTCASQDI-----SNLYNNYQOKPGKAPKLLIYDASNLET 60  
QY 57 GVPSSRFGSGSGGDTFTTINSLOPEDATYVCOYNNLPYSFGQGTKEIKRTVAAPSVP 116  
DB 61 GVPSSRFGSGSGGDTFTTINSLOPEDATYVCOYNNLPYSFGQGTKEIKRTVAAPSVP 120  
QY 117 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 176  
DB 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180  
QY 177 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214

DB 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 6

US-11-144-248-52  
Sequence 52, Application US/11144248  
Publication No. US20050244408A1  
GENERAL INFORMATION:  
APPLICANT: Cohen, Bruce D.  
APPLICANT: Beebe, Jean  
APPLICANT: Miller, Penelope E.  
APPLICANT: Moyer, James D.  
APPLICANT: Corvalan, Jose R.  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
FILE REFERENCE: ABX-PF2  
CURRENT APPLICATION NUMBER: US/11/144,248  
CURRENT FILING DATE: 2005-06-02  
PRIOR APPLICATION NUMBER: US/10/038,591  
PRIOR FILING DATE: 2002-01-04  
PRIOR APPLICATION NUMBER: 60/259,927  
PRIOR FILING DATE: 2001-01-05  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 52  
LENGTH: 236  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-144-248-52

Query Match 89.9%; Score 1002; DB 7; Length 236;

Best Local Similarity 89.7%; Pred. No. 4.5e-47;  
Matches 192; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITTCASQDI-----SNLYNNYQOKPGKAPKLLIYDASNLETGVP 60  
DB 23 DIQMTQSPSSLSASVGRVTITTCASQDI-----SNLYNNYQOKPGKAPKLLIYDASNLETGVP 82  
QY 61 RFGSGSGGDTFTTINSLOPEDATYVCOYNNLPYSFGQGTKEIKRTVAAPSVP 120  
DB 83 RFGSGSGGDTFTTINSLOPEDATYVCOYNNLPYSFGQGTKEIKRTVAAPSVP 142  
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180  
DB 143 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 202  
QY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214  
DB 203 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 7

US-10-923-327-8  
Sequence 8, Application US/10923327  
Publication No. US20050261208A1  
GENERAL INFORMATION:  
APPLICANT: ROBINSON, CYNTHIA B.  
APPLICANT: BALL, HOWARD A.  
TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR  
TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE  
TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE  
TITLE OF INVENTION: PULMONARY DISEASE  
FILE REFERENCE: 30775-723.501  
CURRENT APPLICATION NUMBER: US/10/923,327  
CURRENT FILING DATE: 2004-08-20  
PRIOR APPLICATION NUMBER: PCT/US04/25054  
PRIOR FILING DATE: 2004-07-30  
PRIOR APPLICATION NUMBER: 10/698,073  
PRIOR FILING DATE: 2003-10-29  
PRIOR APPLICATION NUMBER: 60/492,231  
PRIOR FILING DATE: 2003-07-31  
NUMBER OF SEQ ID NOS: 19



Gap8 0;

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QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 60
Db 23 DIQMTQSPSSLSASVGDRTVITTCRASQIRNDLGMWYQKPGKAPKRLIYAASRLHRGVP 82
QY 61 RFGSGSGTDFTTINSLOPEDIAITYCOEYNNLPYSFGQGTGLEIKRTVAAPSFIIPP 120
Db 83 RFGSGSGTDFTTINSLOPEDIAITYCLOHNSYPCSFQGTGLEIKRTVAAPSFIIPP 142
QY 121 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 180
Db 143 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 202
QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214
Db 203 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 236
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```
RESULT 13
US-11-094-625-9
; Sequence 9, Application US/11094625
; Publication No. US20050260711A1
; GENERAL INFORMATION:
; APPLICANT: Datta, Deepshikha
; APPLICANT: Goddard, William A.
; APPLICANT: Tirrell, David
; APPLICANT: Peng, Joyce Yaochun
; TITLE OF INVENTION: MODULATING PH-SENSITIVE BINDING USING
; FILE OF INVENTION: NON-NATURAL AMINO ACIDS
; CURRENT APPLICATION NUMBER: CTCH-P01-031
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US/11/094,625
; PRIOR FILING DATE: 2005-03-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-094-625-9
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Query Match 88.7%; Score 989; DB 7; Length 214;
Best Local Similarity 89.3%; Pred. No. 2e-46;
Matches 191; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQDVTAVAWYQKPGKAPKLLIYASFLYSGVP 60
QY 61 RFGSGSGTDFTTINSLOPEDIAITYCOEYNNLPYSFGQGTGLEIKRTVAAPSFIIPP 120
Db 61 RFGSGSGTDFTTINSLOPEDIAITYCOOHTTPTTFQGTGKVEIKRTVAAPSFIIPP 120
QY 121 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 180
Db 121 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 180
QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214
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RESULT 14
US-11-144-248-51
; Sequence 51, Application US/11144248
; Publication No. US2005024408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
```

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; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PP2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 51
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-51
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Query Match 88.5%; Score 987; DB 7; Length 236;
Best Local Similarity 88.8%; Pred. No. 2.8e-46;
Matches 190; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 60
Db 23 DIQMTQSPSSLSASVGDRTVITTCRASQDIRDLGMWYQKPGKAPKRLIYAASRLQSGVP 82
QY 61 RFGSGSGTDFTTINSLOPEDIAITYCOEYNNLPYSFGQGTGLEIKRTVAAPSFIIPP 120
Db 83 RFGSGSGTDFTTINSLOPEDIAITYCLOHNTPTTFQGTGKVEIKRTVAAPSFIIPP 142
QY 121 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 180
Db 143 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 202
QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214
Db 203 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 236
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RESULT 15
US-11-120-338-13
; Sequence 13, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 13
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-13
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Query Match 88.4%; Score 985.5; DB 7; Length 213;
Best Local Similarity 89.3%; Pred. No. 3.1e-46;
Matches 191; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQSVS-YMHYQKPGKAPKPLIYAPSNLASGVP 59
QY 61 RFGSGSGTDFTTINSLOPEDIAITYCOEYNNLPYSFGQGTGLEIKRTVAAPSFIIPP 120
Db 60 RFGSGSGTDFTTINSLOPEDIAITYCQWNSFPPTTFQGTGKVEIKRTVAAPSFIIPP 119
QY 121 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 180
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Db 120 SDEQLKSGTASVVCLLNFFYPREAKVQWVDNALQSGNSQESVTEQDSKDSTYSLSSTLT 179  
Qy 181 LSKADYERKHVYACEVTHOGLSSPVTKSFNRGEC 214  
Db 180 LSKADYERKHVYACEVTHOGLSSPVTKSFNRGEC 213

Search completed: December 17, 2005, 01:29:50  
Job time : 5.53939 secs

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GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.  
 OM protein - protein search, using sw model  
 Run on: February 6, 2006, 14:23:38 ; Search time 251 Seconds  
 (without alignments)  
 44.974 Million cell updates/sec

Title: US-10-644-277-149\_COPY\_20\_35  
 Perfect score: 73

Sequence: 1 ISVQRLASYRRITSSK 16

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1000 summaries

Database : UniProt\_05.80.\*

1: uniprot\_eprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	100.0	99	1 CCL2_HUMAN	P13500 homo sapien
2	73	100.0	99	1 CCL2_MACFA	P61274 macaca fasc
3	73	100.0	99	1 CCL2_MACMU	P61275 macaca mula
4	73	100.0	99	1 CCL2_PONPY	Q5ra36 pongo pygma
5	73	100.0	99	2 Q6XVn5_MACNE	Q6xvn5 macaca neme
6	73	100.0	99	2 Q71ME7_MACMU	Q71me7 macaca mula
7	68	83.2	101	1 CCL2_CANFA	P52203 canis famil
8	64	87.7	74	1 MCPB_BOVIN	P80343 bos taurus
9	64	87.7	97	2 Q9TTS6_BOVIN	Q9ttt6 bos taurus
10	64	87.7	99	1 CCL2_PIG	P42831 sus scrofa
11	61	83.6	99	1 MCPA_BOVIN	P28291 bos taurus
12	60	82.2	100	1 CCL1_HORSE	Q9ttq4 equus cabal
13	59	80.8	99	1 CCL2_HORSE	Q9ttq3 equus cabal
14	57	78.1	97	2 Q9Z318_CAVPO	Q9z318 cavia porce
15	56	76.7	97	1 CCL11_HUMAN	P51671 homo sapien
16	56	76.7	97	2 Q619T4_HUMAN	Q619t4 homo sapien
17	56	76.7	125	1 CCL2_RABIT	P28292 oryctolagus
18	54	74.0	99	2 Q516F8_CANFA	Q516f8 canis famil
19	52	71.2	96	1 CCL11_CAVPO	P80325 cavia porce
20	52	71.2	104	1 CCL12_MOUSE	Q62401 mus musculu
21	52	71.2	104	2 Q5SVB4_MOUSE	Q5svb4 mus musculu
22	52	71.2	109	2 Q8T6F3_MACNE	Q8t6f3 macaca neme
23	51	69.9	81	2 Q8TTO2_HORSE	Q8ttt2 equus cabal
24	50	68.5	97	1 CCL11_MACMU	Q8mit7 macaca mula
25	50	68.5	97	2 Q8HXZ5_MACMU	Q8hxx5 macaca mula
26	50	68.5	106	2 Q9Z292_9RODE	Q9z292 cricetus
27	50	68.5	150	2 Q8CGM5_SIGHI	Q8cgm5 sigmodon hi
28	49	67.1	65	2 Q7TMS1_MOUSE	Q7tms1 mus musculu
29	49	67.1	99	2 Q5KSU7_CANFA	Q5ksu7 canis famil
30	49	67.1	148	1 CCL2_MOUSE	P10148 mus musculu
31	49	67.1	148	2 Q5SVU3_MOUSE	Q5svu3 mus musculu

32	48	65.8	99	2 Q8MKC8_HORSE	Q8mkc8 equus cabal
33	47	64.4	99	1 CCL7_HUMAN	P80098 homo sapien
34	47	64.4	99	2 Q569J6_HUMAN	Q569j6 homo sapien
35	47	64.4	109	2 Q7Z7Q8_HUMAN	Q7z7q8 homo sapien
36	46	63.0	44	2 Q9BG83_PONPY	Q9bg83 pongo pygma
37	46	63.0	99	2 Q865F4_MACNE	Q865f4 macaca neme
38	46	63.0	99	2 Q8HYQ0_MACMU	Q8hyq0 macaca mula
39	46	63.0	148	1 CCL2_RAT	P14844 rattus norv
40	46	63.0	148	2 Q549R5_RAT	Q549r5 rattus norv
41	45	61.6	97	1 CCL7_MOUSE	Q03366 mus musculu
42	45	61.6	97	2 Q5SVU0_MOUSE	Q5svu0 mus musculu
43	45	61.6	97	2 Q4PIY1_92ZZZ	Q4piy1 unidentified
44	44	60.3	99	1 CCL8_CANFA	Q68av9 canis famil
45	44	60.3	99	1 CCL8_HUMAN	P80075 homo sapien
46	44	60.3	253	2 Q621J4_CABER	Q621j4 caenorhabdi
47	44	60.3	271	2 Q5XPM8_ERWAM	Q5xpm8 erwinia amy
48	43	58.9	421	2 Q8D3D7_WIGBR	Q8d3d7 wigleswort
49	43	58.9	447	2 Q4Q1I5_LEIMA	Q4q1i5 leishmania
50	42	57.5	60	1 YRH1_AZOVI	Q44557 azotobacter
51	42	57.5	97	1 CCL7_RAT	Q9qxy8 rattus norv
52	42	57.5	298	2 Q9D3J9_MOUSE	Q9d3j9 mus musculu
53	42	57.5	301	2 Q9HAI6_HUMAN	Q9hai6 homo sapien
54	42	57.5	305	2 Q5CQI7_CRYPV	Q5cqi7 cryptospori
55	42	57.5	306	2 Q5CL59_CRYHO	Q5cl59 cryptospori
56	42	57.5	377	1 FLAE_VIBAN	Q56570 vibrio angu
57	42	57.5	399	2 Q8P9C4_XANCP	Q8p9c4 xanthomonas
58	42	57.5	401	2 Q4U0H3_XANCP	Q4uuh3 xanthomonas
59	42	57.5	436	2 Q41WF4_AZOVI	Q41wf4 azotobacter
60	42	57.5	526	2 Q707N2_HUMAN	Q707n2 homo sapien
61	42	57.5	625	2 Q7Z441_HUMAN	Q7z441 homo sapien
62	42	57.5	1477	2 Q6A8J4_PROAC	Q6a8j4 propionibac
63	41	56.2	75	2 Q5WEZ4_BACSK	Q5wez4 bacillus cl
64	41	56.2	120	1 CCL2_CAVPO	Q08782 cavia porce
65	41	56.2	339	1 ENG_C_PSEAE	Q9nul3 pseudomonas
66	41	56.2	422	2 Q5GZN6_XANOR	Q5gzn6 xanthomonas
67	41	56.2	550	2 Q9S4M6_ECOLI	Q9s4m6 escherichia
68	41	56.2	588	2 Q6L984_HUMAN	Q6l984 homo sapien
69	41	56.2	859	2 Q6L985_HUMAN	Q6l985 homo sapien
70	41	56.2	919	1 SNCAP_HUMAN	Q9y6h5 homo sapien
71	41	56.2	919	2 Q6L986_HUMAN	Q6l986 homo sapien
72	41	56.2	919	2 Q9HC59_HUMAN	Q9hc59 homo sapien
73	41	56.2	973	2 Q57XV4_9TRYP	Q57xv4 trypanosoma
74	41	56.2	1199	1 MFD_SVNY3	Q55750 synecocyst
75	40	54.8	191	2 Q8JPJ3_9HEPC	Q8jpj3 hepatitis c
76	40	54.8	327	2 Q8XMM6_LEGPN	Q8xmm6 legionella
77	40	54.8	337	2 Q6SGS9_9BACT	Q6sgs9 uncultured
78	40	54.8	361	2 Q8KMN0_LEGPN	Q8kmn0 legionella
79	40	54.8	399	2 Q8PL31_XANAC	Q8pl31 xanthomonas
80	40	54.8	440	2 Q5JCA4_9LILI	Q5jca4 monotagma p
81	40	54.8	451	2 Q5JCA3_9LILI	Q5jca3 monotagma s
82	40	54.8	475	2 Q48824_LEGPN	Q48824 legionella
83	40	54.8	475	2 Q7ATT9_LEGPN	Q7att9 legionella
84	40	54.8	475	2 Q8KID5_LEGLO	Q8kid5 legionella
85	40	54.8	475	2 Q8KMM8_LEGPN	Q8kmm8 legionella
86	40	54.8	475	2 Q5WX06_LEGPL	Q5wx06 legionella
87	40	54.8	475	2 Q5X5M6_LEGPA	Q5x5m6 legionella
88	40	54.8	475	2 Q5ZVVO_LEGPH	Q5zvv0 legionella
89	40	54.8	476	2 Q8KMM7_LEGPN	Q8kmm7 legionella
90	40	54.8	489	2 Q8KMR7_LEGBO	Q8kmr7 legionella
91	40	54.8	491	2 Q8KMM9_LEGPN	Q8kmm9 legionella
92	40	54.8	492	2 Q3FAE7_9BURK	Q3fae7 acidovorax
93	40	54.8	492	2 Q9FAE8_9BURK	Q9fae8 acidovorax
94	40	54.8	493	2 Q8KMN1_LEGPN	Q8kmn1 legionella
95	40	54.8	1132	2 Q5BFT4_EMENI	Q5bft4 aspergillus
96	40	54.8	1148	2 Q66A16_DICDI	Q66a16 dictyosteli
97	39.5	54.1	98	1 CCL13_CANFA	Q68y88 canis famil
98	39	53.4	62	2 Q95690_HUMAN	Q95690 homo sapien
99	39	53.4	118	2 Q5L0Y3_GEOKA	Q5l0y3 geobacillus
100	39	53.4	125	2 Q6MPQ1_BDEBA	Q6mpq1 bdellovibri
101	39	53.4	132	2 Q5L3T7_GEOKA	Q5l3t7 geobacillus
102	39	53.4	150	2 Q5ZNT9_9VIRU	Q5znt9 coeselia con
103	39	53.4	181	2 Q4UK19_RICPE	Q4uk19 rickettsia
104	39	53.4	329	2 Q7VHR6_HELHP	Q7vhr6 helicobacte



105	39	53.4	365	1	ENG C METMA	Q8ptz6 methanosarc	178	37	50.7	379	2	Q58FG3_VIBHA	Q58fg3 vibrio harv
106	39	53.4	377	1	FLAF_VIBPA	Q87081 vibrio para	179	37	50.7	399	2	Q842C5_ECOLI	Q842c5 escherichia
107	39	53.4	377	2	Q5E3K6_VIBF1	Q5e3n6 vibrio fisc	180	37	50.7	408	2	Q51PJ3_MAGGR	Q51pj3 magnaporth
108	39	53.4	377	2	Q8R4Q1_VIBF1	Q8r4q1 vibrio fisc	181	37	50.7	408	2	Q70LL6_ECOLI	Q70ll6 escherichia
109	39	53.4	377	2	Q8DB99_VIBVU	Q8db99 vibrio vuln	182	37	50.7	420	2	Q6VMU1_ECOLI	Q6vmu1 escherichia
110	39	53.4	377	2	Q7MIM3_VIBVU	Q7mim3 vibrio vuln	183	37	50.7	420	2	Q9L9M3_ECOLI	Q9l9m3 escherichia
111	39	53.4	398	1	YFHE_SCHPO	Q42851 schizosacch	184	37	50.7	420	2	Q842D5_ECOLI	Q842d5 escherichia
112	39	53.4	558	2	Q6AHD0_LEIFXX	Q6ahd0 leifsonia x	185	37	50.7	426	2	Q6VMV1_ECOLI	Q6vmv1 escherichia
113	39	53.4	765	2	Q4TLJ5_TETNG	Q4tlj5 tetradon n	186	37	50.7	426	2	Q6VMV4_ECOLI	Q6vmv4 escherichia
114	39	53.4	893	2	Q5X1G2_THEMA	Q5x1g2 thermotoga	187	37	50.7	426	2	Q9L9M1_ECOLI	Q9l9m1 escherichia
115	39	53.4	1020	2	Q5SL67_CRYNE	Q5sl67 cryptococcu	188	37	50.7	426	2	Q842B2_ECOLI	Q842b2 escherichia
116	39	53.4	1020	2	Q5KAB4_CRYNE	Q5kab4 cryptococcu	189	37	50.7	428	2	Q93ES3_ECOLI	Q93es3 escherichia
117	39	53.4	1652	2	Q5NAA4_ORYSA	Q5naa4 oryza sativ	190	37	50.7	428	2	Q842B8_ECOLI	Q842b8 escherichia
118	38	52.1	99	1	CCL8_PIG	P49873 sus scrofa	191	37	50.7	432	2	Q842B4_ECOLI	Q842b4 escherichia
119	38	52.1	125	2	Q5ANF7_CANAL	Q5anf7 candida alb	192	37	50.7	436	2	Q6VMV2_ECOLI	Q6vmv2 escherichia
120	38	52.1	178	2	Q89ZJ1_BACTN	Q89zj1 bacteroides	193	37	50.7	436	2	Q9S0T9_ECOLI	Q9s0t9 escherichia
121	38	52.1	216	2	Q5AS19_EMENI	Q5asl9 aspergillus	194	37	50.7	436	2	Q842A7_ECOLI	Q842a7 escherichia
122	38	52.1	241	2	Q6BQC9_DEBHA	Q6bcq9 debaryomyce	195	37	50.7	440	2	Q6VMT9_ECOLI	Q6vmt9 escherichia
123	38	52.1	242	2	Q9PF23_XYLFA	Q9pf23 xyella fas	196	37	50.7	442	2	Q9FZP0_ARATH	Q9fzp0 arabidopsis
124	38	52.1	244	2	Q87AK3_XYLFT	Q87ak3 xyella fas	197	37	50.7	443	2	Q842C0_ECOLI	Q842c0 escherichia
125	38	52.1	282	2	Q7NRA4_CHRVO	Q7nra4 chromobacte	198	37	50.7	447	2	Q6VMU8_ECOLI	Q6vmu8 escherichia
126	38	52.1	304	2	Q6EHX7_SHEON	Q6ehx7 shewanella	199	37	50.7	447	2	Q6VMV5_ECOLI	Q6vmv5 escherichia
127	38	52.1	306	2	Q5P1X4_AZOSE	Q5p1x4 azoarcus sp	200	37	50.7	447	2	Q842A8_ECOLI	Q842a8 escherichia
128	38	52.1	311	2	Q62942_RAT	Q62942 rattus norv	201	37	50.7	447	2	Q842B5_ECOLI	Q842b5 escherichia
129	38	52.1	402	2	Q4KCK5_PSEF5	Q4kck5 pseudomonas	202	37	50.7	460	2	Q72KY4_THET2	Q72ky4 thermus the
130	38	52.1	422	2	Q7QJG3_ANOGA	Q7qjg3 anopheles g	203	37	50.7	461	2	Q842C6_ECOLI	Q842c6 escherichia
131	38	52.1	430	2	Q5L5U8_CHLAB	Q5l5u8 chlamydophi	204	37	50.7	474	1	FLA_LEGMI	P53606 legionella
132	38	52.1	479	2	Q5Z080_PSEPU	Q5z080 pseudomonas	205	37	50.7	475	2	Q7T3Q3_BRARE	Q7t3q3 brachydanio
133	38	52.1	486	2	Q68384_PSEPU	Q68384 pseudomonas	206	37	50.7	497	1	FLIC_ECOLI	P04949 escherichia
134	38	52.1	505	2	Q8XPW2_RALSO	Q8xpw2 ralstonia s	207	37	50.7	501	2	Q9L9M0_ECOLI	Q9l9m0 escherichia
135	38	52.1	535	2	Q5L4M6_ORYSA	Q5l4m6 oryza sativ	208	37	50.7	508	2	Q9S4M1_ECOLI	Q9s4m1 escherichia
136	38	52.1	628	2	Q5LEB4_ENTHI	Q5led4 entamoeba h	209	37	50.7	517	2	Q9S4M0_ECOLI	Q9s4m0 escherichia
137	38	52.1	732	2	Q5OUU5_ENTHI	Q5ouu5 entamoeba h	210	37	50.7	521	2	Q9XCS3_ECOLI	Q9xcs3 escherichia
138	38	52.1	754	2	Q7F9F8_ORYSA	Q7f9f8 oryza sativ	211	37	50.7	521	2	Q9XCS4_ECOLI	Q9xcs4 escherichia
139	38	52.1	818	2	Q86XFP_HUMAN	Q86xpf homo sapien	212	37	50.7	523	2	Q93ES2_ECOLI	Q93es2 escherichia
140	38	52.1	857	2	Q6AJQ8_DESPS	Q6ajq8 desulfotale	213	37	50.7	545	2	Q842B7_ECOLI	Q842b7 escherichia
141	38	52.1	888	1	GOGA2_MOUSE	Q921m4 mus musculu	214	37	50.7	545	2	Q70LL8_ECOLI	Q70ll8 escherichia
142	38	52.1	890	2	Q7UWJ7_RHOBA	Q7uwj7 rhodopirell	215	37	50.7	548	2	Q842D7_ECOLI	Q842d7 escherichia
143	38	52.1	1022	2	Q5DTH1_MOUSE	Q5dth1 mus musculu	216	37	50.7	549	2	Q53969_SHIDY	Q53969 shigella dy
144	38	52.1	1187	2	Q7XN13_ORYSA	Q7xnl1 oryza sativ	217	37	50.7	550	1	FLIC_SHIFL	Q98860 shigella fl
145	38	52.1	1574	2	Q8GU62_ORYSA	Q8gu62 oryza sativ	218	37	50.7	550	2	Q842D3_ECOLI	Q842d3 escherichia
146	38	52.1	3320	2	Q6CFU1_YARLI	Q6cfl1 yarrowia li	219	37	50.7	550	2	Q9KJAO_ECOLI	Q9kja0 escherichia
147	37.5	51.4	146	1	LCCR_YERPE	P69959 yersinia pe	220	37	50.7	554	2	Q842D0_ECOLI	Q842d0 escherichia
148	37.5	51.4	146	1	LCCR_YERPE	P69960 yersinia ps	221	37	50.7	554	2	Q842B3_ECOLI	Q842b3 escherichia
149	37.5	51.4	146	1	LCCR_YERPS	P69919 tupatia glis	222	37	50.7	555	2	Q9R3X4_ECOLI	Q9r3x4 escherichia
150	37	50.7	73	2	Q5G9J9_TUGGB	Q5g9j9 bos taurus	223	37	50.7	555	2	Q842B9_ECOLI	Q842b9 escherichia
151	37	50.7	99	1	CCL8_BOVIN	Q99141 mus musculu	224	37	50.7	556	2	Q9S4M3_ECOLI	Q9s4m3 escherichia
152	37	50.7	147	2	Q8BN49_MOUSE	Q8bn49 mus musculu	225	37	50.7	557	2	Q6VMU0_ECOLI	Q6vmu0 escherichia
153	37	50.7	169	2	Q70518_MOUSE	Q70616 mus musculu	226	37	50.7	557	2	Q842C4_ECOLI	Q842c4 escherichia
154	37	50.7	171	2	Q70616_MOUSE	Q70616 mus musculu	227	37	50.7	557	2	Q842C4_ECOLI	Q842c4 escherichia
155	37	50.7	171	2	Q70619_MOUSE	Q70619 mus musculu	228	37	50.7	559	2	Q9S4M2_ECOLI	Q9s4m2 escherichia
156	37	50.7	178	2	Q52AY2_MAGGR	Q52ay2 magnaporth	229	37	50.7	560	2	Q9S4M5_ECOLI	Q9s4m5 escherichia
157	37	50.7	194	2	Q62061_CABEL	Q62061 caenorhabdi	230	37	50.7	560	2	Q842B6_ECOLI	Q842b6 escherichia
158	37	50.7	197	2	Q82Z13_ENTFA	Q82z13 enterococcu	231	37	50.7	561	2	Q842D2_ECOLI	Q842d2 escherichia
159	37	50.7	214	2	Q7YYU0_CRYPV	Q7yyu0 cryptospori	232	37	50.7	562	2	Q93ES1_ECOLI	Q93es1 escherichia
160	37	50.7	214	2	Q5CWM1_CRYPV	Q5cwm1 cryptospori	233	37	50.7	564	2	Q842A9_ECOLI	Q842a9 escherichia
161	37	50.7	214	2	Q5CF90_CRYHO	Q5cf90 cryptospori	234	37	50.7	564	2	Q9S0T3_ECOLI	Q9s0t3 escherichia
162	37	50.7	216	2	Q4J416_AZOVI	Q4j416 azotobacter	235	37	50.7	565	2	Q9S4M4_ECOLI	Q9s4m4 escherichia
163	37	50.7	274	2	Q66XA2_9BACT	Q66xa2 endosymbion	236	37	50.7	565	2	Q47226_ECOLI	Q47226 shigella bo
164	37	50.7	274	2	Q66XC2_9BACT	Q66xc2 endosymbion	237	37	50.7	568	2	Q53789_SHIBO	Q53789 shigella bo
165	37	50.7	281	2	Q32FD6_9GAMM	Q32fd6 endosymbion	238	37	50.7	568	2	Q9S0T5_ECOLI	Q9s0t5 escherichia
166	37	50.7	295	2	Q4KEW7_PSEF5	Q4kem7 pseudomonas	239	37	50.7	568	2	Q842B1_ECOLI	Q842b1 escherichia
167	37	50.7	305	2	Q6ATN3_RAT	Q6ayn3 rattus norv	240	37	50.7	570	2	Q9AL29_ECOLI	Q9al29 escherichia
168	37	50.7	348	2	Q5Z3D3_NOCFA	Q5z3d3 nocardia fa	241	37	50.7	570	2	Q9S0T4_ECOLI	Q9s0t4 escherichia
169	37	50.7	349	2	Q5QS23_ECOLI	Q5qs23 escherichia	242	37	50.7	570	2	Q842C1_ECOLI	Q842c1 escherichia
170	37	50.7	349	2	Q5QS23_ECOLI	Q5qs23 escherichia	243	37	50.7	572	2	Q842B0_ECOLI	Q842b0 escherichia
171	37	50.7	349	2	Q70UW9_ECOLI	Q70uw9 escherichia	244	37	50.7	573	2	Q4RQ66_TETNG	Q4rq66 tetraodon n
172	37	50.7	349	2	Q83XMS_ECOLI	Q83xms escherichia	245	37	50.7	576	2	Q842C8_ECOLI	Q842c8 escherichia
173	37	50.7	349	2	Q9S0U0_ECOLI	Q9s0u0 escherichia	246	37	50.7	579	1	YGT6_YEAST	P53099 saccharomyc
174	37	50.7	360	2	Q6BV22_DEBHA	Q6bv22 debaryomyce	247	37	50.7	579	2	Q874L4_SACPS	Q874l4 saccharomyc
175	37	50.7	374	2	Q9ZSH6_ARATH	Q9zsh6 arabidopsis	248	37	50.7	579	2	Q842C2_ECOLI	Q842c2 escherichia
176	37	50.7	378	1	FLAE_VIBCH	Q9kq60 vibrio chol	249	37	50.7	584	2	Q06352_ECOLI	Q06352 escherichia
177	37	50.7	379	1	FLAA_VIBCH	Q30858 vibrio chol	250	37	50.7				

251	37	50.7	585	2	P71246	escherichia	324	36	49.3	191	2	Q8BBL6	9HEPC	Q8BBL6	hepatitis c
252	37	50.7	585	2	Q9K2X8	escherichia	325	36	49.3	191	2	Q8BBL8	9HEPC	Q8BBL8	hepatitis c
253	37	50.7	585	2	Q9L736	escherichia	326	36	49.3	191	2	Q8BBL0	9HEPC	Q8BBL0	hepatitis c
254	37	50.7	585	2	Q9S0T8	escherichia	327	36	49.3	191	2	Q8BBL1	9HEPC	Q8BBL1	hepatitis c
255	37	50.7	585	2	Q7AD06	ECO57	328	36	49.3	191	2	Q8BBL2	9HEPC	Q8BBL2	hepatitis c
256	37	50.7	585	2	Q9K2Y6	escherichia	329	36	49.3	191	2	Q8BBL3	9HEPC	Q8BBL3	hepatitis c
257	37	50.7	585	2	Q7DB10	ECO57	330	36	49.3	191	2	Q8BBL5	9HEPC	Q8BBL5	hepatitis c
258	37	50.7	588	2	Q9S0N6	escherichia	331	36	49.3	191	2	Q8BBL7	9HEPC	Q8BBL7	hepatitis c
259	37	50.7	595	2	Q6G351	escherichia	332	36	49.3	191	2	Q8BBL8	9HEPC	Q8BBL8	hepatitis c
260	37	50.7	595	2	Q6G353	escherichia	333	36	49.3	191	2	Q8BBL9	9HEPC	Q8BBL9	hepatitis c
261	37	50.7	595	2	Q6VMU7	escherichia	334	36	49.3	191	2	Q8BBL0	9HEPC	Q8BBL0	hepatitis c
262	37	50.7	595	2	Q6VMV0	escherichia	335	36	49.3	191	2	Q8BBL1	9HEPC	Q8BBL1	hepatitis c
263	37	50.7	595	2	Q9S0T7	escherichia	336	36	49.3	191	2	Q8BBL3	9HEPC	Q8BBL3	hepatitis c
264	37	50.7	595	2	Q9S0U7	escherichia	337	36	49.3	191	2	Q8BBL4	9HEPC	Q8BBL4	hepatitis c
265	37	50.7	595	2	Q8FGM2	ECO16	338	36	49.3	191	2	Q8BBL6	9HEPC	Q8BBL6	hepatitis c
266	37	50.7	605	2	Q9S0T2	escherichia	339	36	49.3	191	2	Q8BBL7	9HEPC	Q8BBL7	hepatitis c
267	37	50.7	610	2	Q9T6U4	USEUD	340	36	49.3	191	2	Q8BBL8	9HEPC	Q8BBL8	hepatitis c
268	37	50.7	610	2	Q6VMU3	escherichia	341	36	49.3	191	2	Q8BBL9	9HEPC	Q8BBL9	hepatitis c
269	37	50.7	613	2	Q842C9	escherichia	342	36	49.3	191	2	Q8BBL0	9HEPC	Q8BBL0	hepatitis c
270	37	50.7	670	2	Q85825	escherichia	343	36	49.3	191	2	Q8BBL2	9HEPC	Q8BBL2	hepatitis c
271	37	50.7	681	2	Q7ZTU7	BRARE	344	36	49.3	191	2	Q8BBL3	9HEPC	Q8BBL3	hepatitis c
272	37	50.7	725	2	Q55M00	CRYNE	345	36	49.3	191	2	Q8BBL4	9HEPC	Q8BBL4	hepatitis c
273	37	50.7	725	2	Q5K8R8	CRYNE	346	36	49.3	191	2	Q8BBL5	9HEPC	Q8BBL5	hepatitis c
274	37	50.7	730	2	Q4UOL0	XANCP	347	36	49.3	191	2	Q8BBL6	9HEPC	Q8BBL6	hepatitis c
275	37	50.7	730	2	Q8PCU0	XANCP	348	36	49.3	191	2	Q8BBL7	9HEPC	Q8BBL7	hepatitis c
276	37	50.7	786	2	Q940Y3	ARATH	349	36	49.3	191	2	Q8BBL8	9HEPC	Q8BBL8	hepatitis c
277	37	50.7	786	2	Q67Y76	ARATH	350	36	49.3	191	2	Q8BBL9	9HEPC	Q8BBL9	hepatitis c
278	37	50.7	788	2	Q57XU7	TRYYP	351	36	49.3	191	2	Q8BBL0	9HEPC	Q8BBL0	hepatitis c
279	37	50.7	809	2	Q7QRF3	GIALA	352	36	49.3	191	2	Q8BBL1	9HEPC	Q8BBL1	hepatitis c
280	37	50.7	840	2	Q9X8B0	STRCO	353	36	49.3	191	2	Q8BBL3	9HEPC	Q8BBL3	hepatitis c
281	37	50.7	880	2	Q51VF6	MAGGR	354	36	49.3	191	2	Q8BBL4	9HEPC	Q8BBL4	hepatitis c
282	37	50.7	897	2	Q4HZ42	GIBZE	355	36	49.3	191	2	Q8BBL5	9HEPC	Q8BBL5	hepatitis c
283	37	50.7	1119	2	Q9LK04	ARATH	356	36	49.3	191	2	Q8BBL6	9HEPC	Q8BBL6	hepatitis c
284	37	50.7	1175	2	Q9ZPF3	ARATH	357	36	49.3	191	2	Q8BBL7	9HEPC	Q8BBL7	hepatitis c
285	37	50.7	1198	2	Q9C6N9	ARATH	358	36	49.3	191	2	Q8BBL8	9HEPC	Q8BBL8	hepatitis c
286	37	50.7	1265	2	Q5AAU3	CANAL	359	36	49.3	191	2	Q8BBL9	9HEPC	Q8BBL9	hepatitis c
287	37	50.7	1285	2	Q9ZR01	ARATH	360	36	49.3	191	2	Q8BBL0	9HEPC	Q8BBL0	hepatitis c
288	37	50.7	1305	2	Q9ZU21	ARATH	361	36	49.3	191	2	Q8BBL2	9HEPC	Q8BBL2	hepatitis c
289	37	50.7	1312	2	Q9M0W7	ARATH	362	36	49.3	191	2	Q8BBL3	9HEPC	Q8BBL3	hepatitis c
290	37	50.7	1314	2	Q9M194	ARATH	363	36	49.3	191	2	Q8BBL4	9HEPC	Q8BBL4	hepatitis c
291	37	50.7	1444	2	Q9LTG8	ARATH	364	36	49.3	191	2	Q8BBL5	9HEPC	Q8BBL5	hepatitis c
292	37	50.7	1444	2	Q9SFV0	ARATH	365	36	49.3	191	2	Q8BBL6	9HEPC	Q8BBL6	hepatitis c
293	37	50.7	1472	2	Q9SL11	ARATH	366	36	49.3	191	2	Q8BBL7	9HEPC	Q8BBL7	hepatitis c
294	37	50.7	1473	2	Q9SBT9	NEUCR	367	36	49.3	191	2	Q8BBL8	9HEPC	Q8BBL8	hepatitis c
295	37	50.7	1756	2	Q80975	ARATH	368	36	49.3	191	2	Q8BBL9	9HEPC	Q8BBL9	hepatitis c
296	37	50.7	1821	2	Q64E21	TENMO	369	36	49.3	217	1	ATL2K	ARATH	Q8BBL0	hepatitis c
297	36.5	50.0	261	2	Q9KW84	PSESP	370	36	49.3	223	1	GOS11	ARATH	Q8BBL1	hepatitis c
298	36	49.3	65	2	Q9ZTN3	PETHY	371	36	49.3	228	2	Q4WJB0	ASPFO	Q8BBL2	hepatitis c
299	36	49.3	74	2	Q5LD25	BACFN	372	36	49.3	252	2	Q832P5	ENTFA	Q8BBL3	hepatitis c
300	36	49.3	113	1	LCCI	LEUGE	373	36	49.3	266	2	Q5CPG2	CRYPV	Q8BBL4	hepatitis c
301	36	49.3	113	1	MESI	LEUME	374	36	49.3	269	1	CALB2	CHICK	Q8BBL5	hepatitis c
302	36	49.3	113	2	Q6LD90	LEUCA	375	36	49.3	290	2	Q23376	ARATH	Q8BBL6	hepatitis c
303	36	49.3	113	2	Q791W0	LEUME	376	36	49.3	295	2	Q4LYQ3	9BURK	Q8BBL7	hepatitis c
304	36	49.3	156	2	Q49945	SOLTU	377	36	49.3	326	2	Q9RBR1	9PROT	Q8BBL8	hepatitis c
305	36	49.3	158	2	Q8BBL5	9HEPC	378	36	49.3	326	2	Q8BBL6	9HEPC	Q8BBL9	hepatitis c
306	36	49.3	170	2	Q917Q1	9HEPC	379	36	49.3	331	2	Q6SYW1	PASMU	Q8BBL0	hepatitis c
307	36	49.3	170	2	Q917S1	9HEPC	380	36	49.3	331	2	Q9VT05	DROME	Q8BBL1	hepatitis c
308	36	49.3	171	2	Q8QR70	9HEPC	381	36	49.3	335	2	Q5JC79	9LILI	Q8BBL2	hepatitis c
309	36	49.3	180	2	Q5MMF5	9HEPC	382	36	49.3	336	2	Q8PP26	XANAC	Q8BBL3	hepatitis c
310	36	49.3	183	2	Q5L230	PICTO	383	36	49.3	343	2	Q7N812	PHOLI	Q8BBL4	hepatitis c
311	36	49.3	183	2	Q6A2A4	RABIN	384	36	49.3	345	2	Q83918	TREPA	Q8BBL5	hepatitis c
312	36	49.3	183	2	Q4QPF5	HAB18	385	36	49.3	386	2	Q5QLS4	ORYSA	Q8BBL6	hepatitis c
313	36	49.3	185	2	Q7VMK6	HABDU	386	36	49.3	387	2	Q86265	PSEAE	Q8BBL7	hepatitis c
314	36	49.3	186	2	Q91YB7	9HEPC	387	36	49.3	387	2	Q86266	PSEAE	Q8BBL8	hepatitis c
315	36	49.3	188	2	Q91YB7	PROMA	388	36	49.3	387	2	Q83TF1	PSEAE	Q8BBL9	hepatitis c
316	36	49.3	189	2	Q8BBK5	9HEPC	389	36	49.3	387	2	Q83WT8	PSEAE	Q8BBL0	hepatitis c
317	36	49.3	190	2	Q8BPH1	9HEPC	390	36	49.3	393	1	FLICA	PSEAE	Q8BBL1	hepatitis c
318	36	49.3	191	2	Q8BBK6	9HEPC	391	36	49.3	393	2	Q68383	PSEFL	Q8BBL2	hepatitis c
319	36	49.3	191	2	Q8BBK7	9HEPC	392	36	49.3	394	2	Q53ZR9	PSEAE	Q8BBL3	hepatitis c
320	36	49.3	191	2	Q8BBK9	9HEPC	393	36	49.3	394	2	Q53ZS1	PSEAE	Q8BBL4	hepatitis c
321	36	49.3	191	2	Q8BBL1	9HEPC	394	36	49.3	394	2	Q5TJ08	DICLA	Q8BBL5	hepatitis c
322	36	49.3	191	2	Q8BBL2	9HEPC	395	36	49.3	413	2	Q7NZQ6	CHRCV	Q8BBL6	hepatitis c
323	36	49.3	191	2	Q8BBL3	9HEPC	396	36	49.3	430	2	Q822X8	CHLCV	Q8BBL7	hepatitis c

397	Q3JC78_9LILI	2	439	36	49.3	36	Q3jc78 thalia geni	470	35	47.9	65	1	CSRA_SHEON	Q8eb83 shewanella
398	Q9HZC7_PSEAE	2	455	36	49.3	36	Q9hzc7 pseudomonas	471	35	47.9	83	2	Q8CQ6_PSEBK	Q8ccq6 pseudomonas
399	Q73UZ0_MYCPA	2	457	36	49.3	36	Q73uz0 mycobacteri	472	35	47.9	93	2	Q7WCE6_BORPA	Q7wce6 bordetella
400	MS3LI_HUMAN	1	521	36	49.3	36	Q8n5v2 homo sapien	473	35	47.9	94	2	Q8W2U6_ORYSA	Q8w2u6 oryza sativ
401	QSR6Y9_PONPY	1	521	36	49.3	36	Q8r6y9 pongo pygma	474	35	47.9	105	2	Q5F4U5_CABEL	Q5f4u5 caenorhabdi
402	LNT_CAUCR	330	530	36	49.3	36	Q8acl6 caulobacter	475	35	47.9	111	2	Q95X71_CABEL	Q95x71 caenorhabdi
403	Q8ZTW4_PYRAE	2	547	36	49.3	36	Q8ztw4 pyrobaculum	476	35	47.9	118	2	Q8G5F8_BIFLO	Q8g5f8 bifidobacte
404	Q9T6S7_AMBTC	2	547	36	49.3	36	Q9t6s7 amborella t	477	35	47.9	120	2	Q7RLY6_PLAYO	Q7rly6 plasmodium
405	Q8GHN2_PSERE	2	552	36	49.3	36	Q8ghn2 pseudomonas	478	35	47.9	137	2	Q9KGI4_BACHD	Q9kgi4 bacillus ha
406	Q4P982_USTMA	2	575	36	49.3	36	Q4p982 ustilago ma	479	35	47.9	141	2	Q5TRP2_ANOGA	Q5trp2 anopheles g
407	Q4W903_ASPFU	2	580	36	49.3	36	Q4w903 aspergillus	480	35	47.9	152	2	Q6CST0_KLULA	Q6cst0 kluyveromyc
408	Q4QD44_LEIMA	2	599	36	49.3	36	Q4qd44 leishmania	481	35	47.9	156	2	Q6N179_SHOAP	Q6n179 rhodospseudo
409	Q5WP98_BUBBU	2	606	36	49.3	36	Q5wp98 bubalus bub	482	35	47.9	158	2	Q936G6_STAAU	Q936g6 staphylococ
410	Q5ZQP4_BUBBU	2	606	36	49.3	36	Q5zqp4 bubalus bub	483	35	47.9	163	2	Q9SY46_ARATH	Q9sy46 arabidopsis
411	Q68GD0_BUBBU	2	606	36	49.3	36	Q68gd0 bubalus bub	484	35	47.9	171	2	Q98BB8_RHILO	Q98bb8 rhizobium l
412	Q6AKB8_DESPS	2	607	36	49.3	36	Q6akb8 desulfofale	485	35	47.9	176	2	Q9JJY2_MOUSE	Q9jjy2 mus musculu
413	Q5A8N5_CANAL	2	622	36	49.3	36	Q5a8n5 candida alb	486	35	47.9	177	2	Q56D00_DUNSA	Q56d00 dunaliella
414	Q61CN2_CAEBR	2	626	36	49.3	36	Q61cn2 caenorhabdi	487	35	47.9	178	2	Q7WSB3_RICJA	Q7wsb3 rickettsia
415	Q6CC93_YARLI	2	658	36	49.3	36	Q6cc93 yarrowia li	488	35	47.9	178	2	Q7WSB8_RICSI	Q7wsb8 rickettsia
416	Q9BE94_MACFA	2	705	36	49.3	36	Q9be94 macaca fasc	489	35	47.9	178	2	Q7WSB9_RICAK	Q7wsb9 rickettsia
417	Q9H961_HUMAN	2	762	36	49.3	36	Q9h961 homo sapien	490	35	47.9	178	2	Q7WSC0_RICCN	Q7wsc0 rickettsia
418	Q6BY95_DEBHA	2	779	36	49.3	36	Q6by95 debaryomyc	491	35	47.9	179	2	Q4RIS8_TETNG	Q4ris8 tetraodon n
419	Q6AMS9_DESPS	2	782	36	49.3	36	Q6ams9 desulfofale	492	35	47.9	197	2	Q8HY68_MACPL	Q8hy68 macropus fu
420	Q7W542_BORPA	2	786	36	49.3	36	Q7w542 bordetella	493	35	47.9	205	2	Q41200_LYCPE	Q41200 lycopersico
421	Q7WCM4_BORBR	2	786	36	49.3	36	Q7wcm4 bordetella	494	35	47.9	206	2	Q6Y7S0_9VIRU	Q6y7s0 staphylococ
422	Q7VW05_BORPE	2	789	36	49.3	36	Q7vw05 bordetella	495	35	47.9	209	2	Q4ZAI9_9CAUD	Q4zai9 bacterioph
423	SVFB_RICPR	815	815	36	49.3	36	Q7vw05 bordetella	496	35	47.9	209	1	HIS7_ANASP	Q50568 anabaena sp
424	SVFB_RICCN	818	818	36	49.3	36	Q8zdb4 rickettsia	497	35	47.9	216	2	Q6P079_PELPU	Q6p079 pelvicachro
425	Q7PBUI_RICSI	2	818	36	49.3	36	Q8zdb4 rickettsia	498	35	47.9	219	2	Q9VG22_DROME	Q9vg22 drosophila
426	Q4ULS4_RICPE	2	829	36	49.3	36	Q7pbui rickettsia	499	35	47.9	242	2	Q4K171_PSEFS	Q4k171 pseudomonas
427	Q6ZNL0_HUMAN	2	829	36	49.3	36	Q6znl0 homo sapien	500	35	47.9	242	2	Q4KG32_CHLTE	Q4kg32 chlorobium
428	Q9LE38_ARATH	2	844	36	49.3	36	Q9le38 arabidopsis	501	35	47.9	253	2	Q4SFC7_TETNG	Q4sfc7 tetraodon n
429	Q9Z50_FUGRU	2	851	36	49.3	36	Q9z50 fugu rubrip	502	35	47.9	256	2	Q9K7R4_BACHD	Q9k7r4 bacillus ha
430	Q953J1_9CAUD	2	874	36	49.3	36	Q953j1 mycobacteri	503	35	47.9	259	2	Q9AKF8_RICRI	Q9akf8 rickettsia
431	Q6CKC3_KLULA	2	931	36	49.3	36	Q6ckc3 kluyveromyc	504	35	47.9	259	2	Q9AKL2_RICMO	Q9akl2 rickettsia
432	Q4S4S0_BACFR	2	970	36	49.3	36	Q4s4s0 bacteroides	505	35	47.9	263	2	Q6DCX9_XENLA	Q6dcx9 xenopus lae
433	Q4K7J4_PSEFS	2	974	36	49.3	36	Q4k7j4 pseudomonas	506	35	47.9	268	2	Q8WI51_9MAGN	Q8wi51 ciassampelos
434	Q6R703_HUMAN	2	979	36	49.3	36	Q6r703 homo sapien	507	35	47.9	271	2	Q7MA67_WOLSU	Q7ma67 wolinnella s
435	Q4FSR5_9GAMM	2	1001	36	49.3	36	Q6r703 homo sapien	508	35	47.9	272	2	Q8ECA6_SHEON	Q8eca6 shewanella
436	MKL2_MOUSE	1	1080	36	49.3	36	Q6r703 homo sapien	509	35	47.9	273	2	Q8ECA5_SHEON	Q8eca5 shewanella
437	Q5DTX3_MOUSE	2	1080	36	49.3	36	P59759 mas musculu	510	35	47.9	275	2	Q82UA3_NITBU	Q82ua3 nitrosomona
438	Q5AQI2_EMENI	2	1086	36	49.3	36	Q5dtz3 mus musculu	511	35	47.9	281	2	Q9KDU4_BACHD	Q9kdj4 bacillus ha
439	Q9M180_ARATH	2	1113	36	49.3	36	Q5aqi2 aspergillus	512	35	47.9	282	2	Q7NRA5_CHRVO	Q7nra5 chromobacte
440	MFD_ECOLI	1	1148	36	49.3	36	Q9m180 arabidopsis	513	35	47.9	285	2	Q9SGQ2_ARATH	Q9sgq2 arabidopsis
441	Q7UCQ0_SHIFL	2	1148	36	49.3	36	P30958 escherichia fl	514	35	47.9	286	2	Q65PE5_BACLD	Q65pe5 bacillus li
442	Q7AP75_ECO57	2	1148	36	49.3	36	Q7ucw0 shigella fl	515	35	47.9	287	1	FLAA_LISIN	Q92dw3 listeria in
443	Q7QD9_SALCH	2	1148	36	49.3	36	Q7af75 escherichia	516	35	47.9	287	1	FLAA_LISMO	Q92dw3 listeria in
444	Q8ZQ01_SALTY	2	1148	36	49.3	36	Q57qd9 salmonella	517	35	47.9	287	1	Q5Y832_LISMO	Q5y832 listeria mo
445	Q8X8E7_ECO57	2	1148	36	49.3	36	Q8zq01 salmonella	518	35	47.9	287	2	Q5Y833_LISMO	Q5y833 listeria mo
446	Q83R81_SHIFL	2	1148	36	49.3	36	Q8x8e7 escherichia	519	35	47.9	287	2	Q5Y831_LISMO	Q5y831 listeria mo
447	Q7N3M4_PHOLL	2	1148	36	49.3	36	Q83r81 shigella fl	520	35	47.9	287	2	Q722K7_LISMF	Q722k7 listeria mo
448	Q8Z711_SALTI	2	1148	36	49.3	36	Q7n3a4 photorhabdu	521	35	47.9	287	2	Q81SF2_BACAN	Q81sf2 bacillus an
449	Q5PGK4_SALPA	2	1148	36	49.3	36	Q8z7i1 salmonella	522	35	47.9	300	2	Q916U1_PSEAE	Q916u1 pseudomonas
450	Q6D666_ERWCT	2	1149	36	49.3	36	Q5pgk4 salmonella	523	35	47.9	304	2	Q5DY03_ECOLI	Q5dy03 escherichia
451	KCNT1_CHICK	1	1201	36	49.3	36	Q6d666 erwinia car	524	35	47.9	311	2	Q7CPA3_SALCH	Q7cpa3 salmonella
452	Q7YSX3_9TRYP	2	1219	36	49.3	36	Q7qfv0 gallus gall	525	35	47.9	311	2	Q5PEP7_SALPA	Q5pep7 salmonella
453	KCNT1_HUMAN	2	1230	36	49.3	36	Q7ysx3 trypanosoma	526	35	47.9	311	2	Q8XGD5_SALTI	Q8xgd5 salmonella
454	Q7PRW4_ANOGA	2	1383	36	49.3	36	Q5juk3 homo sapien	527	35	47.9	311	2	Q8BUT1_MOUSE	Q8bvt1 m mus muscu
455	Q7PCB3_ARATH	2	1397	36	49.3	36	Q7prw4 anopheles g	528	35	47.9	318	2	Q7SAH9_NEUCR	Q7sah9 neurospora
456	Q7PCB9_ARATH	2	1400	36	49.3	36	Q7pcb3 arabidopsis	529	35	47.9	323	2	Q7SAH9_NEUCR	Q7sah9 neurospora
457	Q9ZUT8_ARATH	2	1413	36	49.3	36	Q7pcb9 arabidopsis	530	35	47.9	324	2	Q97397_PHACE	Q97397 phaeodon coc
458	Q7S0S1_NEUCR	2	1559	36	49.3	36	Q9zut8 arabidopsis	531	35	47.9	326	2	Q8VEB6_9HEPC	Q8veb6 hepatitis c
459	GUNA_CALSA	2	1742	36	49.3	36	Q7s0s1 neurospora	532	35	47.9	327	2	Q6CWR4_KLULA	Q6cwr4 kluyveromyc
460	Q4ST61_TETNG	2	2195	36	49.3	36	P22534 caldocellum	533	35	47.9	328	2	Q9AQV6_ORYSA	Q9aqv6 oryza sativ
461	Q4FY29_LEIMA	2	3155	36	49.3	36	Q4st61 tetraodon n	534	35	47.9	329	2	Q9AQV6_ORYSA	Q9aqv6 oryza sativ
462	Q4QEB7_LEIMA	2	3551	36	49.3	36	Q4fy29 leishmania	535	35	47.9	333	2	Q4KAL3_PSEFS	Q4kal3 pseudomonas
463	Q15142_HUMAN	2	3638	36	49.3	36	Q4qeb7 leishmania	536	35	47.9	334	2	Q9VA93_DROME	Q9va93 drosophila
464	PKD1_HUMAN	2	4303	36	49.3	36	Q15142 homo sapien	537	35	47.9	335	2	Q614N9_CAEER	Q614n9 caenorhabdi
465	COLL3_HUMAN	98	4303	36	49.3	36	P98161 homo sapien	538	35	47.9	338	1	G3P_TRIHA	P87197 trichoderma
466	Q6ICQ6_HUMAN	98	4303	36	49.3	36	Q99616 h small ind	539	35	47.9	341	2	Q71P88_9MAGN	Q71p88 coccullus la
467	Q9KKM5_VIBCH	319	4303	36	49.3	36	Q6icq6 homo sapien	540	35	47.9	343	1	ENG6_PSEBK	Q8adca pseudomonas
468	Q4IDL6_GIBZE	2	468	36	49.3	36	Q9kkm5 vibrio chol	541	35	47.9	343	2	Q5SU6_CANAL	Q5su6 candida alb
469	Q4P0H2_USTMA	2	649	36	49.3	36	Q4idl6 gibberella	542	35	47.9	343	2	Q4KJ82_PSEFS	Q4kj82 pseudomonas
							Q4p0h2 ustilago ma							

543	35	47.9	345	2	Q87UD4_PSESM	Q87ud4 pseudomonas
544	35	47.9	347	1	ADH_SULSO	P39462 sulfolobus
545	35	47.9	348	2	Q57WF4_9TRYP	Q57wf4 trypanosoma
546	35	47.9	353	1	EGSA_METKA	Q8tw08 methanopyru
547	35	47.9	353	2	Q5M6T9_CAMJE	Q5m6t9 campylobact
548	35	47.9	354	2	Q4V4B1_DROME	Q4v4b1 dirosophila
549	35	47.9	357	2	Q6ANG3_DRSPS	Q6ang3 desulfotale
550	35	47.9	367	1	FLIC2_PROMI	P42273 proteus mir
551	35	47.9	368	2	Q6CLV8_KLUOLA	Q6cli8 kluyveromyc
552	35	47.9	368	2	Q9TMG5_9ASPA	Q9tmg5 polyxena co
553	35	47.9	373	2	Q9TMF7_9ASPA	Q9tmf7 nolina recu
554	35	47.9	373	2	Q9TMG6_9ASPA	Q9tmg6 maesonida de
555	35	47.9	377	2	Q9TMG7_9ASPA	Q9tmg7 hvacinthus
556	35	47.9	378	2	Q9TMH1_POLOD	Q9tmh1 polygonatum
557	35	47.9	381	2	Q7S8S6_NEUCR	Q7s8s6 neurospora
558	35	47.9	402	2	Q8TIJ8_METAC	Q8tij8 methanosarc
559	35	47.9	403	2	Q6C3I5_YARLI	Q6c3i5 yarrowia li
560	35	47.9	407	2	Q8HW65_9WAGN	Q8hw65 cocculus or
561	35	47.9	408	1	CH60_RICFI	O3a198 rickettsia
562	35	47.9	423	2	Q4TGT1_TETNG	Q4tgt1 tetraodon n
563	35	47.9	425	2	Q7IMV8_9LILI	Q7imv8 heliconia s
564	35	47.9	425	2	Q7IMV9_HELRS	Q7imv9 heliconia r
565	35	47.9	427	2	Q5V142_HALMA	Q5v142 haloarcula
566	35	47.9	430	2	QANE91_9NICC	Qane91 arthrobacte
567	35	47.9	438	1	TOLC_VIBCH	Q8k2y1 vibrio chol
568	35	47.9	450	2	Q5X8Z7_LEGPA	Q5x8z7 legionella
569	35	47.9	454	2	Q6ITT7_SPISO	Q6itt7 episula sol
570	35	47.9	454	2	Q7N5K3_PHOLL	Q7n5k3 photorhabdu
571	35	47.9	455	2	Q6ITT6_SPISO	Q6itt6 episula sol
572	35	47.9	458	2	Q6AZI8_XENLA	Q6azi8 xenopus lae
573	35	47.9	463	1	DESM_CHICK	P02542 gallus gall
574	35	47.9	464	2	Q6IWI7_CABBR	Q6iwi7 caenorhabdi
575	35	47.9	466	2	Q7S7P9_ASHGO	Q7s7p9 ashbya goss
576	35	47.9	466	2	Q5RJQ2_RAT	Q5rjq2 rattus norv
577	35	47.9	468	1	CNRLA_FUGRU	Q8b894 fugu rubrip
578	35	47.9	468	1	DESM_CANFA	Q5xfn2 canis famil
579	35	47.9	468	1	DESM_MESAU	P02541 mesocricetu
580	35	47.9	468	1	DESM_MOUSE	P13001 mus muscucu
581	35	47.9	468	1	DESM_RAT	P48075 rattus norv
582	35	47.9	468	1	Q4ROX1_TETNG	Q4rox1 tetraodon n
583	35	47.9	469	1	DESM_BOVIN	O62654 bos taurus
584	35	47.9	469	1	DESM_HUMAN	P17661 homo sapien
585	35	47.9	469	2	Q54A94_MESAU	Q54a94 mesocricetu
586	35	47.9	469	2	Q6P725_RAT	Q6p725 rattus norv
587	35	47.9	470	1	DESM_PIG	P02540 sus scrofa
588	35	47.9	470	2	Q9H3I9_HUMAN	Q9h3i9 homo sapien
589	35	47.9	470	2	Q53S85_HUMAN	Q53sb5 homo sapien
590	35	47.9	470	2	Q549R7_HUMAN	Q549r7 homo sapien
591	35	47.9	470	2	Q549R8_HUMAN	Q549r8 homo sapien
592	35	47.9	470	2	Q549R9_HUMAN	Q549r9 homo sapien
593	35	47.9	470	2	Q80IM1_XENLA	Q80im1 xenopus lae
594	35	47.9	473	1	CISY_SCHPO	Q10306 schizosacch
595	35	47.9	473	2	Q9DDC8_LAMFL	Q9ddc8 lampetra fl
596	35	47.9	487	2	Q75HW3_ORYSA	Q75hw3 oryza sativ
597	35	47.9	488	2	Q8XSR9_RALSO	Q8xsr9 ralsconla s
598	35	47.9	489	2	Q977W6_METTE	Q977w6 methanosarc
599	35	47.9	491	2	Q6IFV0_RAT	Q6ifv0 rattus norv
600	35	47.9	499	2	Q8RP06_BACAM	Q8rpq6 bacillus am
601	35	47.9	500	2	Q6AU71_ORYSA	Q6au71 oryza sativ
602	35	47.9	502	2	Q5ZJG6_CHICK	Q5zjg6 gallus gall
603	35	47.9	504	2	Q7VRW4_CANFB	Q7vrw4 candidatus
604	35	47.9	505	2	Q82Y67_NITEPL	Q82y67 nitrosomona
605	35	47.9	506	2	Q5WUQ1_LEGPL	Q5wuq1 legionella
606	35	47.9	506	2	Q5X394_LEGPA	Q5x394 legionella
607	35	47.9	511	2	Q5YAS1_9POAL	Q5yas1 tillandsia
608	35	47.9	511	2	Q5YAS2_9POAL	Q5yas2 tillandsia
609	35	47.9	511	2	Q5YAS3_9POAL	Q5yas3 tillandsia
610	35	47.9	511	2	Q8HV05_9LILI	Q8hv05 heliconia i
611	35	47.9	517	2	Q5ZTG9_LEGPH	Q5ztg9 legionella
612	35	47.9	518	2	Q6LA16_9ASPA	Q6lal6 pleomele th
613	35	47.9	518	2	Q9TN83_9ASPA	Q9tn83 asparagus f
614	35	47.9	518	2	Q9TN84_9ASPA	Q9tn84 asparagus c
615	35	47.9	518	2	Q9TN85_9ASPA	Q9tn85 dracaena dr

Q9tn86	dracaena an
Q9cn98	ophiopogon
Q9tn87	ruscus acul
Q5tky9	beaucarnea
Q7jdn5	diaporopsis
Q9ghb6	polygonatum
Q8t3z6	diaporopsis
Q9chn7	peliosanth
Q9thl2	ophiopogon
Q9thl3	ophiopogon
Q9tn89	nolina recu
Q9tn91	peliosanth
Q9tn92	peliosanth
Q9cn93	ophiopogon
Q9tn94	ophiopogon
Q9tn95	ophiopogon
Q9tn96	ophiopogon
Q9tn97	ophiopogon
Q9tn99	ophiopogon
Q9tna0	liriope spi
Q9tna1	liriope pia
Q9tna2	liriope min
Q9tnb5	disporopsis
Q9tnb6	heteropolys
Q9cnb7	polygonatum
Q9cnb8	polygonatum
Q9cnb9	polygonatum
Q9tnc0	polygonatum
Q9tn90	peliosanth
Q9wv99	mus muscucu
Q6fnj1	candida gla
Q4twp3	leishmania
Q7p996	rickettsia
Q4umf2	rickettsia
Q8a2j6	bacteroides
Q92h04	rickettsia
Q89x76	bradyrhizob
Q83ye7	streptomyce
Q7mv80	porphyromon
Q83032	streptomyce
Q10i01	streptomyce
Q8h6i9	zea mays (m
Q7sdj1	neurospora
Q4qn06	leishmania
Q5grx2	wolbachia s
Q75cl7	ashbya goss
Q4kry9	tomato chlo
Q9ke00	bacillus ha
Q7xv75	oryza sativ
Q7fvc7	oryza sativ
Q5ipb6	magnaporthe
Q9sfw8	arabidopsis
Q3823	saccharomyc
Q4lhn8	burkholderi
Q4sp11	tetradodon n
Q4in90	gibberella
Q14186	schizosacch
Q61ly5	caenorhabdi
Q4wnl3	aspergillus
Q5lht6	bacteroides
Q4lyt8	bacteroides
Q4n733	theileria p
Q5lni1	magnaporthe
Q6bk70	debaromyce
Q5pge6	aspergillus
Q8lbr5	plasmodium
Q4q9r1	leishmania
Q4n216	theileria p
Q6amn5	desulfotale
Q4ubk4	theileria a
Q4peb1	ustilago ma
Q7s8g1	neurospora

Q9TN86_9ASPA	2	518	47.9	35	616
Q9TN98_9ASPA	2	518	47.9	35	617
Q9TN88_9ASPA	2	519	47.9	35	618
MATK_RUSAC	1	520	47.9	35	619
Q5TKY9_9ASPA	2	520	47.9	35	620
Q7JDN5_9ASPA	2	520	47.9	35	621
Q9GHB6_9ASPA	2	520	47.9	35	622
Q8T3Z6_9ASPA	2	520	47.9	35	623
Q9THK7_9ASPA	2	520	47.9	35	624
Q9THL2_9ASPA	2	520	47.9	35	625
Q9THL3_9ASPA	2	520	47.9	35	626
Q9TN89_9ASPA	2	520	47.9	35	627
Q9TN91_9ASPA	2	520	47.9	35	628
Q9TN92_9ASPA	2	520	47.9	35	629
Q9TN93_9ASPA	2	520	47.9	35	630
Q9TN94_9ASPA	2	520	47.9	35	631
Q9TN95_9ASPA	2	520	47.9	35	632
Q9TN96_9ASPA	2	520	47.9	35	633
Q9TN97_9ASPA	2	520	47.9	35	634
Q9TN99_9ASPA	2	520	47.9	35	635
Q9TNA0_9ASPA	2	520	47.9	35	636
Q9TNA1_LRPL	2	520	47.9	35	637
Q9TNA2_9ASPA	2	520	47.9	35	638
Q9TNB5_9ASPA	2	520	47.9	35	639
Q9TNB6_9ASPA	2	520	47.9	35	640
Q9TNB7_9ASPA	2	520	47.9	35	641
Q9TNB8_9ASPA	2	520	47.9	35	642
Q9TNB9_9ASPA	2	520	47.9	35	643
Q9TNCO_9ASPA	2	520	47.9	35	644
Q9TN90_9ASPA	2	522	47.9	35	645
M33L1_MOUSE	1	525	47.9	35	646
Q6FNU1_CANGA	2	528	47.9	35	647
Q4FWP3_LEIMA	2	533	47.9	35	648
Q7P996_RICSI	2	547	47.9	35	649
Q4UMF2_RICPTE	2	547	47.9	35	650
Q8A2J6_BACTN	2	547	47.9	35	651
CH60_RICCN	1	548	47.9	35	652
Q89X76_BRAJA	2	548	47.9	35	653
Q83YE7_STRHY	2	548	47.9	35	654
Q7MV80_FORGI	2	595	47.9	35	655
Q83032_STRCO	2	598	47.9	35	656
Q9L010_STRCO	2	599	47.9	35	657
Q8H6I9_WAIZE	2	639	47.9	35	658
Q7SDJ1_NEUCR	2	646	47.9	35	659
Q4QH06_LEIMA	2	653	47.9	35	660
Q5GRX2_WOLTR	2	654	47.9	35	661
Q75CL7_ASHGO	2	657	47.9	35	662
Q4KRY9_9CLOS	2	669	47.9	35	663
Q9KE00_BACHD	2	682	47.9	35	664
Q7XV75_ORYSA	2	693	47.9	35	665
Q9FVC7_ORYSA	2	736	47.9	35	666
Q51PB6_MAGGR	2	760	47.9	35	667
Q9SPW8_ARATH	2	808	47.9	35	668
YN35_YEAST	1	816	47.9	35	669
Q4LHN8_9BURK	2	820	47.9	35	670
Q4SP11_TETNG	2	828	47.9	35	671
Q4IN90_GIBZE	2	840	47.9	35	672
YDSB_SCHPO	1	846	47.9	35	673
Q61LY5_CAEBR	2	857	47.9	35	674
Q4WNL3_ASPFU	2	921	47.9	35	675
Q5LHT6_BACFN	2	982	47.9	35	676
Q4Y7T8_BACFR	2	982	47.9	35	677
Q4N733_THEPA	2	995	47.9	35	678
Q51LN11_MAGGR	2	1008	47.9	35	679
Q6BK70_DEBHA	2	1050	47.9	35	680
Q5BGE6_EMENI	2	1067	47.9	35	681
Q4IBR5_PLAF7	2	1106	47.9	35	682
Q4Q9R1_LEIMA	2	1118	47.9	35	683
Q4N216_THEPA	2	1123	47.9	35	684
Q6AMN5_DESPS	2	1128	47.9	35	685
Q4UBK4_THEAN	2	1130	47.9	35	686
Q4PEB1_USTMA	2	1173	47.9	35	687
Q7S8G1_NEUCR	2	1286	47.9	35	688

689	35	47.9	1346	2	Q7PU00	ANOQA	Q7puq0	anopheles g	762	34	46.6	93	2	Q7BY0	9HEPC	Q7by0	hepatitis c
690	35	47.9	1378	2	Q8G450	BIFLO	Q8g450	bifidobacte	763	34	46.6	93	2	Q7BY2	9HEPC	Q7by2	hepatitis c
691	35	47.9	1386	2	Q7FMW1	ORYSA	Q7fmw1	oryza sativ	764	34	46.6	93	2	Q7BY3	9HEPC	Q7by3	hepatitis c
692	35	47.9	1431	2	Q8A039	BACTIN	Q8a039	bacteroides	765	34	46.6	93	2	Q7BY4	9HEPC	Q7by4	hepatitis c
693	35	47.9	1474	2	Q5VMX7	ORYSA	Q5vmx7	oryza sativ	766	34	46.6	93	2	Q7BY5	9HEPC	Q7by5	hepatitis c
694	35	47.9	1487	2	Q5NGY2	ORYSA	Q5ngy2	oryza sativ	767	34	46.6	93	2	Q7BY6	9HEPC	Q7by6	hepatitis c
695	35	47.9	1490	2	Q9M1C7	ARATH	Q9m1c7	arabidopsis	768	34	46.6	93	2	Q7BY7	9HEPC	Q7by7	hepatitis c
696	35	47.9	2196	2	Q8ART37	TETUNG	Q8art37	tetradodon n	769	34	46.6	93	2	Q7BY8	9HEPC	Q7by8	hepatitis c
697	35	47.9	3124	2	Q6CQ11	KLULA	Q6cq11	kluyveromyc	770	34	46.6	93	2	Q7BY9	9HEPC	Q7by9	hepatitis c
698	34.5	47.3	431	2	Q26924	METH	Q26924	methanobact	771	34	46.6	93	2	Q7B20	9HEPC	Q7b20	hepatitis c
699	34.5	47.3	470	2	Q16776	CABEL	Q16776	caenorhabdi	772	34	46.6	93	2	Q7B21	9HEPC	Q7b21	hepatitis c
700	34	46.6	52	2	Q6Y229	ORYSA	Q6y229	oryza sativ	773	34	46.6	93	2	Q7B22	9HEPC	Q7b22	hepatitis c
701	34	46.6	52	2	Q8F062	LEPIN	Q8f062	leptosira	774	34	46.6	93	2	Q7B23	9HEPC	Q7b23	hepatitis c
702	34	46.6	57	2	Q6FA86	ACIAD	Q6fa86	acinobact	775	34	46.6	93	2	Q7B24	9HEPC	Q7b24	hepatitis c
703	34	46.6	59	2	Q88M29	PSEPK	Q88m29	pseudomonas	776	34	46.6	93	2	Q7B25	9HEPC	Q7b25	hepatitis c
704	34	46.6	59	2	Q8V5T5	NUCL	Q8v5t5	heilicoverpa	777	34	46.6	93	2	Q7B26	9HEPC	Q7b26	hepatitis c
705	34	46.6	68	2	Q822E1	SALTI	Q822e1	salmonella	778	34	46.6	93	2	Q7B28	9HEPC	Q7b28	hepatitis c
706	34	46.6	69	2	Q57IR4	SALCH	Q57ir4	salmonella	779	34	46.6	93	2	Q7B29	9HEPC	Q7b29	hepatitis c
707	34	46.6	69	2	Q5PLR2	SALPA	Q5plr2	salmonella	780	34	46.6	93	2	Q7C10	9HEPC	Q7c10	hepatitis c
708	34	46.6	69	2	Q8ZL66	SALTY	Q8z166	salmonella	781	34	46.6	93	2	Q7C11	9HEPC	Q7c11	hepatitis c
709	34	46.6	70	2	Q88D99	RHILO	Q88d99	rhizobium l	782	34	46.6	93	2	Q7C12	9HEPC	Q7c12	hepatitis c
710	34	46.6	83	2	Q7VTP5	BORPE	Q7vtp5	borderetella	783	34	46.6	93	2	Q7C13	9HEPC	Q7c13	hepatitis c
711	34	46.6	83	2	Q7W155	BORPA	Q7w155	borderetella	784	34	46.6	93	2	Q7C14	9HEPC	Q7c14	hepatitis c
712	34	46.6	83	2	Q7WNU5	BORBR	Q7wnu5	borderetella	785	34	46.6	93	2	Q7C15	9HEPC	Q7c15	hepatitis c
713	34	46.6	90	2	Q6FVY8	CANGA	Q6fvv8	candida gla	786	34	46.6	93	2	Q7C16	9HEPC	Q7c16	hepatitis c
714	34	46.6	93	2	Q95334	HUMAN	Q95334	homo sapien	787	34	46.6	93	2	Q7C17	9HEPC	Q7c17	hepatitis c
715	34	46.6	93	2	Q7TBR3	9HEPC	Q7tbp3	hepatitis c	788	34	46.6	93	2	Q7C18	9HEPC	Q7c18	hepatitis c
716	34	46.6	93	2	Q7TBP4	9HEPC	Q7tbp4	hepatitis c	789	34	46.6	93	2	Q7C19	9HEPC	Q7c19	hepatitis c
717	34	46.6	93	2	Q7TBP5	9HEPC	Q7tbp5	hepatitis c	790	34	46.6	93	2	Q7C20	9HEPC	Q7c20	hepatitis c
718	34	46.6	93	2	Q7TBP6	9HEPC	Q7tbp6	hepatitis c	791	34	46.6	93	2	Q7C21	9HEPC	Q7c21	hepatitis c
719	34	46.6	93	2	Q7TBP7	9HEPC	Q7tbp7	hepatitis c	792	34	46.6	93	2	Q7C23	9HEPC	Q7c23	hepatitis c
720	34	46.6	93	2	Q7TBP8	9HEPC	Q7tbp8	hepatitis c	793	34	46.6	93	2	Q7C24	9HEPC	Q7c24	hepatitis c
721	34	46.6	93	2	Q7TBP9	9HEPC	Q7tbp9	hepatitis c	794	34	46.6	93	2	Q7C27	9HEPC	Q7c27	hepatitis c
722	34	46.6	93	2	Q7TBO0	9HEPC	Q7tbo0	hepatitis c	795	34	46.6	93	2	Q7C28	9HEPC	Q7c28	hepatitis c
723	34	46.6	93	2	Q7TBO6	9HEPC	Q7tbo6	hepatitis c	796	34	46.6	93	2	Q7C35	9HEPC	Q7c35	hepatitis c
724	34	46.6	93	2	Q7TBO8	9HEPC	Q7tbo8	hepatitis c	797	34	46.6	93	2	Q7C36	9HEPC	Q7c36	hepatitis c
725	34	46.6	93	2	Q7TBR1	9HEPC	Q7tbr1	hepatitis c	798	34	46.6	93	2	Q7C37	9HEPC	Q7c37	hepatitis c
726	34	46.6	93	2	Q7TBR2	9HEPC	Q7tbr2	hepatitis c	799	34	46.6	93	2	Q7C38	9HEPC	Q7c38	hepatitis c
727	34	46.6	93	2	Q7TBR3	9HEPC	Q7tbr3	hepatitis c	800	34	46.6	93	2	Q7C39	9HEPC	Q7c39	hepatitis c
728	34	46.6	93	2	Q7TBR4	9HEPC	Q7tbr4	hepatitis c	801	34	46.6	93	2	Q7C40	9HEPC	Q7c40	hepatitis c
729	34	46.6	93	2	Q7TBR5	9HEPC	Q7tbr5	hepatitis c	802	34	46.6	93	2	Q7C42	9HEPC	Q7c42	hepatitis c
730	34	46.6	93	2	Q7TBR6	9HEPC	Q7tbr6	hepatitis c	803	34	46.6	93	2	Q7C43	9HEPC	Q7c43	hepatitis c
731	34	46.6	93	2	Q7TBR7	9HEPC	Q7tbr7	hepatitis c	804	34	46.6	93	2	Q7C45	9HEPC	Q7c45	hepatitis c
732	34	46.6	93	2	Q7TBR8	9HEPC	Q7tbr8	hepatitis c	805	34	46.6	93	2	Q7C46	9HEPC	Q7c46	hepatitis c
733	34	46.6	93	2	Q7TBR9	9HEPC	Q7tbr9	hepatitis c	806	34	46.6	93	2	Q7C47	9HEPC	Q7c47	hepatitis c
734	34	46.6	93	2	Q7TBS0	9HEPC	Q7tbs0	hepatitis c	807	34	46.6	93	2	Q7C48	9HEPC	Q7c48	hepatitis c
735	34	46.6	93	2	Q7TBS1	9HEPC	Q7tbs1	hepatitis c	808	34	46.6	93	2	Q7C49	9HEPC	Q7c49	hepatitis c
736	34	46.6	93	2	Q7TBS2	9HEPC	Q7tbs2	hepatitis c	809	34	46.6	93	2	Q7C50	9HEPC	Q7c50	hepatitis c
737	34	46.6	93	2	Q7TBS9	9HEPC	Q7tbs9	hepatitis c	810	34	46.6	93	2	Q7C51	9HEPC	Q7c51	hepatitis c
738	34	46.6	93	2	Q7TBV0	9HEPC	Q7tbv0	hepatitis c	811	34	46.6	93	2	Q7C52	9HEPC	Q7c52	hepatitis c
739	34	46.6	93	2	Q7TBV1	9HEPC	Q7tbv1	hepatitis c	812	34	46.6	93	2	Q7C53	9HEPC	Q7c53	hepatitis c
740	34	46.6	93	2	Q7TBV2	9HEPC	Q7tbv2	hepatitis c	813	34	46.6	93	2	Q7C54	9HEPC	Q7c54	hepatitis c
741	34	46.6	93	2	Q7TBV8	9HEPC	Q7tbv8	hepatitis c	814	34	46.6	93	2	Q7C55	9HEPC	Q7c55	hepatitis c
742	34	46.6	93	2	Q7TBW0	9HEPC	Q7tbw0	hepatitis c	815	34	46.6	93	2	Q7C56	9HEPC	Q7c56	hepatitis c
743	34	46.6	93	2	Q7TBW1	9HEPC	Q7tbw1	hepatitis c	816	34	46.6	93	2	Q7C57	9HEPC	Q7c57	hepatitis c
744	34	46.6	93	2	Q7TBW2	9HEPC	Q7tbw2	hepatitis c	817	34	46.6	93	2	Q7C58	9HEPC	Q7c58	hepatitis c
745	34	46.6	93	2	Q7TBW3	9HEPC	Q7tbw3	hepatitis c	818	34	46.6	93	2	Q7C59	9HEPC	Q7c59	hepatitis c
746	34	46.6	93	2	Q7TBW4	9HEPC	Q7tbw4	hepatitis c	819	34	46.6	93	2	Q7C60	9HEPC	Q7c60	hepatitis c
747	34	46.6	93	2	Q7TBW5	9HEPC	Q7tbw5	hepatitis c	820	34	46.6	93	2	Q7C61	9HEPC	Q7c61	hepatitis c
748	34	46.6	93	2	Q7TBW6	9HEPC	Q7tbw6	hepatitis c	821	34	46.6	93	2	Q7C62	9HEPC	Q7c62	hepatitis c
749	34	46.6	93	2	Q7TBW7	9HEPC	Q7tbw7	hepatitis c	822	34	46.6	93	2	Q7C63	9HEPC	Q7c63	hepatitis c
750	34	46.6	93	2	Q7TBW8	9HEPC	Q7tbw8	hepatitis c	823	34	46.6	93	2	Q7C64	9HEPC	Q7c64	hepatitis c
751	34	46.6	93	2	Q7TBW9	9HEPC	Q7tbw9	hepatitis c	824	34	46.6	93	2	Q7C65	9HEPC	Q7c65	hepatitis c
752	34	46.6	93	2	Q7TBX0	9HEPC	Q7tbx0	hepatitis c	825	34	46.6	93	2	Q7C66	9HEPC	Q7c66	hepatitis c
753	34	46.6	93	2	Q7TBX1	9HEPC	Q7tbx1	hepatitis c	826	34	46.6	93	2	Q7C67	9HEPC	Q7c67	hepatitis c
754	34	46.6	93	2	Q7TBX2	9HEPC	Q7tbx2	hepatitis c	827	34	46.6	93	2	Q7C68	9HEPC	Q7c68	hepatitis c
755	34	46.6	93	2	Q7TBX3	9HEPC	Q7tbx3	hepatitis c	828	34	46.6	93	2	Q7C69	9HEPC	Q7c69	hepatitis c
756	34	46.6	93	2	Q7TBX4	9HEPC	Q7tbx4	hepatitis c	829	34	46.6	93	2	Q7C70	9HEPC	Q7c70	hepatitis c
757	34	46.6	93	2	Q7TBX5	9HEPC	Q7tbx5	hepatitis c	830	34	46.6	93	2	Q7C71	9HEPC	Q7c71	hepatitis c
758	34	46.6	93	2	Q7TBX6	9HEPC	Q7tbx6	hepatitis c	831	34	46.6	93	2	Q7C72	9HEPC	Q7c72	hepatitis c
759	34	46.6	93	2	Q7TBX7	9HEPC	Q7tbx7	hepatitis c	832	34	46.6	93	2	Q7C73	9HEPC	Q7c73	hepatitis c
760	34	46.6	93	2	Q7TBX8	9HEPC	Q7tbx8	hepatitis c	833	34	46.6	93	2	Q7C78	9HEPC	Q7c78	hepatitis c
761	34	46.6	93	2	Q7TBX9	9HEPC	Q7tbx9	hepatitis c	834	34	46.6	93	2				





981 34 46.6 130 2 Q91ZN9\_9HEPC Q91zn9 hepatitis c  
 982 34 46.6 130 2 Q91ZP0\_9HEPC Q91zp0 hepatitis c  
 983 34 46.6 130 2 Q91ZP1\_9HEPC Q91zp1 hepatitis c  
 984 34 46.6 130 2 Q91ZP2\_9HEPC Q91zp2 hepatitis c  
 985 34 46.6 130 2 Q91ZP3\_9HEPC Q91zp3 hepatitis c  
 986 34 46.6 130 2 Q91ZP4\_9HEPC Q91zp4 hepatitis c  
 987 34 46.6 130 2 Q91ZP5\_9HEPC Q91zp5 hepatitis c  
 988 34 46.6 130 2 Q91ZQ1\_9HEPC Q91zq1 hepatitis c  
 989 34 46.6 130 2 Q91ZQ2\_9HEPC Q91zq2 hepatitis c  
 990 34 46.6 130 2 Q91ZQ3\_9HEPC Q91zq3 hepatitis c  
 991 34 46.6 130 2 Q91ZQ4\_9HEPC Q91zq4 hepatitis c  
 992 34 46.6 130 2 Q91ZQ5\_9HEPC Q91zq5 hepatitis c  
 993 34 46.6 130 2 Q91ZQ6\_9HEPC Q91zq6 hepatitis c  
 994 34 46.6 130 2 Q66M93\_9HEPC Q66m93 hepatitis c  
 995 34 46.6 132 1 Z1AR\_SYNY3 Q55940 synchocyst  
 996 34 46.6 135 2 Q68190\_9HEPC Q68190 hepatitis c  
 997 34 46.6 135 2 Q68196\_9HEPC Q68196 hepatitis c  
 998 34 46.6 136 2 Q66MA9\_9HEPC Q66ma9 hepatitis c  
 999 34 46.6 137 2 Q66MA8\_9HEPC Q66ma8 hepatitis c  
 1000 34 46.6 137 2 Q911B9\_9HEPC Q911b9 hepatitis c

## ALIGNMENTS

## RESULT 1

CCL2\_HUMAN  
 ID\_CCL2\_HUMAN STANDARD; PRT; 99 AA.  
 AC P13500; Q9UFP3;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic  
 protein 1) (MCP-1) (Monocyte chemoattractant protein 1) (Monocyte  
 chemotactic and activating factor) (MCAF) (Monocyte secretory protein  
 JE) (HC11).  
 DE Name=CCL2; Synonyms=MCP1, SCYA2;  
 GN Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP MEDLINE=89165862; PubMed=2923622;  
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 RX MEDLINE=90097880; PubMed=2513477;  
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 RX MEDLINE=89153605; PubMed=2465924; DOI=10.1016/0014-5793(89)80590-3;  
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 RX MEDLINE=90290466; PubMed=2357211;  
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 RA Yoshimura T., Leonard E.J.;  
 RT "Human monocyte chemoattractant protein-1 (MCP-1).";  
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 RT "Assignment of the human small inducible cytokine A2 gene, SCYA2  
 (encoding JE or MCP-1), to 17q11.2-12: evolutionary relatedness of  
 cytokines clustered at the same locus.";  
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 RP NUCLEOTIDE SEQUENCE.  
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 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,  
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 RT "SeattleSNPs, NHLBI HL66682 program for genomic applications, UW-  
 FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [12]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC TISSUE=Pancreas;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
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RX MEDLINE=91312872; PubMed=1857712;  
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RT "Structural characterization of a monomeric chemokine: monocyte  
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CC -1- FUNCTION: Chemotactic factor that attracts monocytes and basophils  
CC but not neutrophils or eosinophils. Augments monocyte anti-tumor  
CC activity. Has been implicated in the pathogenesis of diseases  
CC characterized by monocyte infiltrates, like psoriasis, rheumatoid  
CC arthritis or atherosclerosis. May be involved in the recruitment  
CC of monocytes into the arterial wall during the disease process of  
CC atherosclerosis. Binds to CCR2 and CCR4.

CC -1- SUBUNIT: Monomer or homodimer; in equilibrium.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- PM: Processing at the N-terminus can regulate receptor and target  
CC cell selectivity. Deletion of the N-terminal residue converts it  
CC from an activator of basophil to an eosinophil chemoattractant.  
CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
Query Match 100.0%; Score 73; DB 1; Length 99;  
Best Local Similarity 100.0%; Pred. No. 5.6e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ISVORLASVREITSSK 16  
DB 43 ISVORLASVRRITSSK 58  
RESULT 2  
CCL2\_MACFA STANDARD; PRT; 99 AA.  
ID CCL2\_MACFA  
AC P61274; Q9MYN4;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic  
DE protein 1) (MCP-1) (Monocyte chemoattractant protein 1).  
GN Name=CCL2; Synonyms=MCPI, SCYA2;  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopithecoidea; Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Studer C., Urfer R.;  
RT "Cloning and expression of cynomolgus monkey chemoattractant protein-  
RT 1.";  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Chemotactic factor that attracts monocytes and basophils  
CC but not neutrophils or eosinophils. Binds to CCR2 and CCR4 (By  
CC similarity).  
CC -1- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; AF276081; AAF81899.1; -; mRNA.  
CC HSSP; P13500; 1DOK.  
DR SMR; P61274; 24-93.  
DR InterPro; IPR000827; CC\_chemokine\_sml.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR InterPro; IPR008097; Fractalkine.  
DR Pfam; PF00048; IL8; 1.  
DR PRINTS; PR01721; FRACTALKINE.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
KW Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;  
KW Pyroglutamate carboxylic acid; Sensory transduction; Signal.  
FT SIGNAL 1 23  
FT CHAIN 24 99  
FT MOD\_RES 24 24  
FT CARBOHYD 37 37  
FT DISULFID 34 59  
FT DISULFID 35 75  
FT SEQUENCE 99 AA; 11007 MW; 433CB88C64EE7A4F CRC64;



Query Match 100.0%; Score 73; DB 1; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYYRITSSK 16  
 |||||  
 Db 43 ISVQRLASYYRITSSK 58

## RESULT 3

CCL2 MACMU CCL2 MACMU STANDARD; PRT; 99 AA.  
 AC P61275; Q9MYN4;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic protein 1) (MCP-1) (Monocyte chemoattractant protein 1).  
 GN Name=CCL2; Synonyms=MC1, SCYA2;  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopithecoidea; Cercopithecinae; Macaca.  
 NCBI\_TaxID=9544;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Studer C., Urfer R.;  
 RT "Cloning and expression of rhesus monkey monocyte chemoattractant protein-1."  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Chemotactic factor that attracts monocytes and basophils but not neutrophils or eosinophils. Binds to CCR2 and CCR4 (By similarity).  
 CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.

-----  
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EMBL; AF255343; AAF67756.1; -; mRNA.  
 HSP; P13500; IDOX.  
 SMR; P61275; 24-93.  
 InterPro; IPR000827; CC\_chemokine\_sml.  
 InterPro; IPR001811; Chemokine IL8.  
 Pfam; PF00048; IL8; 1.  
 PRINTS; PR01721; FRACTALKINE.  
 SMART; SM00199; SCY; 1.  
 PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
 Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;  
 Pyrilidone carboxylic acid; Sensory transduction; Signal.  
 SIGNAL 1 23 By similarity.  
 CHAIN 24 99 Small inducible cytokine A2.  
 MOD\_RES 24 24 Pyrrolidone carboxylic acid (By similarity).  
 CARBOHYD 37 37 N-linked (GlcNAc...) (Potential).  
 DISULFID 34 59 By similarity.  
 DISULFID 35 75 By similarity.  
 SEQUENCE 99 AA; 11007 MW; 433CB88C64EE7A4F CRC64;

Query Match 100.0%; Score 73; DB 1; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYYRITSSK 16  
 |||||  
 Db 43 ISVQRLASYYRITSSK 58

## RESULT 4

CCL2 PONPY CCL2 PONPY STANDARD; PRT; 99 AA.  
 AC OSRA36;  
 DT 13-SEP-2005 (Rel. 48, Created)  
 DT 13-SEP-2005 (Rel. 48, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Small inducible cytokine A2 precursor (CCL2).  
 GN Name=CCL2;  
 OS Pongo pygmaeus (Orangutan).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Pongo.  
 NCBI\_TaxID=9600;  
 [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC The German cDNA consortium;  
 RG Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Chemotactic factor that attracts monocytes and basophils but not neutrophils or eosinophils. Binds to CCR2 and CCR4 (By similarity).  
 CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -!- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.

-----  
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EMBL; CR859186; CAH91374.1; -; mRNA.  
 SMR; OSRA36; 24-94.  
 InterPro; IPR000827; CC\_chemokine\_sml.  
 InterPro; IPR001811; Chemokine IL8.  
 InterPro; IPR008097; Fractalkine.  
 Pfam; PF00048; IL8; 1.  
 PRINTS; PR01721; FRACTALKINE.  
 SMART; SM00199; SCY; 1.  
 PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
 Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;  
 Pyrilidone carboxylic acid; Sensory transduction; Signal.  
 SIGNAL 1 23 By similarity.  
 CHAIN 24 99 Small inducible cytokine A2.  
 MOD\_RES 24 24 Pyrrolidone carboxylic acid (By similarity).  
 CARBOHYD 37 37 N-linked (GlcNAc...) (Potential).  
 DISULFID 34 59 By similarity.  
 DISULFID 35 75 By similarity.  
 SEQUENCE 99 AA; 11015 MW; 45FCA8CC64FF8A4F CRC64;

Query Match 100.0%; Score 73; DB 1; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYYRITSSK 16  
 |||||  
 Db 43 ISVQRLASYYRITSSK 58

## RESULT 5

O6XVNS MACNE O6XVNS MACNE PRELIMINARY; PRT; 99 AA.  
 AC O6XVNS; 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Monocyte chemoattractant protein-1.  
 OS Macaca nemestrina (Pig-tailed macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopithecoidea; Cercopithecinae; Macaca.

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OX NCBI_TaxID=9545;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Coleman G.D., Clements J.E., Zink M.C.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY206692; AAO52733.1; -; mRNA.
DR HSP; P78423; 1B2T.
DR SMR; Q6XVNS; 24-93.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemokine; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR008097; Fractalkine.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR01721; FRACTALKINE.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 99 AA; 11007 MW; 433CB88C64BE7A4F CRC64;

Query Match 100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISVQRLASYRRITSSK 58

RESULT 6
Q71ME7_MACMU
ID Q71ME7 MACMU PRELIMINARY; PRT; 99 AA.
AC Q71ME7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Chemokine CCL2/MCP-1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=22123042; PubMed=12126650; DOI=10.1006/cyto.2002.0875;
RX Baev S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
RT "Molecular cloning and sequencing of 25 different rhesus macaque
RT chemokine cDNAs reveals evolutionary conservation among C, CC, CXCL,
RT and CX3C families of chemokines.";
RL Cytokine 18:140-148(2002).
DR EMBL; AF449265; AAN76069.1; -; mRNA.
SQ SEQUENCE 99 AA; 11007 MW; 433CB88C64BE7A4F CRC64;

Query Match 100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISVQRLASYRRITSSK 58

RESULT 7
CCL2_CANPA
ID CCL2 CANPA STANDARD; PRT; 101 AA.
AC P52203;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant protein 1) (MCP-1) (Monocyte chemoattractant protein 1).

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GN Name=CCL2; Synonyms=MCP1, SCYA2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Jugular vein endothelial;
RC MEDLINE=97176620; PubMed=9024159;
RA Kumar A.G., Ballantyne C.M., Michael L.H., Kukielka G.L., Youker K.A.,
RA Lindsey M.L., Hawkins H.K., Birdsall H.H., Mackay C.R., Larosa G.J.,
RA Rossen R.D., Smith C.W., Batman M.L.;
RT "Induction of monocyte chemoattractant protein-1 in the small veins of
RT the ischemic and reperfused canine myocardium.";
RL Circulation 95:693-700(1997).
CC -!- FUNCTION: Chemotactic factor that attracts monocytes, but not
CC neutrophils. Important factor in the course of the inflammatory
CC reaction to reperfusion of the previously ischemic myocardium. May
CC play a significant role in monocyte trafficking into the
CC reperfused myocardium.
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Endothelium of small veins and intrafascicular
CC veins, and infiltrating leukocytes.
CC -!- INDUCTION: By TNF-alpha.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U29653; AAA84911.1; -; mRNA.
DR HSP; P13500; LDOM.
DR SMR; P52203; 24-94.
DR Ensembl; ENSCAFG00000018349; Canis familiaris.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR008097; Fractalkine.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR01721; FRACTALKINE.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Inflammatory response;
KW Pyroldione carboxylic acid; Sensory transduction; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 101 Small inducible cytokine A2.
FT MOD_RES 24 24 Pyrrolidone carboxylic acid (By
FT similarity).
FT DISULFID 34 59 By similarity.
FT DISULFID 35 75 By similarity.
SQ SEQUENCE 101 AA; 11121 MW; CDD7E2B1901A7267 CRC64;

Query Match 93.2%; Score 68; DB 1; Length 101;
Best Local Similarity 81.2%; Pred. No. 5.4e-05;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISVQRLASYRRITSSK 58

RESULT 8
MCPB_BOVIN
ID MCPB BOVIN STANDARD; PRT; 74 AA.
AC P80343;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Monocyte chemoattractant protein 1B (MCP-1B) (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Euthera; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP PROTEIN SEQUENCE.  
RC TISSUE=Kidney;  
RX MEDLINE=95034774; PubMed=7947749;  
RA Proost P., Wuyts A., Lenaerts J.-P., van Damme J.:  
RT "Purification, sequence analysis, and biological characterization of a  
RL second bovine monocyte chemoattractant protein-1 (Bo MCP-1B).";  
RL Biochemistry 33:13406-13412(1994).  
CC -1- FUNCTION: Chemoattractant factor that attracts monocytes, but not  
CC neutrophils. Augments monocyte anti-tumor activity. Also induces  
CC the release of gelatinase B. This protein can bind heparin.  
CC -1- P1M: The N-terminus is blocked.  
CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.  
CC -----  
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CC removed.  
CC -----  
DR HSSP; P13500; 1DOK.  
DR SMR; P80343; 1-68.  
DR InterPro; IPR000827; CC\_chemokine\_sml.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
DR Chemotaxis; Cytokine; direct protein sequencing; Heparin-binding;  
KW Sensory transduction.  
FT DISULFID 9 34 By similarity.  
FT DISULFID 10 50 By similarity.  
FT NON\_TER 1 1  
SQ SEQUENCE 74 AA; 8363 MW; FAAF72B970EB16E3 CRC64;

Query Match 87.7%; Score 64; DB 1; Length 74;  
Best Local Similarity 81.2%; Pred. No. 0.00023;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 ISVORLASVRRITSSK 16  
DB 18 ISMQRLMSVRRITSSK 33  
|||:|||||:|||||

RESULT 9  
Q9TTS6 BOVIN PRELIMINARY; PRT; 97 AA.  
AC Q9TTS6;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE Eotaxin.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Vogel B., Klinder A., Sittig D., Aust G.:  
RT "Bovine eotaxin (CCL11) - an unusual member of the eotaxin group -  
RT attracts eosinophils in vitro but is not responsible for eosinophilia  
RT in the ovary.";  
RL Vet. Immunol. Immunopathol. 107:67-77(2005).  
DR EMBL; AJ132003; CAB61617.1; -; mRNA.  
DR HSSP; P51671; 1EOT.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0008009; F:chemokine activity; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.

DR SMART; SM00199; SCY; 1.  
SQ SEQUENCE 97 AA; 10965 MW; 9B65F23E1DDEB743 CRC64;

Query Match 87.7%; Score 64; DB 2; Length 97;  
Best Local Similarity 81.2%; Pred. No. 0.00031;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 ISVORLASVRRITSSK 16  
DB 41 ISIQLQSYRKITSSK 56  
|||:|||||:|||||

RESULT 10  
CCL2\_PIG STANDARD; PRT; 99 AA.  
AC P42831;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DB Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant protein 1) (MCP-1) (MCP-1) (Monocyte chemoattractant protein 1).  
DE Name=CCL2; Synonyms=SCYA2;  
GN Sus scrofa (Pig).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
OX Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=94183284; PubMed=7510962;  
RA Hosang K., Knoke I., Klaudiny J., Wempe P., Wuttke W., Scheit K.H.;  
RT "Porcine luteal cells express monocyte chemoattractant protein-1 (MCP-1): analysis by polymerase chain reaction and cDNA cloning.";  
RL Biochem. Biophys. Res. Commun. 199:962-968(1994).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Brain;  
RA Zach O.R.P.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Chemoattractant factor that attracts monocytes, but not  
CC neutrophils.  
CC -1- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR EMBL; Z48479; CAA8370.1; -; mRNA.  
DR EMBL; X79416; CAA55945.1; -; mRNA.  
DR PIR; JC2136; JC2136.  
DR HSSP; P13500; 1DOM.  
DR SMR; P42831; 24-98.  
DR InterPro; IPR000827; CC\_chemokine\_sml.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
DR Chemotaxis; Cytokine; Inflammatory response;  
KW Pyrrolidone carboxylic acid; Sensory transduction; Signal.  
FT SIGNAL 1 23 By similarity.  
FT CHAIN 24 99 Pyrrolidone carboxylic acid (By  
FT MOD\_RES 24 24 similarity).  
FT DISULFID 34 59 By similarity.  
FT DISULFID 35 75 By similarity.  
SQ SEQUENCE 99 AA; 10976 MW; 4C0AC6278D4F0A09 CRC64;

Query Match 87.7%; Score 64; DB 1; Length 99;  
Best Local Similarity 81.2%; Pred. No. 0.00032;

Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISVQRLASRYRRTSSK 16  
 ||:|||||:|||||  
 Db 43 ISMQLRMYYRRTSSK 58

## RESULT 11

MCPA\_BOVIN STANDARD; PRT; 99 AA.  
 ID P28291;  
 AC 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Monocyte chemotactic protein 1A precursor (MCP-1A) (MCP-1) (Acidic  
 DE seminal fluid protein).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Seminal plasma;  
 RX MEDLINE=92096117; PubMed=1721821;  
 RA Wempe F., Henschen A., Scheit K.H.;  
 RT "Gene expression and cDNA cloning identified a major basic protein  
 RT constituent of bovine seminal plasma as bovine monocyte-  
 RT chemoattractant protein-1 (MCP-1).";  
 RL DNA Cell Biol. 10:671-679 (1991).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Seminal plasma;  
 RX MEDLINE=92181448; PubMed=1543494;  
 RA Wempe F., Einspanier R., Scheit K.H.;  
 RT "Characterization by cDNA cloning of the mRNA of a new growth factor  
 RT from bovine seminal plasma: acidic seminal fluid protein.";  
 RL Biochem. Biophys. Res. Commun. 183:232-237 (1992).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=94338337; PubMed=8060303;  
 RA Wempe F., Kuhlmann J.K., Scheit K.H.;  
 RT "Characterization of the bovine monocyte chemoattractant protein-1  
 RT gene.";  
 RL Biochem. Biophys. Res. Commun. 202:1272-1279 (1994).  
 CC -!- FUNCTION: Chemotactic factor that attracts monocytes, but not  
 CC neutrophils.  
 CC -!- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.  
 CC  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC EMBL; L32659; AAA60956.1; -; Genomic\_DNA.  
 CC EMBL; M84602; AAA30651.1; -; mRNA.  
 CC PIR; A39296; A39296.  
 CC HSSP; P13500; 1ML0.  
 CC SMR; P28291; 24-98.  
 CC InterPro; IPR000827; CC\_chemkine eml.  
 CC InterPro; IPR001811; Chemokine\_IL8.  
 CC Pfam; PF00048; IL8; 1.  
 CC SMART; SM00199; SCY; 1.  
 CC PROSITE; PS00472; SMALL\_CYTOKINES CC; 1.  
 CC Chemotaxis; Cytokine; Pyrolidone carboxylic acid;  
 CC Sensory transduction; Signal.  
 CC SIGNAL 1 23 By similarity.  
 CC CHAIN 24 99 Monocyte chemotactic protein 1A.  
 CC MOD\_RES 24 24 Pyrrolidone carboxylic acid (By  
 CC similarity).  
 CC DISULFID 34 59 By similarity.  
 CC FT DISULFID 35 75 By similarity.

SQ SEQUENCE 99 AA; 11114 MW; 0FD79FC1AB0CB88 CRC64;

Query Match 83.6%; Score 61; DB 1; Length 99;  
 Best Local Similarity 75.0%; Pred. No. 0.0012;  
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISVQRLASRYRRTSSK 16

Db 43 ISMQLRMYYRRTSSK 58

## RESULT 12

CCL11\_HORSE STANDARD; PRT; 100 AA.  
 ID CCL11\_HORSE  
 AC Q9TTQ4;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Botaxin precursor (Small inducible cytokine A11) (CCL11).  
 GN Name=CCL11; Synonyms=SCYA11;  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21061912; PubMed=11044560; DOI=10.1016/S0165-2427(00)00222-1;  
 RA Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W.,  
 RA Collins M.E.;  
 RT "Cloning of equine chemokines eotaxin, monocyte chemoattractant  
 RT protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and  
 RT induction by IL-4 in dermal fibroblasts.";  
 RL Vet. Immunol. Immunopathol. 76:283-298 (2000).  
 CC -!- FUNCTION: In response to the presence of allergens, this protein  
 CC directly promotes the accumulation of eosinophils, a prominent  
 CC feature of allergic inflammatory reactions. Binds to CCR3 (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.  
 CC  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC EMBL; AJ251188; CAB61624.1; -; mRNA.  
 CC HSSP; P51671; 1EOT.  
 CC SMR; Q9TTQ4; 25-96.  
 CC InterPro; IPR000827; CC\_chemkine eml.  
 CC InterPro; IPR001811; Chemokine\_IL8.  
 CC InterPro; IPR008097; Fractalkine.  
 CC Pfam; PF00048; IL8; 1.  
 CC PRINTS; PR01721; FRACTALKINE.  
 CC SMART; SM00199; SCY; 1.  
 CC PROSITE; PS00472; SMALL\_CYTOKINES CC; 1.  
 CC Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;  
 CC Sensory transduction; Signal.  
 CC SIGNAL 1 23 By similarity.  
 CC CHAIN 24 100 Eotaxin.  
 CC CARBOHYD 94 94 O-linked (GalNAc. .) (By similarity).  
 CC DISULFID 32 57 By similarity.  
 CC FT DISULFID 33 73 By similarity.  
 CC SQ SEQUENCE 100 AA; 11247 MW; 11F08EC00E75D50B CRC64;

Query Match 82.2%; Score 60; DB 1; Length 100;  
 Best Local Similarity 81.2%; Pred. No. 0.0019;  
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ISVQRLASRYRRTSSK 16

Db 41 ISFQRLQSYRRTSSK 56

```
RESULT 13
CCL2_HORSE
ID CCL2_HORSE STANDARD; PRT; 99 AA.
AC Q9TTQ3;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant protein 1).
DE protein 1) (MCP-1) (Monocyte chemoattractant protein 1).
GN Name=CCL2; Synonyms=MCP1, SCYA2;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=97996;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=21061912; PubMed=11044560; DOI=10.1016/S0165-2427(00)00222-1;
RA Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W.,
RA Collins M.E.;
RA "Cloning of equine chemokines eotaxin, monocyte chemoattractant protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and induction by IL-4 in dermal fibroblasts.";
RL Vet. Immunol. Immunopathol. 76:283-298(2000).
CC -1- FUNCTION: Chemotactic factor that attracts monocytes, but not neutrophils (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
-----
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-----
DR EMBL; AJ251189; CAB61625.1; -; mRNA.
DR HSP; P13500; 1DOM.
DR SMR; Q9TTQ3; 24-38.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Inflammatory response;
KW Pyroglutamate carboxylic acid; Sensory transduction; Signal.
FT SIGNAL 1 23
FT CHAIN 24 99 Small inducible cytokine A2.
FT MOD_RES 24 24 Pyroglutamate carboxylic acid (By similarity).
FT DISULFID 34 59 By similarity.
FT DISULFID 35 75 By similarity.
SQ SEQUENCE 99 AA; 10790 MW; BA1448F79F3423D2 CRC64;

Query Match 80.8%; Score 59; DB 1; Length 99;
Best Local Similarity 75.0%; Pred. No. 0.003;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASRYRITSSK 16
||| ||| ||| ||| |||
Db 43 ISSQRLGSGYKRVITSSK 58

RESULT 14
Q92318_CAVPO
ID Q92318_CAVPO PRELIMINARY; PRT; 97 AA.
AC Q92318;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Monocyte Chemoattractant Protein-3 (MCP-3).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Asano K., Nakamura M., Oguma T., Fukunaga K., Matsubara H.,
RA Ishizaka A., Yanaguchi K., Kanazawa M.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB014340; BAA36456.1; -; mRNA.
DR HSP; P51671; 1EOT.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 97 AA; 11159 MW; E1B9A17C165C2421 CRC64;

Query Match 78.1%; Score 57; DB 2; Length 97;
Best Local Similarity 81.2%; Pred. No. 0.0071;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVQRLASRYRITSSK 16
||| ||| ||| ||| |||
Db 41 IRVQRLSYRITSSK 56

RESULT 15
CCL11_HUMAN
ID CCL11_HUMAN STANDARD; PRT; 97 AA.
AC P51671; P50877; Q92490; Q92491;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Eotaxin precursor (Small inducible cytokine A11) (CCL11) (Eosinophil chemotactic protein)-SCYA11;
DE Name=CCL11; Synonyms=SCYA11;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96181758; PubMed=8597956; DOI=10.1038/nm0496-449;
RA Garcia-Zepeda E.A., Rothenberg M.E., Ownbey T.R., Leder P.,
RA Luster A.D.;
RA "Human eotaxin is a specific chemoattractant for eosinophil cells and provides a new mechanism to explain tissue eosinophilia.";
RL Nat. Med. 2:449-456(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96189337; PubMed=8609214;
RA Ponath P.D., Qin S., Ringler D.J., Clark-Lewis I., Wang J., Kassam N.,
RA Smith H., Shi X., Gonzalo J.A., Newman W., Gutierrez-Ramos J.C.,
RA Mackay C.R.;
RA "Cloning of the human eosinophil chemoattractant, eotaxin. Expression, receptor binding, and functional properties suggest a mechanism for the selective recruitment of eosinophils.";
RL J. Clin. Invest. 97:604-612(1996).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Small intestine;
RX MEDLINE=96205964; PubMed=8631813; DOI=10.1074/jbc.271.13.7725;
RA Kitaura M., Nakajima T., Imai T., Harada S., Combadiere C.,
RA Tiffany H.L., Murphy P.M., Yoshie O.;
RT Molecular cloning of human eotaxin, an eosinophil-selective CC chemokine, and identification of a specific eosinophil eotaxin receptor, CC chemokine receptor 3.;
RT receptor, CC chemokine receptor 3.;
```

RL J. Biol. Chem. 271:7725-7730(1996).

RP [4]

RP NUCLEOTIDE SEQUENCE, PROTEIN SEQUENCE OF 60-65 AND 75-88, AND VARIANTS.

RC TISSUE=Foreskin;

RA MEDLINE=96374440; PubMed=8780731; DOI=10.1006/bbrc.1996.1292;

RA Bartels J., Schluter C., Richter E., Noso N., Kulke R.,

RA Christophers E., Schroeder J.-M.;

RT "Human dermal fibroblasts express eotaxin: molecular cloning, mRNA expression, and identification of eotaxin sequence variants.";

RL Biochem. Biophys. Res. Commun. 225:1045-1051(1996).

RN [5]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Placenta;

RA MEDLINE=97312708; PubMed=9169149; DOI=10.1006/geno.1997.4656;

RA Garcia-Zepeda E.A., Rothenberg M.E., Weremowicz S., Sarafi M.N.,

RA Morton C.C., Luster A.D.;

RT "Genomic organization, complete sequence, and chromosomal location of the gene for human eotaxin (SCYA11), an eosinophil-specific CC chemokine.";

RL Genomics 41:471-476(1997).

RN [6]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Lung;

RA MEDLINE=97445071; PubMed=9299399; DOI=10.1006/bbrc.1997.7169;

RA Hein H., Schluter C., Kulke R., Christophers E., Schroeder J.-M.,

RA Bartels J.;

RT "Genomic organization, sequence, and transcriptional regulation of the human eotaxin gene.";

RL Biochem. Biophys. Res. Commun. 237:537-542(1997).

RN [7]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC TISSUE=Lung;

RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [8]

RP CARBOHYDRATE-LINKAGE SITE.

RC TISSUE=Blood;

RA MEDLINE=98237580; PubMed=9578468;

RA Noso N., Bartels J., Maillet A.I., Mochizuki M., Christophers E.,

RA Schroeder J.-M.;

RT "Delayed production of biologically active O-glycosylated forms of human eotaxin by tumor-necrosis-factor-alpha-stimulated dermal fibroblasts.";

RL Eur. J. Biochem. 253:114-122(1998).

RN [9]

RP STRUCTURE BY NMR.

RA MEDLINE=98380469; PubMed=9712872; DOI=10.1074/jbc.273.35.22471;

RA Crump M.P., Rajaratnam K., Kim K.S., Clark-Lewis I., Sykes B.D.;

RT "Solution structure of eotaxin, a chemokine that selectively recruits eosinophils in allergic inflammation.";

RL J. Biol. Chem. 273:22471-22479(1998).

CC -1- FUNCTION: In response to the presence of allergens, this protein directly promotes the accumulation of eosinophils, a prominent

feature of allergic inflammatory reactions. Binds to CCR3.

-1- SUBCELLULAR LOCATION: Secreted.

-1- INDUCTION: By TNF-alpha, interleukin-1 alpha and interferon gamma.

-1- PTM: O-linked glycan consists of a Gal-GalNAc disaccharide which is modified with up to 2 sialic acid residues.

-1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.

-1- DATABASE: NAME=RD Systems' cytokine source book: SCYA11; WWW="http://www.rndsystems.com/asp/g\_sitebuilder.asp?bodyId=196".

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EMBL; U46573; AAA98957.1; -; mRNA.

EMBL; U34780; AAC50369.1; -; Genomic\_DNA.

EMBL; D49372; BAA08370.1; -; mRNA.

EMBL; D69291; CAA93258.1; -; mRNA.

EMBL; Z75668; CAA99997.1; -; mRNA.

EMBL; Z75669; CAA99998.1; -; mRNA.

EMBL; U46572; AAC51297.1; -; Genomic\_DNA.

EMBL; Z92709; CAB07027.1; -; Genomic\_DNA.

EMBL; BC017850; AAH17850.1; -; mRNA.

PIR; JC4912; JC4912.

PDB; 1BOT; NMR; @=24-97.

PDB; 2BOT; NMR; @=24-97.

ENSMBL; ENSG00000172156; Homo sapiens.

HGNC; HGNC:10610; CCL11.

H-InvDB; HIX0013715; -.

MIM; 601156; -.

GO; GO:0008009; F:chemokine activity; TAS.

GO; GO:0006874; P:calcium ion homeostasis; TAS.

GO; GO:0007155; P:cell adhesion; TAS.

GO; GO:0006935; P:chemotaxis; TAS.

GO; GO:0006954; P:inflammatory response; TAS.

GO; GO:0006488; P:protein amino acid phosphorylation; TAS.

GO; GO:0009334; P:response to radiation; TAS.

GO; GO:0009615; P:response to virus; TAS.

GO; GO:0007165; P:signal transduction; TAS.

InterPro; IPR000827; CC chemokine sm.

InterPro; IPR001811; Chemokine\_IL8.

Pfam; PF00048; IL8; 1.

PROSITE; PS00472; SMALL CYTOKINES CC; 1.

3D-structure; Chemotaxis; Cytokine; Direct protein sequencing;

Glycoprotein; Inflammatory response; Polymorphism;

Sensory transduction; Signal.

SIGNAL 1 23

CHAIN 24 97 Botaxin.

CARBOHYD 94 94 O-linked (GalNAc. .).

DISULFID 32 57

DISULFID 33 73

VARIANT 7

VARIANT 23 23 L -> P (in clone 34).

VARIANT 51 51 /FTID=VAR\_001634.

VARIANT 79 79 A -> T (in clone 53; dbSNP:3744508).

VARIANT 79 79 R -> S (in clone 34).

VARIANT 79 79 K -> R (in clone 53).

TURN 44 45 /FTID=VAR\_001636.

STRAND 46 52 /FTID=VAR\_001637.

TURN 61 66

TURN 67 68

TURN 71 74

TURN 76 77

TURN 79 91

HELEX 79 91

SEQUENCE 97 AA; 10732 MW; B433C30FDA4C71A7 CRC64;

Query Match 76.7%; Score 56; DB 1; Length 97;

Best Local Similarity 75.0%; Pred. No. 0.011; Indels 0; Gaps 0;

Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY 1 ISVQRLASYRRITSSK 16
  -||| ||||| |
Db 41 IPLQRLSYRRITSSK 56

RESULT 16
Q619T4 HUMAN
ID Q619T4 HUMAN PRELIMINARY; PRT; 97 AA.
AC Q619T4
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE CCL11 protein.
GN Name=CCL11;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; CR457421; CAG33702.1; -; mRNA.
SQ SEQUENCE 97 AA; 10732 MW; B433C30FDA4C71A7 CRC64;

Query Match 76.7%; Score 56; DB 2; Length 97;
Best Local Similarity 75.0%; Pred. No. 0.011;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16
  -||| ||||| |
Db 41 IPLQRLSYRRITSSK 56

RESULT 17
CCL2 RABIT
ID CCL2 RABIT STANDARD; PRT; 125 AA.
AC P28292;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant protein 1) (MCP-1) (MCP-1) (Monocyte chemoattractant protein 1).
GN Name=CCL2; Synonyms=SCYA2;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=New Zealand white; TISSUE=Spleen;
RX MEDLINE=91225489; PubMed=2026877;
RA Yoshimura T., Yuhki N.;
RT "Neutrophil attractant/activation protein-1 and monocyte chemoattractant protein-1 in rabbit. cDNA cloning and their expression in spleen cells.";
RL J. Immunol. 146:3483-3488(1991).
CC -!- FUNCTION: Chemoattractant factor that attracts monocytes, but not neutrophils.
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
-----
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DR EMBL; M57440; AAA31386.1; -; mRNA.
PIR; I46857; I46857.
```

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DR HSSP; P13500; 1DOM.
DR SMR; P28292; 24-99.
DR InterPro; IPR000827; CC chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL CYTOKINES CC; 1.
KW Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;
KW Pyrrolidone carboxylic acid; Sensory transduction; Signal.
FT SIGNAL 1 23
FT CHAIN 24 125
FT MOD_RES 24 24
FT CARBOHYD 40 40
FT CARBOHYD 55 55
FT CARBOHYD 112 112
FT DISULFID 34 59
FT DISULFID 35 75
SQ SEQUENCE 125 AA; 13776 MW; 24C3A542CB6A47EE CRC64;

Query Match 76.7%; Score 56; DB 1; Length 125;
Best Local Similarity 75.0%; Pred. No. 0.015;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16
  -||| ||||| |
Db 43 ISVKRLMSYRRINSTK 58

RESULT 18
Q516F8 CANFA
ID Q516F8 CANFA PRELIMINARY; PRT; 99 AA.
AC Q516F8;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE Monocyte chemoattractant protein 3.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Peters I.R., Peeters D., Clercx C., Day M.J.;
RT "Identification of Coding Sequence of Canine MCP-3 (CCL-7).";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY849795; AAW34061.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; P:chemokine activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemokine_sml.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL CYTOKINES CC; 1.
SQ SEQUENCE 99 AA; 11236 MW; 48A5B4A7932DEEC9 CRC64;

Query Match 74.0%; Score 54; DB 2; Length 99;
Best Local Similarity 73.3%; Pred. No. 0.028;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSS 15
  -||| ||||| |
Db 43 IPIQKLKSYRRITSS 57

RESULT 19
CCL11 CAVPO
ID CCL11 CAVPO STANDARD; PRT; 96 AA.
AC P80325;
DT 01-JUN-1994 (Rel. 29, Created)
```



01-OCT-1996 (Rel. 34, Last sequence update)  
 10-MAY-2005 (Rel. 47, Last annotation update)  
 Eotaxin precursor (Small inducible cytokine A11) (CCL11) (Eosinophil chemotactic protein)  
 Name=CCL11; Synonyms=SCV11;  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Hystriocognathi; Caviidae; Cavia.  
 NCBI\_TaxID=10141;  
 (1)  
 NUCLEOTIDE SEQUENCE.  
 TISSUE=Lung;  
 MEDLINE=95173589; PubMed=7869037; DOI=10.1084/jem.181.3.1211;  
 RA Rothenberg M.E., Luster A.D., Lilly C.M., Drazen J.M., Leder P.;  
 RT "Constitutive and allergen-induced expression of eotaxin mRNA in the guinea pig lung.";  
 RL J. Exp. Med. 181:1211-1216 (1995).  
 (2)  
 NUCLEOTIDE SEQUENCE.  
 MEDLINE=95091818; PubMed=7999113;  
 RA Jose P.J., Adcock I.M., Griffiths-Johnson D.A., Berkman N., Wells T.C., Williams T.J., Power C.A.;  
 RT "Eotaxin: cloning of an eosinophil chemoattractant cytokine and increased mRNA expression in allergen-challenged guinea-pig lungs.";  
 RL Biochem. Biophys. Res. Commun. 205:788-794 (1994).  
 (3)  
 PROTEIN SEQUENCE OF 24-96.  
 STRAIN=Hartley; TISSUE=Lung;  
 MEDLINE=94157409; PubMed=7509365; DOI=10.1084/jem.179.3.881;  
 RA Jose P.J., Griffiths-Johnson D.A., Collins P.D., Walsh D.T., Moser R., Totty N.P., Truong O., Huan J.J., Williams T.J.;  
 RT "Eotaxin: a potent eosinophil chemoattractant cytokine detected in a guinea pig model of allergic airways inflammation.";  
 RL J. Exp. Med. 179:881-887 (1994).  
 CC -I- FUNCTION: In response to the presence of allergens, this protein directly promotes the accumulation of eosinophils, a prominent feature of allergic inflammatory reactions.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- TISSUE SPECIFICITY: Lung.  
 CC -I- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
 -----  
 DR EMBL; U18941; AAC52180.1; -; mRNA.  
 DR EMBL; X77603; CAA54698.1; -; mRNA.  
 DR PIR; I48099; I48099.  
 DR HSP; P51671; 180T.  
 DR InterPro; IPR000827; CC chemokine sm1.  
 DR InterPro; IPR001811; Chemokine\_IL8.  
 DR Pfam; PF00048; IL8; 1.  
 DR SMART; SM00199; SCY; 1.  
 DR PROSITE; PS00472; SMALL CYTOKINES CC; 1.  
 DR Chemotaxis; Cytokine; Direct protein sequencing; Glycoprotein; Inflammatory response; Sensory transduction; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 96 Eotaxin.  
 FT CARBOHYD 93 93 O-linked (Potential).  
 FT DISULFID 31 56 By similarity.  
 FT DISULFID 32 72 By similarity.  
 FT CONFLICT 88 88 D -> G (in Ref. 2).  
 FT SEQUENCE 96 AA; 10753 MW; 62C856645BC6AC99 CRC64;  
 Query Match 71.2%; Score 52; DB 1; Length 96;  
 Best Local Similarity 75.0%; Pred. No. 0.066;  
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 || ||| ||: |||||

Qy

Db 40 ISFORLKSXKIITSSK 55  
 RESULT 20  
 CCL12 MOUSE  
 ID CCL12\_MOUSE STANDARD; PRT; 104 AA.  
 AC Q62401; O9QYD6;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Small inducible cytokine A12 precursor (CCL12) (Monocyte chemotactic protein 5) (MCP-5) (MCP-1-related chemokine).  
 DE Name=CCL12; Synonyms=Mcp5, Scyal2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 (1)  
 NUCLEOTIDE SEQUENCE.  
 MEDLINE=97079149; PubMed=8920881; DOI=10.1084/jem.184.5.1939;  
 RA Jia G.-Q., Gonzalo J.A., Lloyd C., Kremer L., Lu L., Martinez A.C., Werahil B.K., Gutierrez-Ramos J.C.;  
 RT "Distinct expression and function of the novel mouse chemokine monocyte chemotactic protein-5 in lung allergic inflammation.";  
 RL J. Exp. Med. 184:1939-1951 (1996).  
 (2)  
 NUCLEOTIDE SEQUENCE.  
 MEDLINE=97149438; PubMed=8996246; DOI=10.1084/jem.185.1.99;  
 RA Sarafi M.N., Garcia-Zepeda E.A., McLean J.A., Charo I.F., Luster A.D.;  
 RT "Murine monocyte chemoattractant protein (MCP)-5: a novel CC chemokine that is a structural and functional homologue of human MCP-1.";  
 RL J. Exp. Med. 185:99-109 (1997).  
 (3)  
 NUCLEOTIDE SEQUENCE.  
 STRAIN=B10.S/J, BALB/c, DBA/2J, NOD/LtJ, and SJL/J; TISSUE=Spleen;  
 MEDLINE=99370037; PubMed=10438970;  
 RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W., Blankenhorn B.P.;  
 RT "Sequence polymorphisms in the chemokines Scyal (TCA-3) and Scyal2 (monocyte chemoattractant protein (MCP)-1), and Scyal2 (MCP-5) are candidates for eae7, a locus controlling susceptibility to monophasic remitting/nonrelapsing experimental allergic encephalomyelitis.";  
 RL J. Immunol. 163:2262-2266 (1999).  
 (4)  
 NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 TISSUE=Mammary gland;  
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 CC -I- FUNCTION: Chemotactic factor that attracts eosinophils, monocytes, and lymphocytes but not neutrophils. Potent monocyte active chemokine that signals through CCR2. Involved in allergic inflammation and the host response to pathogens and may play a pivotal role during early stages of allergic lung inflammation.



```

CC CC -1- SUBUNIT: Homodimer (By similarity).
CC CC -1- SUBCELLULAR LOCATION: Secreted.
CC CC -1- TISSUE SPECIFICITY: Predominantly expressed in the lymph nodes and
CC CC thymus. Also found in the salivary glands containing lymph nodes,
CC CC breast, heart, lung, brain, small intestine, kidney and colon.
CC CC -1- INDUCTION: By interferon gamma and lipopolysaccharides (LPS).
CC CC -1- POLYMORPHISM: The polymorphism in strain SJL/J may be associated
CC CC with severity of clinical symptoms of experimental allergic
CC CC encephalomyelitis, an animal model of multiple sclerosis, and
CC CC susceptibility to the monophasic remitting/nonrelapsing form of
CC CC the disease.
CC CC -1- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
CC CC
CC CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use as long as its content is in no way modified and this statement is not
CC CC removed.
CC CC
CC CC EMBL; U50712; AB50053.1; -; mRNA.
CC CC EMBL; U66670; AB49424.1; -; mRNA.
CC CC EMBL; AF065934; AAF15384.1; -; mRNA.
CC CC EMBL; AF065935; AAF15385.1; -; mRNA.
CC CC EMBL; AF065936; AAF15386.1; -; mRNA.
CC CC EMBL; AF065937; AAF15387.1; -; mRNA.
CC CC EMBL; AF065938; AAF15388.1; -; mRNA.
CC CC EMBL; BC027520; AAH27520.1; -; mRNA.
CC CC HSSP; P13500; IDOL.
CC CC
CC CC Ensembl; ENSMUSG00000035352; Mus musculus.
CC CC MGI; MGI:108224; Ccl12.
CC CC GO; GO:0005615; C:extracellular space; TAS.
CC CC InterPro; IPR000827; CC_chemokine_sml.
CC CC InterPro; IPR001811; Chemokine_IL8.
CC CC Pfam; PF00048; IL8; 1.
CC CC PROSITE; PS00472; SMALL CYTOKINES CC; 1.
CC CC Conserved; Cytokine; Inflammatory response; Polymorphism;
CC CC Sensory transduction; Signal.
CC CC
CC CC SIGNAL 1 22 By similarity.
CC CC CHAIN 23 104 Small inducible cytokine A12.
CC CC DISULFID 33 58 By similarity.
CC CC DISULFID 34 74 By similarity.
CC CC VARIANT 94 104 QTFILEPSCLG -> RT (in strain SJL/J).
CC CC SEQUENCE 104 AA; 11659 MW; 8D102P4FF4CC3DBF CRC64;
CC CC
CC CC Query Match 71.2%; Score 52; DB 1; Length 104;
CC CC Best Local Similarity 68.8%; Pred. NO. 0.073;
CC CC Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
CC CC
CC CC Qy 1 ISVQRLASVYRITSSK 16
CC CC Db 42 IHVRKLKSYRRITSSQ 57
CC CC
CC CC RESULT 21
CC CC Q5SVB4_MOUSE PRELIMINARY; PRT; 104 AA.
CC CC
CC CC 01-FEB-2005 (TrEMBLrel. 29, Created)
CC CC 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
CC CC 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
CC CC Chemokine (C-C motif) ligand 12 (11 days embryo whole body cDNA, RIKEN
CC CC full-length enriched library, clone:2700043D19 product:small inducible
CC CC cytokine A12, full insert sequence).
CC CC GN Name=Ccl12; Synonyms=OTTMUSP0000000792; ORFNames=RP23-301E19.2-001;
CC CC Mus musculus (Mouse).
CC CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
CC CC Muridae; Murinae; Mus.
CC CC NCBI_TaxID=10090;
CC CC [1]
CC CC NUCLEOTIDE SEQUENCE.
CC CC RP Matthews L.;
CC CC RA Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

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RN RP NUCLEOTIDE SEQUENCE.
RN RC STRAIN=C57BL/6J; TISSUE=Whole body;
RN RX MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RN RA Carninci P., Hayashizaki Y.;
RN RT "High-efficiency full-length cDNA cloning.";
RN RL Meth. Enzymol. 303:19-44(1999).
RN [3]
RN RP NUCLEOTIDE SEQUENCE.
RN RC STRAIN=C57BL/6J; TISSUE=Whole body;
RN RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RN RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Iehi Y.,
RN RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RN RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RN RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RN RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RN RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochava H.,
RN RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RN RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RN RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RN RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RN RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RN RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RN RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RN RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RN RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RN RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RN RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RN RA Hayashizaki Y.;
RN RT "Functional annotation of a full-length mouse cDNA collection.";
RN RL Nature 409:685-690(2001).
RN [4]
RN RP NUCLEOTIDE SEQUENCE.
RN RC STRAIN=C57BL/6J; TISSUE=Whole body;
RN RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RN RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RN RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RN RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RN RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RN RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RN RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RN RA Della E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RN RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RN RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RN RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RN RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RN RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RN RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RN RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RN RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RN RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RN RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RN RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RN RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
RN RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RN RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RN RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RN RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RN RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RN RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RN RA Birney E., Hayashizaki Y.;
RN RT "Analysis of the mouse transcriptome based on functional annotation of
RN RT 60,770 full-length cDNAs.";
RN RL Nature 420:563-573(2002).
RN [5]
RN RP NUCLEOTIDE SEQUENCE.
RN RC STRAIN=C57BL/6J; TISSUE=Whole body;
RN RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RN RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RN RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RN RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RN RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RN RL Genome Res. 10:1617-1630(2000).

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RN NUCLEOTIDE SEQUENCE
RC STRAIN=C57BL/6J; TISSUE=Whole body; DOI=10.1101/gr.152600;
EX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama S., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:11757-1771(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Horii F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toyota T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL645596; CA125041.1; -; Genomic_DNA.
DR EMBL; AK012356; BAB28185.1; -; mRNA.
DR MGI; MGI:108224; Cc112.
DR GO; GO:0005615; C:extracellular space; TAS.
SQ SEQUENCE 104 AA; 11659 MW; 8D102F4FF4CC3DBF CRC64;

Query Match 71.2%; Score 52; DB 2; Length 104;
Best Local Similarity 68.8%; Pred. No. 0.073;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ISVORLASRYRITSSK 16
| : : : : :
Db 42 IHVRKLSYRITSSQ 57

RESULT 22
Q865F3 MACNE
ID Q865F3 MACNE PRELIMINARY; PRT; 109 AA.
AC Q865F3
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Monocyte chemoattractant protein-3.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Coleman G.D., Valli P.J.S., Clements J.E., Zink M.C.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY206694; AA052735.1; -; mRNA.
DR HSSP; P80098; 1B00.
DR SMR; Q865F3; 34-109.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC chemokine sm1.
DR InterPro; IPR001811; CC chemokine_IL6.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.

Query Match 71.2%; Score 52; DB 2; Length 109;
Best Local Similarity 80.0%; Pred. No. 0.077;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ISVORLASRYRITSS 15
| : : : : :
Db 53 IPKORLESYRITSS 67

RESULT 23
Q87TQ2 HORSE
ID Q87TQ2 HORSE PRELIMINARY; PRT; 81 AA.
AC Q87TQ2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Monocyte chemoattractant protein-2 precursor (Fragment).
GN Name=mcp-2;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=21061912; PubMed=11044560; DOI=10.1016/S0165-2427(00)00222-1;
RA Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W.,
RA Collins M.E.;
RT "Cloning of equine chemokines eotaxin, monocyte chemoattractant
RT protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and
RT induction by IL-4 in dermal fibroblasts.";
RL Vet. Immunol. Immunopathol. 76:283-298(2000).
DR EMBL; AJ251190; CAB61626.1; -; mRNA.
DR HSSP; P80075; 1ESR.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR KW Signal.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 >81 by similarity.
FT NON TER 81 81
SQ SEQUENCE 81 AA; 8858 MW; A34ADE103C386B0F CRC64;

Query Match 69.9%; Score 51; DB 2; Length 81;
Best Local Similarity 62.5%; Pred. No. 0.086;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ISVORLASRYRITSSK 16
| : : : : :
Db 43 VP1ORLESYRITSSQ 58

RESULT 24
CCL11 MACMU
ID CCL11 MACMU STANDARD; PRT; 97 AA.
AC Q8M1T7;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Eotaxin precursor (Small inducible cytokine A11) (CCL11).
GN Name=CCL11; Synonyms=SCY11;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
```

RA Zhang L., Soares M.P., Guan Y., Sirotina-Meisher A.,  
RA Macheravidathu S., Iliff S.A., Mudgett J.S., Springer M.S.,  
RA Daugherty B.L.,  
RT "Molecular cloning of ectatin/CC111 and CCR3 from rhesus monkey.  
RT Functional expression and characterization of rhesus monkey CCR3 in  
RT murine Li-2 cells; generation of antibodies against rhesus CCR3.";  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: In response to the presence of allergens, this protein  
CC directly promotes the accumulation of eosinophils, a prominent  
CC feature of allergic inflammatory reactions. Binds to CCR3 (By  
CC similarity).  
CC  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC  
CC -1- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL: AY049019; AAL13086.1; -; mRNA.  
CC SMR: Q8MI77; 24-97.  
CC InterPro: IPR000827; CC\_chemkine\_sml.  
CC InterPro: IPR001811; Chemokine\_IL8.  
CC Pfam: PF00048; IL8; 1.  
CC SMART: SM00199; SCY; 1.  
CC PROSITE: PS00472; SMALL\_CYTOKINES\_CC; 1.  
CC Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;  
KW Sensory transduction; Signal.  
FT SIGNAL 1 23 By similarity.  
FT CHAIN 24 97 Botaxin.  
FT CARBOHYD 94 94 O-linked (GalNAc. .) (By similarity).  
FT DISULFID 32 57 By similarity.  
FT DISULFID 33 73 By similarity.  
SQ SEQUENCE 97 AA; 10855 MW; 9BCA0FD6D95B02DD CRC64;  
  
Query Match 68.5%; Score 50; DB 1; Length 97;  
Best Local Similarity 68.8%; Pred. No. 0.16;  
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 1 ISVORLASYYRITSSK 16  
| : ||| ||||| |  
Db 41 IPLQRLSYRRIISGK 56  
  
RESULT 25  
Q8HXZ5 MACMU PRELIMINARY; PRT; 97 AA.  
AC Q8HXZ5;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Chemokine CC111/BOTAXIN.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopithecoidea; Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22123042; PubMed=12126650; DOI=10.1006/cyto.2002.0875;  
RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;  
RT "Molecular cloning and sequencing of 25 different rhesus macaque  
RT chemokine cDNAs reveals evolutionary conservation among C, CC, CXC,  
RT and CX3C families of chemokines.";  
RL Cytochrome 18:140-148(2002).  
DR EMBL: AF449270; AAN76074.1; -; mRNA.  
DR HSSP: P51671; 1EOT.  
DR SMR: Q8HXZ5; 24-97.  
DR GO: GO:0005576; C:extracellular region; IEA.  
DR GO: GO:0008009; F:chemokine activity; IEA.  
DR GO: GO:0006935; P:chemotaxis; IEA.  
DR GO: GO:0006955; P:immune response; IEA.

DR InterPro: IPR000827; CC\_chemkine\_sml.  
DR InterPro: IPR001811; Chemokine\_IL8.  
DR Pfam: PF00048; IL8; 1.  
DR SMART: SM00199; SCY; 1.  
DR PROSITE: PS00472; SMALL\_CYTOKINES\_CC; 1.  
SQ SEQUENCE 97 AA; 10795 MW; ED0CD4B2860A47C9 CRC64;  
  
Query Match 68.5%; Score 50; DB 2; Length 97;  
Best Local Similarity 68.8%; Pred. No. 0.16;  
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 1 ISVORLASYYRITSSK 16  
| : ||| ||||| |  
Db 41 IPLQRLSYRRIISGK 56  
  
RESULT 26  
Q9Z292\_9RODE PRELIMINARY; PRT; 106 AA.  
AC Q9Z292;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Monocyte chemoattractant protein 1 (fragment).  
OS Cricetulus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Cricetinae; Cricetulus.  
OX NCBI\_TaxID=10031;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Bachrati C.Z., Downes S., Raske I.;  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF081141; AAD03677.1; -; mRNA.  
DR HSSP: P13500; 1ML0.  
DR GO: GO:0005576; C:extracellular region; IEA.  
DR GO: GO:0008009; F:chemokine activity; IEA.  
DR GO: GO:0006955; P:immune response; IEA.  
DR InterPro: IPR001811; Chemokine\_IL8.  
DR Pfam: PF00048; IL8; 1.  
DR SMART: SM00199; SCY; 1.  
FT NON\_TER 1  
SQ SEQUENCE 106 AA; 11876 MW; 3F670AE9F360355A CRC64;  
  
Query Match 68.5%; Score 50; DB 2; Length 106;  
Best Local Similarity 68.8%; Pred. No. 0.18;  
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 ISVORLASYYRITSSK 16  
| : ||| ||||| |  
Db 7 IPEKRLSYRRIISGK 22  
  
RESULT 27  
Q8CGM5 SIGHI PRELIMINARY; PRT; 150 AA.  
AC Q8CGM5;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Monocyte chemoattractant protein-1.  
GN Name=MCP-1/JE;  
OS Sigmodon hispidus (Hispid cotton rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Sigmodontinae; Sigmodon.  
OX NCBI\_TaxID=42415;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=14980081; DOI=10.1089/10799900477219873;  
RA Blanco J.C., Pletneva L., Boukhvalova M., Richardson J.Y.,  
RA Harris K.A., Prince G.A.;  
RT "The cotton rat: an underutilized animal model for human infectious

diseases can now be exploited using specific reagents to cytokines, chemokines, and interferons.";  
 J. Interferon Cytokine Res. 24:21-28(2004).  
 EMBL; AY165953; AAN85636.1; -; mRNA.  
 HSP; P13500; 1DOK.  
 GO: GO:0005576; C:extracellular region; IEA.  
 GO: GO:0008009; F:chemokine activity; IEA.  
 GO: GO:0006935; F:chemotaxis; IEA.  
 GO: GO:0006955; P:immune response; IEA.  
 InterPro; IPR000827; CC chemokine sml.  
 InterPro; IPR001811; Chemokine\_IL8.  
 Pfam; PF00048; IL8; 1.  
 SMART; SM00199; SCY; 1.  
 PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
 SEQUENCE 150 AA; 16480 MW; 16341DBD2C52AF25 CRC64;  
 Query Match 68.5%; Score 50; DB 2; Length 150;  
 Best Local Similarity 68.8%; Pred. No. 0.27;  
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 ISVQRLASYRRITSSK 16  
 : : : : :  
 Db 44 IPEKRLSYKRTSSK 59  
 : : : : :  
 RESULT 28  
 Q7TMS1 MOUSE  
 ID Q7TMS1 MOUSE PRELIMINARY; PRT; 65 AA.  
 AC Q7TMS1  
 DT 01-OCT-2003 (TRENBLrel. 25, Created)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Ccl2 protein.  
 GN Name=Ccl2;  
 OS Mus musculus (Mouse);  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C3H/He; TISSUE=Mesenchymal Stem Cell;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Frange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C3H/He; TISSUE=Mesenchymal Stem Cell;  
 RG NIH MGC Project;  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC055070; AAN55070.1; -; mRNA.  
 DR HSP; P13500; 1DOK.  
 GO: GO:0005576; C:extracellular region; IEA.  
 GO: GO:0008009; F:chemokine activity; IEA.  
 GO: GO:0006955; P:immune response; IEA.

DR InterPro; IPR001811; Chemokine\_IL8.  
 DR Pfam; PF00048; IL8; 1.  
 DR SMART; SM00199; SCY; 1.  
 SQ SEQUENCE 65 AA; 7188 MW; 9FB7F1460A424B80 CRC64;  
 Query Match 67.1%; Score 49; DB 2; Length 65;  
 Best Local Similarity 62.5%; Pred. No. 0.16;  
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 ISVQRLASYRRITSSK 16  
 : : : : :  
 Db 43 IPMSRLSYKRTSSR 58  
 : : : : :  
 RESULT 29  
 Q5KSU7 CANFA  
 ID Q5KSU7 CANFA PRELIMINARY; PRT; 99 AA.  
 AC Q5KSU7  
 DT 10-MAY-2005 (TRENBLrel. 30, Created)  
 DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)  
 DE CC chemokine ligand 7.  
 GN Name=CCL7;  
 OS Canis familiaris (Dog);  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 OC Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Tsukaguchi T., Maeda S., Koyanagi M., Hashimoto R., Masuda K., Ohno K.,  
 Sakaguchi M., Tsujimoto H., Iwabuchi S.;  
 RT "Expression analysis of CCL7 gene in canine atopic dermatitis.";  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB183286; BAD83851.1; -; mRNA.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0008009; F:chemokine activity; IEA.  
 DR GO; GO:0006935; P:chemotaxis; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR000827; CC chemokine sml.  
 DR InterPro; IPR001811; Chemokine\_IL8.  
 DR Pfam; PF00048; IL8; 1.  
 DR SMART; SM00199; SCY; 1.  
 DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
 SQ SEQUENCE 99 AA; 11224 MW; B195B4A7933664E1 CRC64;  
 Query Match 67.1%; Score 49; DB 2; Length 99;  
 Best Local Similarity 66.7%; Pred. No. 0.26;  
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 ISVQRLASYRRITSS 15  
 : : : : :  
 Db 43 IPIQKLKSYRTTSS 57  
 : : : : :  
 RESULT 30  
 CCL2 MOUSE  
 ID CCL2 MOUSE STANDARD; PRT; 148 AA.  
 AC P10148; OSQYD7;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant protein 1) (MCP-1) (MCP-1) (Monocyte chemoattractant protein 1) (Platelet-derived growth factor-inducible protein JE).  
 DE derived growth factor-inducible protein JE).  
 GN Name=Ccl2; Synonyms=Je, Mcp1, Scy2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=89093129; PubMed=2910858;  
RA Kawahara R.S., Devel T.P.;  
RT "Platelet-derived growth factor-inducible gene JE is a member of a  
RT family of small inducible genes related to platelet factor 4.";  
RL J. Biol. Chem. 264:679-682(1989).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=88234501; PubMed=3287374;  
RA Rollins B.J., Morrison E.D., Stiles C.D.;  
RT "Cloning and expression of JE, a gene inducible by platelet-derived  
RT growth factor and whose product has cytokine-like properties.";  
RL Proc. Natl. Acad. Sci. U.S.A. 85:3738-3742(1988).  
RN [3]  
RP NUCLEOTIDE SEQUENCE, AND VARIANTS GLY-50 AND GLN-92.  
RC STRAIN=B10.S/J, BALB/C, DBA/2J, NOD/LtJ, and SJL/J, TISSUE=Spleen;  
RX MEDLINE=99370037; PubMed=10438970;  
RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,  
RA Blankenhorn E.P.;  
RT "Sequence polymorphisms in the chemokines Sclal (TCA-3), Sclal2  
RT (monocyte chemoattractant protein (MCP)-1), and Sclal2 (MCP-5) are  
RT candidates for eae7, a locus controlling susceptibility to monophasic  
RT remitting/nonrelapsing experimental allergic encephalomyelitis.";  
RL J. Immunol. 163:2262-2266(1999).  
RN [4]  
RP PROTEIN SEQUENCE OF 26-42.  
RX MEDLINE=91293127; PubMed=2065676;  
RA van Damme J., Decock B., Bertini R., Conings R., Lenaerts J.-P.,  
RA Put W., Opendakker G., Mancovani A.;  
RT "Production and identification of natural monocyte chemotactic protein  
RT from virally infected murine fibroblasts. Relationship with the  
RT product of the mouse competence (JE) gene.";  
RL Eur. J. Biochem. 199:223-229(1991).  
CC -!- FUNCTION: Chemotactic factor that attracts monocytes, but not  
CC neutrophils.  
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- INDUCTION: By platelet-derived growth factor.  
CC -!- POLYMORPHISM: The polymorphisms in strain SJL/J may be associated  
CC with severity of clinical symptoms of experimental allergic  
CC encephalomyelitis, an animal model of multiple sclerosis, and  
CC susceptibility to the monophasic remitting/nonrelapsing form of  
CC the disease.  
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; J04467; AAA37685.1; -; Genomic DNA.  
CC EMBL; M19681; AAA37684.1; -; Genomic DNA.  
CC EMBL; AF065929; AAF15379.1; -; mRNA.  
CC EMBL; AF065930; AAF15380.1; -; mRNA.  
CC EMBL; AF065931; AAF15381.1; -; mRNA.  
CC EMBL; AF065932; AAF15382.1; -; mRNA.  
CC EMBL; AF065933; AAF15383.1; -; mRNA.  
CC F01; A30209; A30209.  
CC F01; S16226; S16226.  
CC HSSP; P13500; IDOK.  
CC Ensembl; ENSMUSG00000035385; Mus musculus.  
CC MGI; MGI:98259; Ccl2.  
CC GO; GO:0005615; C:extracellular space; TAS.  
CC GO; GO:0001664; F:G-protein-coupled receptor binding; IDA.  
CC GO; GO:0005515; F:protein binding; IDA.  
CC InterPro; IPR000827; CC chemokine sm.  
CC InterPro; IPR001811; Chemokine\_IL8.  
CC Pfam; PF00048; IL8; 1.  
CC SMART; SM00199; SCY; 1.  
CC PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
CC Chemotaxis; Cytokine; Direct protein sequencing; Glycoprotein;  
KW Inflammatory response; Polymorphism; Pyrrolidone carboxylic acid;  
KW Sensory transduction; Signal.

FT SIGNAL 1 23 By similarity.  
FT CHAIN 24 148 Small inducible cytokine A2.  
FT MOD\_RES 24 24 Pyrrolidone carboxylic acid (By  
FT similarity).  
FT CARBOHYD 126 126 N-linked (GlcNAc...) (Potential).  
FT DISULFID 34 59 By similarity.  
FT DISULFID 35 75 By similarity.  
FT VARIANT 50 50 S -> G (in strain SJL/J).  
FT VARIANT 92 92 R -> Q (in strain SJL/J).  
SQ SEQUENCE 148 AA; 16326 MW; 29A5505FC6D94837 CRC64;  
Query Match 67.1%; Score 49; DB 1; Length 148;  
Best Local Similarity 62.5%; Pred. No. 0.42;  
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 ISVORLASYYRRTSSK 16  
| : |||:|||||:  
Db 43 IPMSRLSYKRTSSR 58  
| : |||:|||||:  
RESULT 31  
Q5SVU3\_MOUSE PRELIMINARY; PRT; 148 AA.  
ID Q5SVU3\_MOUSE  
AC Q5SVU3;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 13-FEB-2005 (TrEMBLrel. 31, Last annotation update)  
DE Chemokine (C-C motif) ligand 2 (Ccl2 protein).  
GN Name=Ccl2; ORFNames=RP23-350GL.3-001;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Whitehead S.;  
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Ebert L., Muenstermann E., Schatten R., Henze S., Bohn E.,  
RA Mollenhauer J., Wiemann S., Schick M., Korn B.;  
RT "Cloning of mouse full open reading frames in Gateway(R) system entry  
RT vector (pDONR201)." ;  
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.  
DE EMBL; AL626807; CA125305.1; -; Genomic DNA.  
DE EMBL; CT010187; CA18395.1; -; mRNA.  
DE Ensembl; ENSMUSG00000035385; Mus musculus.  
DE GO; GO:0005576; C:extracellular region; IEA.  
DE GO; GO:0008009; F:chemokine activity; IEA.  
DE GO; GO:0006955; P:immune response; IEA.  
DE InterPro; IPR000827; CC chemokine sm.  
DE InterPro; IPR001811; Chemokine\_IL8.  
DE Pfam; PF00048; IL8; 1.  
DE SMART; SM00199; SCY; 1.  
DE PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
SQ SEQUENCE 148 AA; 16326 MW; 29A5505FC6D94837 CRC64;  
Query Match 67.1%; Score 49; DB 2; Length 148;  
Best Local Similarity 62.5%; Pred. No. 0.42;  
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 ISVORLASYYRRTSSK 16  
| : |||:|||||:  
Db 43 IPMSRLSYKRTSSR 58  
| : |||:|||||:  
RESULT 32  
Q8MKC8\_HORSE PRELIMINARY; PRT; 99 AA.  
ID Q8MKC8\_HORSE  
AC Q8MKC8;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-JUN-2003 (trEMBLrel. 24, Last annotation update)  
 DE MCP-2.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF506972; AAM34214.1; -; mRNA.  
 DR HSSP; P80075; 1ESR.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0008009; F:chemokine activity; IEA.  
 DR GO; GO:0008955; P:immune response; IEA.  
 DR InterPro; IPR001811; Chemokine\_IL8.  
 DR Pfam; PF00048; IL8; 1.  
 DR SMART; SM00199; SCY; 1.  
 SQ SEQUENCE 99 AA; 11028 MW; 94F5D8E540889228 CRC64;  
 Query Match 65.8%; Score 48; DB 2; Length 99;  
 Best Local Similarity 56.2%; Pred. NO. 0.41;  
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 ISVQRLASVRRITSSK 16  
 Db 43 VPIQRVESYTRITSSQ 58  
 RESULT 33  
 CCL7\_HUMAN  
 ID CCL7\_HUMAN STANDARD; PRT; 99 AA.  
 AC P80098;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Small inducible cytokine A7 precursor (CCL7) (Monocyte chemoattractant protein 3) (MCP-3) (MCP-3) (Monocyte chemoattractant protein 3) (NC28).  
 DE Name=CCL7; Synonyms=MCP3, SCYA7;  
 GN Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 31-67 AND 71-99.  
 RA MEDLINE=93213290; PubMed=8461011;  
 RA Opatenacker G., Froyen G., Fiten P., Proost P., van Damme J.;  
 RT "Human monocyte chemoattractant protein-3 (MCP-3): molecular cloning of the cDNA and comparison with other chemokines.";  
 RL Biochem. Biophys. Res. Commun. 191:535-542(1993).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=94375065; PubMed=7916328;  
 RA Opatenacker G., Fiten P., Nys G., Froyen G., van Roy N., Speleman F., Laureys G., van Damme J.;  
 RA Laureys G., van Damme J.;  
 RT "The human MCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the C-C chemokine gene cluster on chromosome 17q11.2-q12.";  
 RL Genomics 21:403-408(1994).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=93305913; PubMed=8318676;  
 RA Minty A., Chalou P., Guillemot J.C., Kaghad M., Liauzun P., Magazin M., Miloux B., Miny C., Ramond P., Vita N., Lupker J., Shire D., Ferrara P., Caput D.;  
 RA Shire D., Ferrara P., Caput D.;  
 RT "Molecular cloning of the MCP-3 chemokine gene and regulation of its expression.";  
 RL Eur. Cytokine Netw. 4:99-110(1993).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE OF 24-99.  
 RA Jang J.S., Kim B.E.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP PROTEIN SEQUENCE OF 30-99.  
 RC TISSUE=Osteosarcoma;  
 RX MEDLINE=92308855; PubMed=16133466; DOI=10.1084/jem.176.1.59;  
 RA van Damme J., Proost P., Lenaerts J.-P., Opatenacker G.;  
 RT "Structural and functional identification of two human, tumor-derived monocyte chemoattractant proteins (MCP-2 and MCP-3) belonging to the chemokine family.";  
 RL J. Exp. Med. 176:59-65(1992).  
 RN [6]  
 RP PROTEIN SEQUENCE OF 24-38.  
 RX PubMed=15340161; DOI=10.1110/ps.04682504;  
 RA Zhang Z., Hensel W.J.;  
 RT "Signal peptide prediction based on analysis of experimentally verified cleavage sites.";  
 RL Protein Sci. 13:2819-2824(2004).  
 RN [7]  
 RP STRUCTURE BY NMR, AND SUBUNIT.  
 RX MEDLINE=97053697; PubMed=8898111; DOI=10.1016/0014-5793(96)01024-1;  
 RA Kim K.-S., Rajarathnam K., Clark-Lewis I., Sykes B.D.;  
 RT "Structural characterization of a monomeric chemokine: monocyte chemoattractant protein-3.";  
 RL FEBS Lett. 395:277-282(1996).  
 RN [8]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=97263733; PubMed=9109648; DOI=10.1021/bi9627929;  
 RA Meunier S., Bernasau J.-M., Guillemot J.-C., Ferrara P., Darbon H.;  
 RT "Determination of the three-dimensional structure of CC chemokine monocyte chemoattractant protein 3 by 1H two-dimensional NMR spectroscopy.";  
 RL Biochemistry 36:4412-4422(1997).  
 RN [9]  
 RP STRUCTURE BY NMR.  
 RA Kwon D., Lee D., Sykes B.D., Kim K.-S.;  
 RL Submitted (AUG-1998) to the PDB data bank.  
 CC -!- FUNCTION: Chemotactic factor that attracts monocytes and eosinophils, but not neutrophils. Augments monocyte anti-tumor activity. Also induces the release of gelatinase B. This protein can bind heparin. Binds to CCR1, CCR2 and CCR3.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- PTM: O-glycosylated.  
 CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
 CC EMBL; X72308; CAA51055.1; ALT INIT; mRNA.  
 CC EMBL; X72309; -; NOT ANNOTATED CDS; Genomic\_DNA.  
 CC EMBL; X71087; CAA50407.1; -; mRNA.  
 CC EMBL; X71087; CAA50406.1; ALT INIT; mRNA.  
 CC EMBL; X71087; CAA50405.1; ALT INIT; mRNA.  
 CC EMBL; AF043338; AAC03538.1; -; mRNA.  
 CC PDB; 1BOO; NMR; @=24-99.  
 CC PDB; 1NCV; NMR; A/B=24-99.  
 CC Eneembl; ENSG00000108688; Homo sapiens.  
 CC HGNC; HGNC:10634; CCL7.  
 CC MIM; 158106; -.  
 CC GO; GO:0005615; C:extracellular space; TAS.  
 CC GO; GO:0008009; F:chemokine activity; TAS.  
 CC GO; GO:0006874; P:calcium ion homeostasis; TAS.  
 CC GO; GO:0007267; P:cell-cell signaling; TAS.  
 CC GO; GO:0006935; P:chemotaxis; TAS.  
 CC GO; GO:0007165; P:signal transduction; TAS.  
 CC InterPro; IPR000827; CC chemokine sm1.  
 CC InterPro; IPR001811; Chemokine\_IL8.  
 CC Pfam; PF00048; IL8; 1.  
 CC SMART; SM00199; SCY; 1.  
 CC PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
 CC 3D-structure; Chemotaxis; Cytokine; Direct protein sequencing;  
 KW

KW Glycoprotein; Heparin-binding; Inflammatory response;  
KW Pyrrolidone carboxylic acid; Sensory transduction; Signal.  
FT SIGNAL 1 23  
FT CHAIN 24 99  
FT MOD RES 24 24 Small inducible cytokine A7.  
FT CARBOHYD 29 29 Pyrrolidone carboxylic acid.  
FT DISULFID 34 59 N-linked (GlcNAc...) (Potential).  
FT DISULFID 35 75  
FT CONFLICT 30 30  
FT CONFLICT 68 70  
FT TURN 45 47  
FT TURN 48 48 T -> K (in Ref. 5).  
FT STRAND 53 53 Missing (in Ref. 5).  
FT TURN 56 58  
FT STRAND 64 68  
FT TURN 69 70  
FT STRAND 73 76  
FT TURN 78 79  
FT HELIX 81 91  
SQ SEQUENCE 99 AA; 11200 MW; 96048B371C25D00E CRC64;

Query Match 64.4%; Score 47; DB 1; Length 99;  
Best Local Similarity 73.3%; Pred. No. 0.65;  
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSS 15  
| | | | | | | | | |  
Db 43 IPKQRLSYRRITSS 57

RESULT 34  
Q569J6 HUMAN  
ID Q569J6\_HUMAN PRELIMINARY; PRT; 99 AA.  
AC Q569J6; PubMed=12477932; DOI=10.1073/pnas.242603899;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Chemokine (C-C motif) ligand 7.  
GN Name=CCL7;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Blood;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Blood;  
RG NIH MGC Project;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC092436; AAH92436.1; -; mRNA.

SQ SEQUENCE 99 AA; 11200 MW; 96048B371C25D00E CRC64;  
Query Match 64.4%; Score 47; DB 2; Length 99;  
Best Local Similarity 73.3%; Pred. No. 0.65;  
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 ISVQRLASYRRITSS 15  
| | | | | | | | | |  
Db 43 IPKQRLSYRRITSS 57

RESULT 35  
Q727Q8 HUMAN  
ID Q727Q8\_HUMAN PRELIMINARY; PRT; 109 AA.  
AC Q727Q8;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Monocyte chemotactic protein-3.  
GN Name=MCP-3;

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=94375065; PubMed=7916328;  
RA Opdenakker G., Fiten P., Nys G., Froyen G., van Roy N., Speleman F.,  
RA Laureys G., van Damme J.;  
RT "The human MCP-3 gene (SCYA7): cloning, sequence analysis, and  
RT assignment to the C-C chemokine gene cluster on chromosome 17q11.2-  
RT Q12."  
RL Genomics 21:403-408(1994).  
DR EMBL; X72309; CAB59723.1; -; Genomic\_DNA.  
DR HSSP; P80098; 1B00.  
DR SMR; Q727Q8; 34-109.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0008009; F:chemokine activity; IEA.  
DR GO; GO:0006935; P:chemotaxis; IEA.  
DR GO; GO:0006935; P:immune response; IEA.  
DR InterPro; IPR000827; CC chemokine smi.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
SQ SEQUENCE 109 AA; 12356 MW; 69980669F0A2157D CRC64;

Query Match 64.4%; Score 47; DB 2; Length 109;  
Best Local Similarity 73.3%; Pred. No. 0.72;  
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSS 15  
| | | | | | | | | |  
Db 53 IPKQRLSYRRITSS 67

RESULT 36  
Q9BG83 PONPY  
ID Q9BG83\_PONPY PRELIMINARY; PRT; 44 AA.  
AC Q9BG83;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Monocyte chemotactic protein 1 (Fragment).  
GN Name=MCP1;

OS Pongo pygmaeus (Orangutan).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Pongo.  
OX NCBI\_TaxID=9600;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.



```

RA Avi T.C., Chew X.L.A., Yap P.H.E.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF324469; AAK13442.1; -; mRNA.
DR HSSP; P13500; 1DOK.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; P:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
FT NON_TER 1 1
FT NON_TER 44 44
SQ SEQUENCE 44 AA; 4830 MW; 1DE3C10EB83CD190 CRC64;

Query Match 63.0%; Score 46; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQLASVSR 10
| | | | | | | | | |
DB 35 ISVQLASVSR 44

RESULT 37
Q865F4_MACNE PRELIMINARY; PRT; 99 AA.
ID Q865F4;
AC Q865F4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 24, Last annotation update)
DE Monocyte chemoattractant protein-2.
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Coleman G.D., Clements J.E., Zink M.C.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY206693; AAO52734.1; -; mRNA.
DR HSSP; P80075; 1ESR.
DR SMR; Q865F4; 24-99.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008009; P:chemokine activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC chemokine sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR01721; FRCTALKINE.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 99 AA; 11261 MW; 9D6797974A88B9BF CRC64;

Query Match 63.0%; Score 46; DB 2; Length 99;
Best Local Similarity 56.2%; Pred. No. 1;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 ISVQLASVRRITSSK 16
| | | | | | | | | | | | | | | |
DB 43 IPIQLQSYTRITNTQ 58

RESULT 38
Q8HYQ0_MACMU PRELIMINARY; PRT; 99 AA.
ID Q8HYQ0;
AC Q8HYQ0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chemokine CCL8/MCP-2.

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OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22123042; PubMed=12126650; DOI=10.1006/cyto.2002.0875;
RA Babu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinart T.A.;
RT "Molecular cloning and sequencing of 25 different rhesus macaque
RT chemokine cDNAs reveals evolutionary conservation among C, CC, CXC,
RT and CX3C families of chemokines.";
RL Cytokine 18:140-148(2002).
DR EMBL; AF449269; AAN76073.1; -; mRNA.
DR HSSP; P80075; 1ESR.
DR SMR; Q8HYQ0; 24-99.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008009; P:chemokine activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC chemokine sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR008097; Fractalkine.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR01721; FRCTALKINE.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 99 AA; 11263 MW; 9D6797974A88B97F CRC64;

Query Match 63.0%; Score 46; DB 2; Length 99;
Best Local Similarity 56.2%; Pred. No. 1;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 ISVQLASVRRITSSK 16
| | | | | | | | | | | | | | | |
DB 43 IPIQLQSYTRITNTQ 58

RESULT 39
CCL2_RAT STANDARD; PRT; 148 AA.
ID CCL2_RAT
AC P14844;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant
DE protein 1) (MCP-1) (Monocyte chemoattractant protein 1) (Immediate-
DE early serum-responsive JE protein).
DE Name=CCL2; Synonyms=Je, Mcp1, Sca2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WAG/RIJ; TISSUE=Kidney;
RX MEDLINE=90174947; PubMed=2106664;
RA Timmers H.T.M., Pronk G.J., Bos J.L., van der Eb A.J.;
RT "Analysis of the rat JE gene promoter identifies an AP-1 binding site
RT essential for basal expression but not for TPA induction.";
RL Nucleic Acids Res. 18:23-34(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91128376; PubMed=1704226;
RA Yoshimura T., Takeya M., Takahashi K.;
RT "Molecular cloning of rat monocyte chemoattractant protein-1 (MCP-1)
RT and its expression in rat spleen cells and tumor cell lines.";
RL Biochem. Biophys. Res. Commun. 174:504-509(1991).
CC -1- FUNCTION: Chemotactic factor that attracts monocytes, but not
CC neutrophils.
CC -1- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).

```



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CC CC -!- SUBCELLULAR LOCATION: Secreted.
CC CC -!- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
CC CC -----
CC CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use as long as its content is in no way modified and this statement is not
CC CC removed.
CC CC -----
DR DR EMBL; X17053; CAA34901.1; -; Genomic_DNA.
DR DR EMBL; M57441; AAA63496.1; -; mRNA.
DR DR PIR; S07723; S07723.
DR DR HSSP; P13500; 1DOK.
DR DR Ensembl; ENSRNOG00000007159; Rattus norvegicus.
DR DR InterPro; IPR000827; CC_chemkine_sml.
DR DR InterPro; IPR001811; Chemokine_IL8.
DR DR Pfam; PF00048; IL8; 1.
DR DR SMART; SM00199; SCY; 1.
DR DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;
KW Pyroliidone carboxylic acid; Sensory transduction; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 148 Small inducible cytokine A2.
FT MOD_RES 24 24 Pyroliidone carboxylic acid (By
FT similarity).
FT CARBOHYD 126 126 N-linked (GlcNAc...) (Potential).
FT DISULFID 34 59 By similarity.
FT DISULFID 35 75 By similarity.
SQ SEQUENCE 148 AA; 16460 MW; 62D4C42BF4B11C9D CRC64;

Query Match 63.0%; Score 46; DB 1; Length 148;
Best Local Similarity 56.2%; Pred. No. 1.6;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVQRLASVRRITSSK 16
Db 43 IPMSRLNKYKRTSSR 58

RESULT 40
Q549R5 RAT PRELIMINARY; PRT; 148 AA.
AC Q549R5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein JE/MCP-1.
GN Name=JE/MCP-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Aortic smooth muscle;
RA Poon M., Taubman M.B.;
RT "Cloning of the full-length rat JE/MCP-1 cDNA.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF058786; AAC15187.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 148 AA; 16460 MW; 62D4C42BF4B11C9D CRC64;

Query Match 63.0%; Score 46; DB 2; Length 148;
Best Local Similarity 56.2%; Pred. No. 1.6;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVQRLASVRRITSSK 16
Db 43 IPMSRLNKYKRTSSR 58

RESULT 41

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CCL7 MOUSE
ID AC Q03366; STANDARD; PRT; 97 AA.
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Small inducible cytokine A7 precursor (CCL7) (Monocyte chemoattractant protein 3) (MCP-3) (Monocyte chemoattractant protein 3)
DE (Interleukine/chemokine MARC) (FIC protein).
GN Name=CCL7; Synonyms=Fic, Mcp3, Scya7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mast cell;
RA Kulmburg P.A., Huber N.E., Scheer B.J., Wrann M., Baumruker T.;
RT "Immunoglobulin B plus antigen challenge induces a novel
interleukine/chemokine in mouse mast cells.";
RL J. Exp. Med. 176:1773-1778 (1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=94271193; PubMed=8002978;
RA Thirion S., Nys G., Fiten P., Masure S., van Damme J., Opdenakker G.;
RT "Mouse macrophage derived monocyte chemoattractant protein-3: cDNA cloning
and identification as MARC/FIC.";
RL Biochem. Biophys. Res. Commun. 201:493-499 (1994).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC Werner F.;
RA Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=93204948; PubMed=8455595;
RA Heinrich J.N., Ryseck R.P., Macdonald-Bravo H., Bravo R.;
RT "The product of a novel growth factor-activated gene, fic, is a
biologically active 'C-C'-type cytokine.";
RL Mol. Cell. Biol. 13:2020-2030 (1993).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=95081620; PubMed=7989769;
RA Jarvin D.I., Kulmburg P.A., Huber N.E., Baumann G.;
RA Prieschl-Strasemayr E.E., Baumruker T.;
RT "A transcription factor with AP3-like binding specificity mediates
gene regulation after an allergic triggering with IGE and Ag in mouse
mast cells.";
RL J. Immunol. 153:5720-5729 (1994).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B10.S/J, and SJL/J; TISSUE=Spleen;
RX MEDLINE=99370037; PubMed=10438970;
RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
RA Blankenhorn E.P.;
RT "Sequence polymorphisms in the chemokines Scya1 (TCA-3), Scya2
(monocyte chemoattractant protein (MCP)-1), and Scya12 (MCP-5) are
candidates for eae7, a locus controlling susceptibility to monophasic
remitting/nonrelapsing experimental allergic encephalomyelitis.";
RL J. Immunol. 163:2262-2266 (1999).
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=22354683; PubMed=12468851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Balzarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,

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RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lennard B., Lyons P.A.,  
RA Maglott D.R., Maitala L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sadelin A., Schneider C., Sempile C.A., Setou M., Shinada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Vardaro R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
RN [8]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE:Testis;  
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T.J., Max S.I., Wang J., Heide F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Kravinsky M.I., Skalska U., Smalls D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
CC -!- FUNCTION: Chemotactic factor that attracts monocytes and  
CC eosinophils, but not neutrophils. Augments monocyte anti-tumor  
CC activity (By similarity).  
CC -!- SUBUNIT: Monomer (By similarity).  
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR EMBL; Z12297; CAA78169.1; -; mRNA.  
DR EMBL; L04694; AAA37516.1; -; mRNA.  
DR EMBL; S71251; AAB30997.1; -; mRNA.  
DR EMBL; X70058; CAA49662.1; -; Genomic\_DNA.  
DR EMBL; AF128193; AAF22534.1; -; mRNA.  
DR EMBL; AF128194; AAF22535.1; -; mRNA.  
DR EMBL; AK078827; BAC37413.1; -; mRNA.  
DR EMBL; BC061126; AAG61126.1; -; mRNA.  
DR PIR; A48093; A48093.  
DR HSP; P80098; 1800.  
DR Ensembl; ENSMUSG00000035373; Mus musculus.  
DR MGI; MGI-99512; Ccl17.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR InterPro; IPR000827; CC\_chemokine\_sml.  
DR InterPro; IPR001811; Chemokine\_IL8.

DR Pfam; PF00048; IL8; 1.  
DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
KW Chemotaxis; Cytokine; Glycoprotein; Heparin-binding;  
KW Inflammatory response; Pyrilidone carboxylic acid;  
KW Sensory transduction; Signal.  
FT SIGNAL 1 23 Potential.  
FT CHAIN 24 97 Small inducible cytokine A7.  
FT MOD\_RES 24 24 Pyrrolidone carboxylic acid (By  
FT similarity).  
FT CARBOHYD 29 29 N-linked (GlcNAc..) (Potential).  
FT DISULFID 33 57 By similarity.  
FT DISULFID 34 73 By similarity.  
FT CONFLICT 57 63 Missing (in Ref. 5).  
FT CONFLICT 74 74 A -> R (in Ref. 4).  
SQ SEQUENCE 97 AA; 10999 MW; B94FDA6DF1EF6140 CRC64;  
Query Match 61.6%; Score 45; DB 1; Length 97;  
Best Local Similarity 62.5%; Pred. No. 1.6;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 ISVORLASYYRRTSSK 16  
| : ||||| :  
Db 41 IPKRNLSYYRRTSSR 56  
RESULT 42  
QSSVUO MOUSE  
ID QSSVUO MOUSE PRELIMINARY; PRT; 97 AA.  
AC QSSVUO;  
DT 10-MAY-2005 (TRENBLrel. 30, Created)  
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)  
DE Chemokine (C-C motif) ligand 7.  
GN Name=Ccl17; ORFNames=RP23-350G1.4-001;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Whitehead S.;  
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL626807; CA125304.1; -; Genomic DNA.  
SQ SEQUENCE 97 AA; 10999 MW; B94FDA6DF1EF6140 CRC64;  
Query Match 61.6%; Score 45; DB 2; Length 97;  
Best Local Similarity 62.5%; Pred. No. 1.6;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 ISVORLASYYRRTSSK 16  
| : ||||| :  
Db 41 IPKRNLSYYRRTSSR 56  
RESULT 43  
Q4PIY1 9ZZZZ  
ID Q4PIY1 9ZZZZ PRELIMINARY; PRT; 97 AA.  
AC Q4PIY1;  
DT 13-SEP-2005 (TRENBLrel. 31, Created)  
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)  
DE MARC.  
GN Name=MARC;  
OS unidentified.  
OC unclassified.  
OX NCBI\_TaxID=32644;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=93094785; PubMed=1281219; DOI=10.1084/jem.176.6.1773;  
RA Kulmburg P.A., Huber N.E., Scheer B.J., Wrann M., Baumruker T.;  
RT "Immunoglobulin E plus antigen challenge induces a novel  
RT intercrine/chemokine in mouse mast cells."

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RL J. Exp. Med. 176:1773-1778 (1992).
DR EMBL: S50588; AA12542.1; -; mRNA
SQ SEQUENCE 97 AA; 1099 MW; B94FDA6DF1EF6140 CRC64;

Query Match 61.6%; Score 45; DB 2; Length 97;
Best Local Similarity 62.5%; Pred. No. 1.6;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
Db 41 IPKENLKSYYRITSSR 56
| : | | | | | | | | | |
| : | | | | | | | | | |

RESULT 44
CCL8 CANFA STANDARD; PRT; 99 AA.
AC Q69AY9;
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Small inducible cytokine A8 precursor (CCL8) (Monocyte chemotactic
DE protein 2) (MCP-2) (Monocyte chemoattractant protein 2).
GN Name=CCL8; Synonyms=MCP2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OC NCBI_TaxID=9615;
RX [1]
RN NUCLEOTIDE SEQUENCE [MRNA].
RA Tsukui T., Sakaguchi M., Maeda S., Koyanagi M., Masuda K., Ohno K.,
RA Tsujimoto H., Iwabuchi S.;
RA "Expression analysis of chemokine gene in canine atopic dermatitis.";
RT Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RL [2]
RN NUCLEOTIDE SEQUENCE [MRNA].
RA Peters I.R., Peeters D., Clercx C., Day M.J.;
RA "Identification of coding sequences for canine monocyte chemotactic
RT protein-2 (CCL8), eotaxin 2 (CCL24), eotaxin 3 (CCL26) and C-C
RT chemokine receptor 3 (CCR3).";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Chemotactic factor that attracts monocytes. This protein
CC can bind heparin (By similarity).
CC -1- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
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DR EMBL: AB163436; BAD37149.1; -; mRNA.
DR EMBL: AY675234; AAU14059.1; -; mRNA.
DR Ensembl: ENSCAFG00000018348; Canis familiaris.
DR InterPro: IPR000827; CC chemokine sm1.
DR InterPro: IPR001811; Chemokine IL8.
DR InterPro: IPR008097; Fractalkine.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR01721; FRACTALKINE.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Heparin-binding; Inflammatory response;
KW Pyrolydione carboxylic acid; Sensory transduction; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 99 Small inducible cytokine A8.
FT MOD_RES 24 24 Pyrrolidone carboxylic acid (By
FT similarity).
FT DISULFID 34 59 By similarity.
FT DISULFID 35 75 By similarity.
SQ SEQUENCE 99 AA; 11263 MW; FD56D8405DC010E8 CRC64;

Query Match 60.3%; Score 44; DB 1; Length 99;
Best Local Similarity 56.2%; Pred. No. 2.5;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
Db 43 IPQKLESYMRITNSQ 58
| : | | | | | | | | | |
| : | | | | | | | | | |

RESULT 45
CCL8 HUMAN STANDARD; PRT; 99 AA.
AC P80075; P78388;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Small inducible cytokine A8 precursor (CCL8) (Monocyte chemotactic
DE protein 2) (MCP-2) (Monocyte chemoattractant protein 2) (HC14)
DE [Contains: MCP-2(6-76)].
DE Name=CCL8; Synonyms=MCP2, SCYA10, SCYA8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RX [1]
RN NUCLEOTIDE SEQUENCE, AND VARIANT GLN-69.
RX MEDLINE=97237052; PubMed=9119400; DOI=10.1006/geno.1996.4594;
RA van Coillie E., Fiten P., Nomiya H., Sakaki Y., Miura R., Fiten P.,
RA van Damme J., Odenakker G.;
RA "The human MCP-2 gene (SCYA8): cloning, sequence analysis, tissue
RT expression, and assignment to the CC chemokine gene contig on
RT chromosome 17q11.2.";
RL Genomics 40:323-331 (1997).
RN [2]
RN NUCLEOTIDE SEQUENCE, AND VARIANT GLN-69.
RP TISSUE=Bone marrow;
RX MEDLINE=97224420; PubMed=9070881; DOI=10.1006/bbrc.1997.6177;
RA van Coillie E., Froyen F., Nomiya H., Miura R., Fiten P.,
RA van Aelst I., van Damme J., Odenakker G.;
RT "Human monocyte chemotactic protein-2: cDNA cloning and regulated
RT expression of mRNA in mesenchymal cells.";
RL Biochem. Biophys. Res. Commun. 231:726-730 (1997).
RN [3]
RN NUCLEOTIDE SEQUENCE OF 23-99.
RX MEDLINE=91207938; PubMed=2518726;
RA Chang H.C., Hsu F., Freeman G.J., Griffin J.D., Reinherz E.L.;
RA "Cloning and expression of a gamma-interferon-inducible gene in
RT monocytes; a new member of a cytokine gene family.";
RL Int. Immunol. 1:388-399 (1989).
RN [4]
RN PROTEIN SEQUENCE OF 26-99.
RC TISSUE=Osteosarcoma;
RX MEDLINE=9230885; PubMed=1613466; DOI=10.1084/jem.176.1.59;
RA van Damme J., Proost P., Lenaerts J.-P., Odenakker G.;
RT "Structural and functional identification of two human, tumor-derived
RT monocyte chemotactic proteins (MCP-2 and MCP-3) belonging to the
RT chemokine family.";
RL J. Exp. Med. 176:59-65 (1992).
RN [5]
RN SUBUNIT.
RP MEDLINE=97053697; PubMed=8898111; DOI=10.1016/0014-5793(96)01024-1;
RA Kim K.-S., Rajaratnam K., Clark-Lewis I., Sykes B.D.;
RT "Structural characterization of a monomeric chemokine: monocyte
RT chemoattractant protein-3.";
RL FEBS Lett. 395:277-282 (1996).
RN [6]
RN IDENTIFICATION OF MCP-2(6-76), MASS SPECTROMETRY, N-TERMINAL
RP PROCESSING, AND FUNCTION.
RX PubMed=9558113;
RA Proost P., Struyf S., Couvreur M., Lenaerts J.-P., Conings R.,
RA Menten P., Verhaert P., Wuyts A., Van Damme J.;
RT "Posttranslational modifications affect the activity of the human

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monocyte chemotactic proteins MCP-1 and MCP-2: identification of MCP-2 (6-76) as a natural chemokine inhibitor.";

J. Immunol. 160:4034-4041(1998).

-1- FUNCTION: Chemotactic factor that attracts monocytes, lymphocytes, basophils and eosinophils. May play a role in neoplasia and inflammatory host responses. This protein can bind heparin. The processed form MCP-2(6-76) does not show monocyte chemotactic activity, but inhibits the chemotactic effect most predominantly of CCL7, and also of CCL2 and CCL5 and CCL8.

-1- SUBUNIT: Monomer or homodimer; in equilibrium.

-1- SUBCELLULAR LOCATION: Secreted.

-1- TISSUE SPECIFICITY: Highest expression found in the small intestine and peripheral blood cells. Intermediate levels seen in the heart, placenta, lung, skeletal muscle, thymus, colon, ovary, spinal cord and pancreas. Low levels seen in the brain, liver, spleen and prostate.

-1- INDUCTION: By interferon gamma, mitogens and interleukin-1.

-1- PTM: N-terminal processed form MCP-2(6-76) is produced by proteolytic cleavage after secretion from peripheral blood monocytes.

-1- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.

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EMBL; X99886; CAA68168.1; ALT INIT; Genomic\_DNA.

EMBL; Y10802; CAA71760.1; -; mRNA.

EMBL; Y16645; CAA76341.1; -; mRNA.

PIR; JC5295; JCS295.

PDB; 1ESR; X-ray; A=24-99.

Ensembl; ENSG00000108700; Homo sapiens.

HGNC; HGNC:10635; CCL8.

MIM; 602283; -.

GO; GO:0008009; F:chemokine activity; TAS.

GO; GO:0004871; F:signal transducer activity; TAS.

GO; GO:0006816; P:calcium ion transport; TAS.

GO; GO:0007267; P:cell-cell signaling; TAS.

GO; GO:0006935; P:chemotaxis; TAS.

GO; GO:0006887; P:exocytosis; TAS.

GO; GO:0009615; P:response to virus; TAS.

GO; GO:0007165; P:signal transduction; TAS.

InterPro; IPR000827; CC chemokine sm1.

InterPro; IPR001811; Chemokine IL8.

Pfam; PF00048; IL8; 1.

PRINTS; PR01721; FRACTALKINE.

PROSITE; PS00472; SMALL CYTOKINES CC; 1.

3D-structure; Chemotaxis; Cytokine; Direct protein sequencing; Heparin-binding; Inflammatory response; Polymorphism; Pyrrolidone carboxylic acid; Sensory transduction; Signal.

SIGNAL 1 23 Probable.

CHAIN 24 99 Small inducible cytokine A8.

CHAIN 29 99 MCP-2(6-76).

MOD RES 24 24 Pyrrolidone carboxylic acid.

DISULFID 34 59 By similarity.

DISULFID 35 75 By similarity.

VARIANT 69 69 K->Q (in dbSNP:3138038).

FT 26 29 /FTId=VAR\_001633.

FT TURN 45 47

FT HELIX 48 53

FT STRAND 57 58

FT TURN 64 68

FT STRAND 69 70

FT TURN 73 76

FT STRAND 78 79

FT TURN 81 96

SEQUENCE 99 AA; 11246 MW; 9D67976BB9422F2A CRC64;

Query Match 60.3%; Score 44; DB 1; Length 99;

Best Local Similarity 64.3%; Pred. No. 2.5; Mismatches 9; Conservative 2; Indels 0; Gaps 0;

QY 1 ISVQLASVRRITS 14  
|:|:|:|:|:|:|:  
Db 43 IPIQLRSYTRITN 56

RESULT 46  
Q621J4\_CABBR  
ID Q621J4\_CABBR PRELIMINARY; PRT; 253 AA.  
AC Q621J4;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE Hypothetical protein CBG02465.  
GN Name=CBG02465;  
OS Caenorhabditis briggsae.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6238;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RG The C.briggsae Sequencing Consortium;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
CC -! CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.  
DR EMBL; CAC01000012; CAB59159.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 253 AA; 28604 MW; 46174476A01B3EF CRC64;

Query Match 60.3%; Score 44; DB 2; Length 253;  
Best Local Similarity 71.4%; Pred. No. 7.4; Mismatches 10; Conservative 2; Indels 0; Gaps 0;

QY 2 SVQRLASVRRITSS 15  
|:|:|:|:|:|:|:  
Db 56 SLQNLASARKITSS 69

RESULT 47  
Q5XPM8\_ERWAM  
ID Q5XPM8\_ERWAM PRELIMINARY; PRT; 271 AA.  
AC Q5XPM8;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE Flc (Fragment).  
GN Name=flc;  
OS Erwinia amylovora.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Erwinia.  
OX NCBI\_TaxID=552;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
STRAIN=CFBP 1430;  
RC Cesbron S., Bissot M.-N., Tharaud M., Paulin J.-P.;  
RA "Erwinia amylovora genes involved in motility,";  
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY743588; AAU90046.1; -; Genomic\_DNA.  
DR GO; GO:0009420; C:flagellar filament (sensu Bacteria); IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR GO; GO:0001539; P:ciliary or flagellar motility; IEA.  
DR InterPro; IPR001029; Flagellin\_C.  
DR InterPro; IPR001492; Flagellin\_N.  
DR Pfam; PF00700; Flagellin\_C; 1.  
DR Pfam; PF00669; Flagellin\_N; 1.  
DR PRINTS; PR00207; FLAGELLIN.  
DR ProDom; PD000316; Flagellin\_C; 1.  
FT NON TER 271 271  
SQ SEQUENCE 271 AA; 28638 MW; 7F1EDE7853451F27 CRC64;

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Query Match      60.3%; Score 44; DB 2; Length 271;
Best Local Similarity 66.7%; Pred. No. 8;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Caps 0;
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Qy 2 SVQRLASYRRITSSK 16  
|:|:|:|:|:|:|  
Db 28 SMERLSSGSRITSSK 42

RESULT 48

Q8D3D7	WIGBR			PRT;	421 AA.
AC	Q8D3D7_WIGBR	PRELIMINARY;			
ID	Q8D3D7;				
DT	01-MAR-2003	(TReMBLrel. 23, Created)			
DT	01-MAR-2003	(TReMBLrel. 23, Last sequence update)			
DT	01-JUN-2003	(TReMBLrel. 24, Last annotation update)			
DE	FliC protein.				
DE	Name=fliC; OrderedLocusNames=WIGBR0640;				
GN	Wigglesworthia glossinidia Brevipalpis.				
OS	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;				
OC	Enterobacteriaceae; Wigglesworthia.				
OX	NCBI_TaxID=36870;				
RN	[1]	NUCLEOTIDE SEQUENCE.			
RP	MEDLINE=22937718; PubMed=12219091; DOI=10.1038/ng986;				
RX	Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,				
RA	Aksay S.;				
RT	"Genome sequence of the endocellular obligate symbiont of tsetse				
RT	flies, Wigglesworthia glossinidia."				
RL	Nat. Genet. 32:402-407(2002).				
RL	EMBL; BA000021; BAC24210.1; -; Genomic_DNA.				
DR	HSSP; Q67803; IORV;				
DR	GO; GO:0009420; C:flagellar filament (sensu Bacteria); IEA.				
DR	GO; GO:0005198; F:structural molecule activity; IEA.				
DR	GO; GO:0001539; P:ciliary or flagellar motility; IEA.				
DR	InterPro; IPR001029; Flagellin_C.				
DR	InterPro; IPR001492; Flagellin_N.				
DR	Pfam; PF00700; Flagellin_C; 1.				
DR	Pfam; PF00669; Flagellin_N; 1.				
DR	PRINTS; PR00207; FLAGELLIN.				
DR	ProDom; PD000316; FLAGELLIN_C; 1.				
KW	COMPLETE proteome.				
KW	SEQUENCE 421 AA; 45963 MW; AA6952B2CEC2CA8C CRG64;				

Query Match 58.9%; Score 43; DB 2; Length 421;  
Best Local Similarity 66.7%; Pred. No. 21;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

**Qy**            2 SVQR<sup>L</sup>ASVRRITSSK 16  
               | : ||| : | |||||  
**pB**            28 STORI<sup>S</sup>SGI<sup>R</sup>INSSK 42

RESULT 49

AD001		Q40I15_LEIMA	PRT; 447 AA.
ID	Q40I15	LEIMA PRELIMINARY;	
AC	Q40I15	AC Q40I15;	
DT	13-SEP-2005	(TREMBLrel. 31, Created)	
DT	13-SEP-2005	(TREMBLrel. 31, Last sequence update)	
DT	13-SEP-2005	(TREMBLrel. 31, Last annotation update)	
DE	Tyrosine aminotransferase, putative (EC 2.6.1.5).		
GN	ORFNames=LmjJF36.2360;		
OS	Leishmania major.		
OC	Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.		
OX	NCBI_TaxID=5664;		
NP	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=Priedlin;		
RA	Peacock C.S.; Murphy L., Ivens A.C., Berriman M., Blackwell J.,		
RA	Smith D., Collins N., Foster N., Harris D., Oliver K., O'Neill S.,		
RA	Saunders D., Seeger K., Warren T., Rajandream M., and Barrall B.G.,		
RL	Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.		
RR	EMBL; CT005272; CAJ09194.1; -; Genomic DNA.		

KW AminoTRANSFERase; TRANSFERase.  
SQ SEQUENCE 447 AA; 49590 MW; 8AB5E91CFAC64A14 CRC64;  
  
Query Match 58.9%; Score 43; DB 2; Length 447;  
Best Local Similarity 90.0%; Pred. No. 22;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ASYRRITSSK 16  
|||:|||||  
Db 38 ASFRRITSSK 47

RESULT 50

YRHL\_AZOVI  
ID YRHL\_AZOVI STANDARD; PRT; 60 AA.  
AC Q44557;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Hypothetical protein in rhda 5' region (ORF1) (Fragment).  
DS Azotobacter vinelandii.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Azotobacter.  
OX NCBI\_TaxID=354;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RC STRAIN=OP / UMI136;  
FX MEDLINE=96184904; PubMed=8617271;  
RA Coisnaghi R., Paganì S., Kennedy C., Drummond M.;  
RT "Cloning, sequence analysis and overexpression of the rhodanese gene  
of Azotobacter vinelandii.";  
RL Eur. J. Biochem. 236:240-248 (1996)

--  
CC - SIMILARITY: To E.coli YjeQ and H.influenzae HI1714.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.

CC -----  
DR EMBL: L42346: AAB03237.1: -; Genomic DNA.

DR PIR; S62188; S62188.  
DR InterPro: IPR004881; GTPase EngC.

DR Pfam; PF03193; DUF258; 1.  
KW Hypothetical protein.

AN  
 HYPOTHECAIR PROTEIN: 1  
 FT NON TER 1  
 SO SEQUENCE 60 AA: 6999 MW: 91C25433756394200 CRC64:

Query Match 57.5%; Score 42; DB 1; Length 60;  
Best Local Similarity 60.0%; Pred. No. 3.4;  
Matches 9; Conservative 2; Mismatches 4; Indels

Qy 1 ISVQLASYRRITSS 15

Db 40 IQPQRMASYPHILAS 54

Search completed: February 6, 2006, 14:29:19  
Job time : 276 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 6, 2006, 14:29:34 ; Search time 47 Seconds

(without alignments)  
28.145 Million cell updates/sec

Title: US-10-644-277-149\_COPY\_20\_35

Perfect score: 73

Sequence: 1 ISVQRLASYRRTSSK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5 COMB pep:\*

2: /cgn2\_6/ptodata/1/iaa/6 COMB pep:\*

3: /cgn2\_6/ptodata/1/iaa/H COMB pep:\*

4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB pep:\*

5: /cgn2\_6/ptodata/1/iaa/RE COMB pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	73	100.0	68	2	US-09-463-458A-9
2	73	100.0	68	2	US-09-463-458A-26
3	73	100.0	68	2	US-09-463-458A-29
4	73	100.0	68	2	US-09-463-458A-30
5	73	100.0	69	2	US-09-463-458A-31
6	73	100.0	69	2	US-09-463-458A-32
7	73	100.0	76	1	US-07-956-862A-1
8	73	100.0	76	1	US-08-250-958-1
9	73	100.0	76	1	US-08-235-659-1
10	73	100.0	76	1	US-08-716-188-2
11	73	100.0	76	2	US-08-615-232A-5
12	73	100.0	76	2	US-08-470-323-5
13	73	100.0	76	2	US-09-195-457-5
14	73	100.0	76	2	US-09-291-038-5
15	73	100.0	76	2	US-09-043-861-31
16	73	100.0	78	1	US-08-330-163-12
17	73	100.0	78	1	US-08-482-111-12
18	73	100.0	78	2	US-09-567-225-14
19	73	100.0	78	4	PCT-US95-00605-1
20	73	100.0	99	1	US-08-127-499A-35
21	73	100.0	99	1	US-08-482-847-35
22	73	100.0	99	1	US-08-347-492B-8
23	73	100.0	99	1	US-08-480-449-19
24	73	100.0	99	1	US-08-479-126B-5
25	73	100.0	99	1	US-08-421-144A-5
26	73	100.0	99	1	US-08-726-830A-5
27	73	100.0	99	1	US-08-660-542-19

## SUMMARIES

28	73	100.0	99	1	US-08-798-143-8	Sequence 8, Appli
29	73	100.0	99	2	US-07-927-391-24	Sequence 24, Appli
30	73	100.0	99	2	US-08-995-156A-5	Sequence 5, Appli
31	73	100.0	99	2	US-09-044-856A-5	Sequence 5, Appli
32	73	100.0	99	2	US-08-679-493A-152	Sequence 152, App
33	73	100.0	99	2	US-08-479-603-19	Sequence 19, Appli
34	73	100.0	99	2	US-09-419-281-5	Sequence 5, Appli
35	73	100.0	99	2	US-09-366-887A-10	Sequence 10, Appli
36	73	100.0	99	2	US-08-939-107-19	Sequence 19, Appli
37	73	100.0	99	2	US-09-545-894-5	Sequence 5, Appli
38	73	100.0	99	2	US-09-834-795A-28	Sequence 28, Appli
39	73	100.0	99	2	US-09-067-447B-19	Sequence 19, Appli
40	73	100.0	99	2	US-08-517-204-10	Sequence 10, Appli
41	73	100.0	99	2	US-08-437-306-2	Sequence 2, Appli
42	73	100.0	99	2	US-08-479-620-19	Sequence 19, Appli
43	73	100.0	99	2	US-10-054-967-5	Sequence 5, Appli
44	73	100.0	99	2	US-10-141-965-5	Sequence 5, Appli
45	73	100.0	99	2	PCT-US96-10087-5	Sequence 5, Appli
46	73	100.0	99	4	5212073-2	Patent No. 5212073
47	73	100.0	99	6	US-09-133-521-5	Sequence 5, Appli
48	61	83.6	99	2	US-09-366-887A-20	Sequence 20, Appli
49	56	76.7	37	2	US-09-517-204-20	Sequence 20, Appli
50	56	76.7	37	2	US-08-613-822-20	Sequence 20, Appli
51	56	76.7	74	2	US-09-479-729B-20	Sequence 20, Appli
52	56	76.7	74	2	US-09-366-887A-25	Sequence 25, Appli
53	56	76.7	74	2	US-09-717-209-20	Sequence 20, Appli
54	56	76.7	74	2	US-09-517-204-25	Sequence 25, Appli
55	56	76.7	74	2	US-10-125-451-20	Sequence 20, Appli
56	56	76.7	74	2	US-09-366-887A-27	Sequence 27, Appli
57	56	76.7	97	2	US-09-545-894-8	Sequence 8, Appli
58	56	76.7	97	2	US-09-834-795A-26	Sequence 26, Appli
59	56	76.7	97	2	US-09-517-204-27	Sequence 27, Appli
60	56	76.7	97	2	US-09-366-887A-23	Sequence 23, Appli
61	52	71.2	70	2	US-09-517-204-23	Sequence 23, Appli
62	52	71.2	70	2	US-08-615-232A-1	Sequence 1, Appli
63	52	71.2	73	1	US-08-615-232A-2	Sequence 2, Appli
64	52	71.2	73	1	US-08-470-323-2	Sequence 1, Appli
65	52	71.2	73	2	US-08-470-323-2	Sequence 2, Appli
66	52	71.2	73	2	US-09-195-457-1	Sequence 1, Appli
67	52	71.2	73	2	US-09-291-038-2	Sequence 2, Appli
68	52	71.2	73	2	US-08-679-493A-154	Sequence 154, App
69	52	71.2	73	2	US-09-366-887A-8	Sequence 8, Appli
70	52	71.2	96	2	US-09-517-204-8	Sequence 8, Appli
71	52	71.2	96	2	US-08-744-419-2	Sequence 4, Appli
72	52	71.2	96	2	US-03-545-894-4	Sequence 4, Appli
73	52	71.2	104	2	US-09-366-887A-11	Sequence 11, Appli
74	52	71.2	104	2	US-09-517-204-11	Sequence 11, Appli
75	52	71.2	104	2	US-09-545-894-15	Sequence 15, Appli
76	52	71.2	104	2	US-07-927-391-4	Sequence 4, Appli
77	52	71.2	104	2	US-07-927-391-3	Sequence 3, Appli
78	49	67.1	99	2	US-08-127-499A-38	Sequence 38, Appli
79	49	67.1	99	2	US-08-482-847-38	Sequence 38, Appli
80	49	67.1	148	2	US-08-470-323-7	Sequence 7, Appli
81	49	67.1	148	2	US-08-195-457-7	Sequence 7, Appli
82	47	64.4	45	2	US-08-615-232A-7	Sequence 7, Appli
83	47	64.4	61	2	US-09-291-038-7	Sequence 7, Appli
84	47	64.4	63	2	US-08-613-822-19	Sequence 19, Appli
85	47	64.4	67	1	US-09-479-729B-19	Sequence 19, Appli
86	47	64.4	67	1	US-09-717-209-19	Sequence 19, Appli
87	47	64.4	67	2	US-09-043-861-33	Sequence 33, Appli
88	47	64.4	70	1	US-10-125-451-19	Sequence 19, Appli
89	47	64.4	70	2	US-08-567-225-15	Sequence 15, Appli
90	47	64.4	76	2	US-08-480-449-18	Sequence 18, Appli
91	47	64.4	76	2	US-08-660-542-18	Sequence 18, Appli
92	47	64.4	76	2	US-08-479-603-18	Sequence 18, Appli
93	47	64.4	76	2		
94	47	64.4	76	2		
95	47	64.4	76	2		
96	47	64.4	82	2		
97	47	64.4	99	1		
98	47	64.4	99	1		
99	47	64.4	99	2		
100	47	64.4	99	2		

101	47	64.4	99	2	US-09-479-729B-18	Sequence 18, Appl	174	36	49.3	479	2	US-09-252-991A-28691	Sequence 28691, A
102	47	64.4	99	2	US-08-939-107-18	Sequence 18, Appl	175	36	49.3	590	2	US-09-252-991A-23447	Sequence 23447, A
103	47	64.4	99	2	US-09-886-319A-22	Sequence 22, Appl	176	36	49.3	651	2	US-09-248-796A-17444	Sequence 17444, A
104	47	64.4	99	2	US-09-717-209-18	Sequence 18, Appl	177	36	49.3	1154	2	US-09-489-039A-7724	Sequence 7724, Ap
105	47	64.4	99	2	US-09-545-894-7	Sequence 7, Appl	178	36	49.3	1173	2	US-09-543-681A-7965	Sequence 7965, Ap
106	47	64.4	99	2	US-09-834-795A-27	Sequence 27, Appl	179	36	49.3	1614	2	US-09-052-469-2	Sequence 2, Appl
107	47	64.4	99	2	US-09-067-447B-18	Sequence 18, Appl	180	36	49.3	1614	2	US-08-422-362-2	Sequence 2, Appl
108	47	64.4	99	2	US-08-479-620-18	Sequence 18, Appl	181	36	49.3	1614	2	US-09-052-362-2	Sequence 2, Appl
109	47	64.4	99	2	US-10-125-451-18	Sequence 18, Appl	182	36	49.3	4302	2	US-08-658-136-5	Sequence 5, Appl
110	47	64.4	109	1	US-08-421-144A-7	Sequence 7, Appl	183	36	49.3	4302	2	US-09-052-469-6	Sequence 6, Appl
111	47	64.4	109	2	US-07-927-391-16	Sequence 16, Appl	184	36	49.3	4302	2	US-08-422-582-8	Sequence 8, Appl
112	47	64.4	109	2	US-08-679-493A-153	Sequence 153, App	185	36	49.3	4302	2	US-09-052-462-8	Sequence 8, Appl
113	47	64.4	110	2	US-09-366-887A-13	Sequence 13, Appl	186	36	49.3	4303	1	US-08-460-751-2	Sequence 2, Appl
114	47	64.4	110	2	US-09-517-204-13	Sequence 13, Appl	187	36	49.3	4303	2	US-09-479-467A-2	Sequence 2, Appl
115	47	64.4	122	2	US-09-949-016-9711	Sequence 9711, Ap	188	36	49.3	4303	2	US-09-655-160-2	Sequence 2, Appl
116	47	64.4	137	2	US-09-646-028-2	Sequence 2, Appl	189	36	49.3	4339	2	US-09-052-469-6	Sequence 6, Appl
117	47	64.4	151	2	US-09-646-028-2	Sequence 7, Appl	190	36	49.3	4339	2	US-08-422-582-6	Sequence 6, Appl
118	47	64.4	348	2	US-09-646-028-51	Sequence 51, Appl	191	36	49.3	4339	2	US-09-052-462-6	Sequence 6, Appl
119	47	64.4	359	2	US-09-646-028-16	Sequence 16, Appl	192	35.5	48.6	82	2	US-09-567-225-7	Sequence 7, Appl
120	47	64.4	361	2	US-09-646-028-14	Sequence 14, Appl	193	35.5	48.6	89	2	US-09-545-894-29	Sequence 29, Appl
121	47	64.4	601	2	US-09-646-028-52	Sequence 52, Appl	194	35.5	48.6	98	2	US-08-613-822-4	Sequence 4, Appl
122	46	63.0	70	2	US-08-613-822-17	Sequence 17, Appl	195	35.5	48.6	98	2	US-08-852-212-2	Sequence 2, Appl
123	46	63.0	70	2	US-09-479-729B-17	Sequence 17, Appl	196	35.5	48.6	98	2	US-09-479-729B-4	Sequence 4, Appl
124	46	63.0	70	2	US-09-717-209-17	Sequence 17, Appl	197	35.5	48.6	98	2	US-09-261-201A-4	Sequence 4, Appl
125	46	63.0	70	2	US-10-125-451-17	Sequence 17, Appl	198	35.5	48.6	98	2	US-09-717-209-4	Sequence 4, Appl
126	46	63.0	72	2	US-08-793-381A-7	Sequence 7, Appl	199	35.5	48.6	98	2	US-09-545-894-2	Sequence 2, Appl
127	45	61.6	92	2	US-09-366-887A-14	Sequence 14, Appl	200	35.5	48.6	98	2	US-09-834-795A-25	Sequence 25, Appl
128	45	61.6	92	2	US-09-517-204-14	Sequence 14, Appl	201	35.5	48.6	98	2	US-10-164-621-4	Sequence 4, Appl
129	45	61.6	97	2	US-09-886-319A-21	Sequence 21, Appl	202	35.5	48.6	98	2	US-10-125-451-4	Sequence 4, Appl
130	45	61.6	97	2	US-09-545-894-13	Sequence 13, Appl	203	35	47.9	121	2	US-09-902-540-10841	Sequence 10841, A
131	45	61.6	97	2	US-09-545-894-16	Sequence 16, Appl	204	35	47.9	129	2	US-09-252-991A-28493	Sequence 28493, A
132	45	61.6	156	2	US-09-646-028-4	Sequence 4, Appl	205	35	47.9	162	2	US-09-270-767-36191	Sequence 36191, A
133	45	61.6	171	2	US-09-646-028-9	Sequence 9, Appl	206	35	47.9	162	2	US-09-270-767-51408	Sequence 51408, A
134	44	60.3	71	2	US-09-537-859D-3	Sequence 3, Appl	207	35	47.9	274	2	US-09-902-540-11769	Sequence 11769, A
135	44	60.3	71	2	US-09-537-859D-6	Sequence 6, Appl	208	35	47.9	334	2	US-09-248-796A-19521	Sequence 19521, A
136	44	60.3	74	1	US-08-615-232A-6	Sequence 6, Appl	209	35	47.9	415	2	US-09-543-681A-8002	Sequence 8002, Ap
137	44	60.3	74	2	US-09-195-457-6	Sequence 6, Appl	210	35	47.9	469	2	US-09-538-092-948	Sequence 948, App
138	44	60.3	74	2	US-09-291-038-6	Sequence 6, Appl	211	35	47.9	496	2	US-09-949-016-11133	Sequence 11133, A
139	44	60.3	76	1	US-08-480-449-20	Sequence 20, Appl	212	35	47.9	730	2	US-09-107-532A-4752	Sequence 4752, Ap
140	44	60.3	76	1	US-08-716-188-3	Sequence 3, Appl	213	34.5	47.3	1257	2	US-09-252-991A-17290	Sequence 17290, A
141	44	60.3	76	1	US-08-660-542-20	Sequence 20, Appl	214	34	46.6	147	2	US-09-230-637-42	Sequence 42, Appl
142	44	60.3	76	1	US-08-479-603-20	Sequence 20, Appl	215	34	46.6	73	2	US-09-366-887A-24	Sequence 24, Appl
143	44	60.3	76	2	US-08-939-107-20	Sequence 20, Appl	216	34	46.6	73	2	US-09-517-204-24	Sequence 24, Appl
144	44	60.3	76	2	US-09-067-447B-20	Sequence 20, Appl	217	34	46.6	91	2	US-09-252-991A-29046	Sequence 29046, A
145	44	60.3	76	2	US-08-479-620-20	Sequence 20, Appl	218	34	46.6	97	2	US-09-366-887A-6	Sequence 6, Appl
146	44	60.3	76	2	US-09-043-861-32	Sequence 32, Appl	219	34	46.6	97	2	US-09-545-894-14	Sequence 14, Appl
147	44	60.3	76	2	US-08-421-144A-6	Sequence 6, Appl	220	34	46.6	97	2	US-09-517-204-6	Sequence 6, Appl
148	44	60.3	77	1	US-08-347-492B-9	Sequence 9, Appl	221	34	46.6	98	2	US-09-366-887A-7	Sequence 7, Appl
149	44	60.3	77	1	US-08-798-143-9	Sequence 9, Appl	222	34	46.6	98	2	US-09-517-204-7	Sequence 7, Appl
150	44	60.3	77	1	US-09-366-887A-12	Sequence 12, Appl	223	34	46.6	143	2	US-09-270-767-37600	Sequence 37600, A
151	44	60.3	77	2	US-08-545-894-6	Sequence 6, Appl	224	34	46.6	143	2	US-09-270-767-52817	Sequence 52817, A
152	44	60.3	77	2	US-09-834-795A-24	Sequence 24, Appl	225	34	46.6	144	1	US-08-440-103-20	Sequence 20, Appl
153	44	60.3	77	2	US-09-517-204-12	Sequence 12, Appl	226	34	46.6	144	1	US-08-440-103-20	Sequence 20, Appl
154	44	60.3	99	2	US-09-886-319A-30	Sequence 30, Appl	227	34	46.6	144	1	US-08-231-368-20	Sequence 20, Appl
155	44	60.3	99	2	US-09-537-859D-1	Sequence 1, Appl	228	34	46.6	144	1	US-08-440-210-20	Sequence 20, Appl
156	44	60.3	99	2	US-09-537-859D-2	Sequence 2, Appl	229	34	46.6	144	1	US-09-046-604-20	Sequence 20, Appl
157	44	60.3	109	2	US-09-537-859D-2	Sequence 2, Appl	230	34	46.6	165	2	US-10-104-047-2538	Sequence 2538, Ap
158	44	60.3	109	2	US-08-886-319A-71	Sequence 71, Appl	231	34	46.6	174	1	US-08-460-806-19	Sequence 19, Appl
159	43	58.9	76	1	US-08-716-188-4	Sequence 4, Appl	232	34	46.6	174	1	US-08-325-630-19	Sequence 19, Appl
160	41.5	56.8	96	2	US-09-230-637-44	Sequence 44, Appl	233	34	46.6	180	1	US-08-483-695-40	Sequence 40, Appl
161	41	56.2	71	1	US-08-615-232A-8	Sequence 8, Appl	234	34	46.6	180	1	US-07-965-285-40	Sequence 40, Appl
162	41	56.2	71	2	US-08-470-323-8	Sequence 8, Appl	235	34	46.6	180	1	US-08-487-231-40	Sequence 40, Appl
163	41	56.2	71	2	US-09-195-457-8	Sequence 8, Appl	236	34	46.6	180	2	US-09-201-912-40	Sequence 40, Appl
164	41	56.2	71	2	US-09-291-038-8	Sequence 8, Appl	237	34	46.6	221	2	US-09-270-767-36608	Sequence 36608, A
165	41	56.2	321	2	US-09-252-991A-28673	Sequence 28673, A	238	34	46.6	221	2	US-09-270-767-51825	Sequence 51825, A
166	41	56.2	356	2	US-09-252-991A-32731	Sequence 32731, A	239	34	46.6	250	2	US-09-952-572-8	Sequence 8, Appl
167	37	50.7	198	2	US-09-134-000C-4428	Sequence 4428, Ap	240	34	46.6	294	2	US-09-252-991A-29464	Sequence 29464, A
168	37	50.7	500	1	US-08-260-582-77	Sequence 77, Appl	241	34	46.6	305	2	US-08-478-073-2	Sequence 2, Appl
169	37	50.7	500	4	PCT-US95-05471-77	Sequence 77, Appl	242	34	46.6	333	1	US-08-453-552-12	Sequence 12, Appl
170	37	50.7	527	2	US-09-902-540-15230	Sequence 15230, A	243	34	46.6	333	1	US-08-710-637-12	Sequence 12, Appl
171	36	49.3	118	2	US-09-621-976-5403	Sequence 5403, Ap	244	34	46.6	333	4	PCT-US93-00907-12	Sequence 12, Appl
172	36	49.3	257	2	US-09-902-540-13970	Sequence 13970, A	245	34	46.6	337	1	US-08-188-281B-7	Sequence 7, Appl
173	36	49.3	417	2	US-09-252-991A-19725	Sequence 19725, A	246	34	46.6	337	4	PCT-US94-07280-7	Sequence 7, Appl



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248	34	46.6	350	2	US-10-104-966-4	Sequence 4, Appli	321	34	46.6	1648	1	US-08-188-281B-2	Sequence 12, Appli
249	34	46.6	350	2	US-09-929-955-4	Sequence 4, Appli	322	34	46.6	1648	4	PCT-US94-07280-12	Sequence 12, Appli
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255	34	46.6	367	4	PCT-US94-07280-9	Sequence 9, Appli	328	34	46.6	3011	2	US-09-014-416-1	Sequence 1, Appli
256	34	46.6	367	4	PCT-US95-01087-9	Sequence 9, Appli	329	34	46.6	3011	2	US-09-034-756-20	Sequence 20, Appli
257	34	46.6	377	1	US-08-188-281B-17	Sequence 17, Appli	330	34	46.6	3011	2	US-10-104-966-1	Sequence 1, Appli
258	34	46.6	377	4	PCT-US94-07280-17	Sequence 17, Appli	331	34	46.6	3011	2	US-09-953-572-9	Sequence 9, Appli
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264	34	46.6	397	4	PCT-US95-01087-11	Sequence 11, Appli	337	34	46.6	3012	2	US-08-811-566-2	Sequence 2, Appli
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266	34	46.6	399	1	US-08-710-637-10	Sequence 10, Appli	339	33	45.9	242	2	US-09-270-767-43155	Sequence 43155, A
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272	34	46.6	402	1	US-08-325-630-15	Sequence 15, Appli	345	33	45.2	146	2	US-09-252-991A-25506	Sequence 25506, A
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280	34	46.6	409	1	US-08-440-210-21	Sequence 21, Appli	353	33	45.2	277	2	US-09-543-681A-8237	Sequence 8237, Ap
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295	34	46.6	441	4	PCT-US95-01087-21	Sequence 21, Appli	368	33	45.2	472	1	US-08-483-859-5	Sequence 5, Appli
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309	34	46.6	571	2	US-09-248-796A-20375	Sequence 20375, A	382	33	45.2	552	2	US-09-792-024-84	Sequence 84, Appli
310	34	46.6	608	2	US-09-107-532A-5702	Sequence 5702, Ap	383	33	45.2	576	2	US-09-248-796A-27399	Sequence 27399, A
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317	34	46.6	1157	1	US-07-876-280-30	Sequence 30, Appli	390	32	43.8	43	2	US-10-318-675-38	Sequence 38, Appli
318	34	46.6	1157	1	US-07-812-180A-2	Sequence 2, Appli	391	32	43.8	43	2	US-10-318-675-40	Sequence 40, Appli
319	34	46.6	1157	1	US-08-315-468-2	Sequence 2, Appli	392	32	43.8	61	1	US-08-194-211A-3	Sequence 3, Appli



393	32	43.8	61	2	US-08-456-748B-3	Sequence 3, Appl1	466	32	43.8	567	2	US-09-711-164-374	Sequence 374, App
394	32	43.8	61	2	US-09-492-709A-357	Sequence 10090, App	467	32	43.8	623	2	US-10-464-939-12	Sequence 12, Appl
395	32	43.8	67	2	US-03-489-039A-10090	Sequence 3507, App	468	32	43.8	664	2	US-08-957-063-18	Sequence 18, Appl
396	32	43.8	68	2	US-09-543-681A-5321	Sequence 5321, Ap	469	32	43.8	664	2	US-09-487-685-18	Sequence 18, Appl
397	32	43.8	72	2	US-09-134-000C-4792	Sequence 4792, Ap	470	32	43.8	664	2	US-08-802-805D-18	Sequence 18, Appl
398	32	43.8	87	2	US-09-248-796A-22966	Sequence 22966, A	471	32	43.8	664	2	US-09-388-316C-18	Sequence 18, Appl
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403	32	43.8	117	2	US-09-248-796A-19723	Sequence 19723, A	476	32	43.8	831	1	US-08-254-359A-5	Sequence 5, Appl1
404	32	43.8	151	2	US-09-583-110-2927	Sequence 2927, Ap	477	32	43.8	831	1	US-08-483-043-5	Sequence 5, Appl1
405	32	43.8	165	2	US-09-107-433-4649	Sequence 4649, Ap	478	32	43.8	831	1	US-08-481-238-5	Sequence 5, Appl1
406	32	43.8	170	2	US-09-248-796A-19501	Sequence 19501, A	479	32	43.8	831	1	US-08-471-066B-5	Sequence 5, Appl1
407	32	43.8	190	2	US-09-252-991A-22245	Sequence 22245, A	480	32	43.8	831	1	US-08-484-956-5	Sequence 5, Appl1
408	32	43.8	209	2	US-09-270-767-35218	Sequence 35218, A	481	32	43.8	831	1	US-08-757-653-5	Sequence 5, Appl1
409	32	43.8	209	2	US-09-270-767-50435	Sequence 50435, A	482	32	43.8	831	1	US-08-599-491-5	Sequence 5, Appl1
410	32	43.8	218	2	US-09-107-532A-3957	Sequence 3957, Ap	483	32	43.8	831	1	US-08-756-386-5	Sequence 5, Appl1
411	32	43.8	232	1	US-08-456-670B-39	Sequence 39, Appl1	484	32	43.8	831	1	US-08-823-516-5	Sequence 5, Appl1
412	32	43.8	232	2	US-09-372-036-39	Sequence 39, Appl1	485	32	43.8	831	1	US-08-682-853A-5	Sequence 5, Appl1
413	32	43.8	235	2	US-09-252-991A-29622	Sequence 29622, A	486	32	43.8	831	2	US-08-759-038-5	Sequence 5, Appl1
414	32	43.8	258	2	US-09-328-352-6852	Sequence 6852, Ap	487	32	43.8	831	2	US-08-758-314-5	Sequence 5, Appl1
415	32	43.8	263	2	US-09-270-767-57472	Sequence 57472, A	488	32	43.8	831	2	US-09-350-309-5	Sequence 5, Appl1
416	32	43.8	269	2	US-09-252-991A-16773	Sequence 16773, A	489	32	43.8	831	2	US-08-520-346-5	Sequence 5, Appl1
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418	32	43.8	306	2	US-09-270-767-33158	Sequence 33158, A	491	32	43.8	831	2	US-09-308-825A-5	Sequence 5, Appl1
419	32	43.8	306	2	US-09-270-767-48375	Sequence 48375, A	492	32	43.8	831	2	US-09-758-282B-5	Sequence 5, Appl1
420	32	43.8	308	2	US-09-640-211A-644	Sequence 644, App	493	32	43.8	831	2	US-09-655-378A-5	Sequence 5, Appl1
421	32	43.8	311	2	US-09-614-912-198	Sequence 198, App	494	32	43.8	831	2	US-09-940-244-5	Sequence 5, Appl1
422	32	43.8	314	2	US-09-583-545-15	Sequence 15, Appl1	495	32	43.8	831	2	US-09-333-145-5	Sequence 5, Appl1
423	32	43.8	314	2	US-09-134-000C-4530	Sequence 4530, Ap	496	32	43.8	831	2	US-09-577-304A-5	Sequence 5, Appl1
424	32	43.8	314	2	US-09-514-245-24	Sequence 24, Appl1	497	32	43.8	831	2	US-09-381-212-5	Sequence 5, Appl1
425	32	43.8	314	2	US-10-112-540-2	Sequence 2, Appl1	498	32	43.8	831	2	US-10-081-806-5	Sequence 5, Appl1
426	32	43.8	320	2	US-09-212-247C-13	Sequence 13, Appl1	499	32	43.8	831	2	US-10-190-967-16	Sequence 16, Appl1
427	32	43.8	320	2	US-10-076-157-13	Sequence 13, Appl1	500	32	43.8	831	2	US-09-713-601A-5	Sequence 5, Appl1
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436	32	43.8	464	2	US-08-957-063-6	Sequence 6, Appl1	509	31	42.5	43	2	US-10-318-675-42	Sequence 42, Appl1
437	32	43.8	464	2	US-09-487-685-6	Sequence 6, Appl1	510	31	42.5	43	2	US-10-318-675-45	Sequence 45, Appl1
438	32	43.8	464	2	US-08-802-805D-6	Sequence 6, Appl1	511	31	42.5	43	2	US-10-318-675-48	Sequence 48, Appl1
439	32	43.8	464	2	US-08-861-990-2	Sequence 2, Appl1	512	31	42.5	48	1	US-08-637-759B-480	Sequence 480, App
440	32	43.8	464	2	US-09-388-316C-6	Sequence 6, Appl1	513	31	42.5	48	2	US-08-871-355A-480	Sequence 480, App
441	32	43.8	472	2	US-09-826-509-469	Sequence 469, App	514	31	42.5	48	2	US-09-201-945-480	Sequence 480, App
442	32	43.8	474	2	US-09-248-796A-15826	Sequence 15826, A	515	31	42.5	59	1	US-08-637-759B-99	Sequence 99, Appl1
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445	32	43.8	475	1	US-08-472-173-6	Sequence 6, Appl1	518	31	42.5	65	2	US-03-186-276B-65	Sequence 65, Appl1
446	32	43.8	475	1	US-08-487-167-6	Sequence 6, Appl1	519	31	42.5	65	2	US-08-842-445-65	Sequence 65, Appl1
447	32	43.8	475	1	US-08-482-816-6	Sequence 6, Appl1	520	31	42.5	65	2	US-09-186-188B-65	Sequence 65, Appl1
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553	31	42.5	214	2	US-09-577-304A-19	Sequence 19, Appl	626	31	42.5	574	2	US-09-614-912-172	Sequence 172, App
554	31	42.5	216	2	US-09-294-298A-7	Sequence 7, Appl	627	31	42.5	632	2	US-09-640-958-4	Sequence 4, Appl
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573	31	42.5	297	2	US-09-068-195-12	Sequence 12, Appl	646	31	42.5	832	1	US-07-977-434-2	Sequence 2, Appl
574	31	42.5	299	2	US-09-205-258-265	Sequence 265, App	647	31	42.5	832	1	US-08-156-020-2	Sequence 2, Appl
575	31	42.5	299	2	US-10-004-860-265	Sequence 265, App	648	31	42.5	832	1	US-08-156-020-4	Sequence 4, Appl
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579	31	42.5	314	1	US-08-859-201-8	Sequence 8, Appl	652	31	42.5	832	1	US-08-073-384C-4	Sequence 4, Appl
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581	31	42.5	314	2	US-09-968-033C-5	Sequence 5, Appl	654	31	42.5	832	1	US-08-483-043-4	Sequence 4, Appl
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583	31	42.5	336	2	US-09-515-039-70	Sequence 70, Appl	656	31	42.5	832	1	US-08-481-238-4	Sequence 4, Appl
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587	31	42.5	366	2	US-09-605-703B-2132	Sequence 2132, Ap	660	31	42.5	832	1	US-08-599-491-4	Sequence 4, Appl
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591	31	42.5	374	2	US-08-821-994-70	Sequence 70, Appl	664	31	42.5	832	2	US-08-759-038-4	Sequence 4, Appl
592	31	42.5	374	2	US-09-787-084-4	Sequence 4, Appl	665	31	42.5	832	2	US-08-758-314-4	Sequence 4, Appl
593	31	42.5	381	2	US-09-902-540-11854	Sequence 11854, A	666	31	42.5	832	2	US-09-350-309-4	Sequence 4, Appl
594	31	42.5	385	2	US-09-248-796A-17393	Sequence 17393, A	667	31	42.5	832	2	US-08-520-946-4	Sequence 4, Appl
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596	31	42.5	395	1	US-08-841-349-9	Sequence 9, Appl	669	31	42.5	832	2	US-09-684-938-4	Sequence 4, Appl
597	31	42.5	395	2	US-09-431-184A-9	Sequence 9, Appl	670	31	42.5	832	2	US-09-308-825A-4	Sequence 4, Appl
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602	31	42.5	425	2	US-09-489-039A-8386	Sequence 8386, Ap	675	31	42.5	832	2	US-09-577-304A-4	Sequence 4, Appl
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605	31	42.5	432	2	US-09-919-172-9	Sequence 9, Appl	678	31	42.5	832	2	US-10-190-967-3	Sequence 3, Appl
606	31	42.5	432	2	US-09-315-355A-18	Sequence 18, Appl	679	31	42.5	832	2	US-09-713-601A-4	Sequence 4, Appl
607	31	42.5	442	2	US-09-949-016-9762	Sequence 9762, Ap	680	31	42.5	832	1	PCT-US91-07035-2	Sequence 2, Appl
608	31	42.5	467	2	US-08-867-611-24	Sequence 24, Appl	681	31	42.5	833	1	US-08-073-384C-8	Sequence 8, Appl
609	31	42.5	467	2	US-09-690-359-24	Sequence 24, Appl	682	31	42.5	833	1	US-08-254-359A-8	Sequence 8, Appl
610	31	42.5	467	4	PCT-US92-06965A-29	Sequence 29, Appl	683	31	42.5	833	1	US-08-483-043-8	Sequence 8, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 9, Application US/09463458A
; Patent No. 6383782
; GENERAL INFORMATION:
; APPLICANT: Barratt, Derek G
; APPLICANT: Needham, Maurice R.C.
; TITLE OF INVENTION: MCP-1 ANALOGS
; FILE REFERENCE: 1991-186
; CURRENT APPLICATION NUMBER: US/09/463,458A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: PCT/GB98/02179
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
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US-09-463-458A-9

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Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 26, Application US/09463458A
; Patent No. 6383782
; GENERAL INFORMATION:
; APPLICANT: Barratt, Derek G
; APPLICANT: Needham, Maurice R.C.
; TITLE OF INVENTION: MCP-1 ANALOGS
; FILE REFERENCE: 1991-186
; CURRENT APPLICATION NUMBER: US/09/463,458A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: PCT/GB98/02179
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 68
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US-09-463-458A-26

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Db 12 ISVQRLASYRRITSSK 27

RESULT 3
US-09-463-458A-29
; Sequence 29, Application US/09463458A
; Patent No. 6383782
; GENERAL INFORMATION:
; APPLICANT: Barratt, Derek G
; APPLICANT: Needham, Maurice R.C.
; TITLE OF INVENTION: MCP-1 ANALOGS
; FILE REFERENCE: 1991-186
; CURRENT APPLICATION NUMBER: US/09/463,458A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: PCT/GB98/02179
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 32
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; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence:
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US-09-463-458A-29

Query Match 100.0%; Score 73; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 12 ISVQRLASYRRITSSK 27

RESULT 4
US-09-463-458A-30
; Sequence 30, Application US/09463458A
; Patent No. 6383782
; GENERAL INFORMATION:
; APPLICANT: Barratt, Derek G
; APPLICANT: Needham, Maurice R.C.
; TITLE OF INVENTION: MCP-1 ANALOGS
; FILE REFERENCE: 1991-186
; CURRENT APPLICATION NUMBER: US/09/463,458A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: PCT/GB98/02179
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 68
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; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: [V9T]MCP-1(9-76)
US-09-463-458A-30

Query Match 100.0%; Score 73; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
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US-09-463-458A-30

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Db 12 ISVQRLASYRRITSSK 27

#### RESULT 5

US-09-463-458A-31

; Sequence 31, Application US/09463458A

; Patent No. 6383782

; GENERAL INFORMATION:

; APPLICANT: Barratt, Derek G

; APPLICANT: Needham, Maurice R.C.

; TITLE OF INVENTION: MCP-1 ANALOGS

; FILE REFERENCE: 1991-186

; CURRENT APPLICATION NUMBER: US/09/463,458A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: PCT/GB98/02179

; PRIOR FILING DATE: 1998-07-21

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 31

; LENGTH: 69

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Met-MCP1 (9-76)

US-09-463-458A-31

Query Match 100.0%; Score 73; DB 2; Length 69;  
Best Local Similarity 100.0%; Pred. No. 4.7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
| | | | | | | | | | | | | | | |  
Db 13 ISVQRLASYRRITSSK 28

#### RESULT 6

US-09-463-458A-32

; Sequence 32, Application US/09463458A

; Patent No. 6383782

; GENERAL INFORMATION:

; APPLICANT: Barratt, Derek G

; APPLICANT: Needham, Maurice R.C.

; TITLE OF INVENTION: MCP-1 ANALOGS

; FILE REFERENCE: 1991-186

; CURRENT APPLICATION NUMBER: US/09/463,458A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: PCT/GB98/02179

; PRIOR FILING DATE: 1998-07-21

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 32

; LENGTH: 69

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: pglu-MCP1 (9-76)

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: ( )..)

; OTHER INFORMATION: Xaa=pglu

US-09-463-458A-32

Query Match 100.0%; Score 73; DB 2; Length 69;  
Best Local Similarity 100.0%; Pred. No. 4.7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
| | | | | | | | | | | | | | | |  
Db 13 ISVQRLASYRRITSSK 28

#### RESULT 7

US-07-956-862A-1

; Sequence 1, Application US/07956862A

; Patent No. 5413778

; GENERAL INFORMATION:

; APPLICANT: KUNKEL, STEVEN L.

; APPLICANT: LYLE, LEON R.

; APPLICANT: STRIETER, ROBERT M.

; TITLE OF INVENTION: LABELLED MONOCYTE CHEMOATTRACTANT

; TITLE OF INVENTION: PROTEIN MATERIAL AND MEDICAL USES

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rothwell, Figg, Ernst & Kurz

; STREET: Suite 701-E, 555 Thirteenth St., N.W

; CITY: Washington

; STATE: D. C.

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/956,862A

; FILING DATE: 05-OCT-1992

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: REPPER, GEORGE R.

; REGISTRATION NUMBER: 31,414

; REFERENCE/DOCKET NUMBER: 1670-197A

; TELEPHONE: (202)783-6040

; TELEFAX: (202)783-6031

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 76 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: N-terminal

US-07-956-862A-1

Query Match 100.0%; Score 73; DB 1; Length 76;  
Best Local Similarity 100.0%; Pred. No. 5.3e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
| | | | | | | | | | | | | | | |  
Db 20 ISVQRLASYRRITSSK 35

#### RESULT 8

US-08-250-958-1

; Sequence 1, Application US/08250958

; Patent No. 5571713

; GENERAL INFORMATION:

; APPLICANT: LYLE, LEON R.

; APPLICANT: KUNKEL, STEVEN L.

; APPLICANT: STRIETER, ROBERT M.

; TITLE OF INVENTION: THERAPEUTIC TREATMENT FOR INHIBITING

;; TITLE OF INVENTION: VASCULAR RESTENOSIS  
;; NUMBER OF SEQUENCES: 10  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Rothwell, Figg, Ernst & Kurz  
;; STREET: Suite 701-E, 555 Thirteenth St., N.W  
;; CITY: Washington  
;; STATE: D. C.  
;; COUNTRY: U.S.A.  
;; ZIP: 20004  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/250,958  
;; FILING DATE: 27-MAY-1994  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/965,678  
;; FILING DATE: 22-OCT-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: WALKER, Barbara W.  
;; REGISTRATION NUMBER: 35,400  
;; REFERENCE/DOCKET NUMBER: 2077-206A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202)783-6040  
;; TELEFAX: (202)783-6031  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 76 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;; FRAGMENT TYPE: N-terminal  
US-08-250-958-1

Query Match 100.0%; Score 73; DB 1; Length 76;  
Best Local Similarity 100.0%; Pred. No. 5.3e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16  
Db 20 ISVORLASYYRRTSSK 35

RESULT 9  
US-08-235-659-1  
; Sequence 1, Application US/08235659  
; Patent No. 5605871  
; GENERAL INFORMATION:  
; APPLICANT: Lyle, Leon R.  
; APPLICANT: Kunkel, Steven L.  
; APPLICANT: Strieter, Robert M.  
; TITLE OF INVENTION: LABELLED CHEMOKINE MATERIALS AND  
; TITLE OF INVENTION: MEDICAL USES THEREOF  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz  
; STREET: Suite 701-E, 555 Thirteenth St., N.W  
; CITY: Washington  
; STATE: D. C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/235,659

;; FILING DATE: 29-APR-1994  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/956,862  
;; FILING DATE: 05-OCT-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/956,863  
;; FILING DATE: 05-OCT-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: WALKER, Barbara W.  
;; REGISTRATION NUMBER: 35,400  
;; REFERENCE/DOCKET NUMBER: 2077-205A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202)783-6040  
;; TELEFAX: (202)783-6031  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 76 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: not relevant  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FRAGMENT TYPE: N-terminal  
US-08-235-659-1

Query Match 100.0%; Score 73; DB 1; Length 76;  
Best Local Similarity 100.0%; Pred. No. 5.3e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16  
Db 20 ISVORLASYYRRTSSK 35

RESULT 10  
US-08-716-188-2  
; Sequence 2, Application US/08716188  
; Patent No. 5908829  
; GENERAL INFORMATION:  
; APPLICANT: KELLY, RODNEY W  
; TITLE OF INVENTION: USE OF MCP-1 FOR INDUCING RIPENING OF  
; TITLE OF INVENTION: THE CERVIX  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHVE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/716,188  
; FILING DATE: 30-SEP-1996  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB95/00733  
; FILING DATE: 31-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9406463.1  
; FILING DATE: 31-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 117-219  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4091  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 2:



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; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-716-188-2

Query Match 100.0%; Score 73; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
Db 20 ISVORLASYYRRTSSK 35

RESULT 11
US-08-615-232A-5
; Sequence 5, Application US/08615232A
; Patent No. 5993814
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO).
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,232A
; FILING DATE: 13-AUG-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9318984
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: GB 9408602
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 550-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-615-232A-5

Query Match 100.0%; Score 73; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
Db 20 ISVORLASYYRRTSSK 35
```

```

RESULT 12
US-08-470-323-5
; Sequence 5, Application US/08470323A
; Patent No. 6031080
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; FILE REFERENCE: 550-33
; CURRENT APPLICATION NUMBER: US/08/470,323A
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: PCT/GB94/02006
; EARLIER FILING DATE: 1994-09-14
; EARLIER APPLICATION NUMBER: GB 9318984.3
; EARLIER FILING DATE: 1993-09-14
; EARLIER APPLICATION NUMBER: GB 94086902.2
; EARLIER FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 76
; TYPE: PRT
; ORGANISM: human
US-08-470-323-5

Query Match 100.0%; Score 73; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
Db 20 ISVORLASYYRRTSSK 35

RESULT 13
US-09-195-457-5
; Sequence 5, Application US/09195457
; Patent No. 6605702
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; FILE REFERENCE: 550-33
; CURRENT APPLICATION NUMBER: US/09/195,457
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/470,323
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/GB94/02006
; PRIOR FILING DATE: 1994-09-14
; PRIOR APPLICATION NUMBER: GB 9318984.3
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: GB 94086902.2
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 76
; TYPE: PRT
; ORGANISM: human
US-09-195-457-5

Query Match 100.0%; Score 73; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
Db 20 ISVORLASYYRRTSSK 35
```



## RESULT 14

US-09-291-038-5  
; Sequence 5, Application US/09291038  
; Patent No. 6635251  
; GENERAL INFORMATION:  
; APPLICANT: WILLIAMS, TIMOTHY J.  
; JOSE, PETER J.  
; GRIFFITHS-JOHNSON, DAVID A.  
; HSUAN, JOHN J.  
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/291,038  
; FILING DATE: 14-Apr-1999  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/615,232A  
; FILING DATE: 13-AUG-1996  
; APPLICATION NUMBER: GB 9318984  
; FILING DATE: 14-SEP-1993  
; APPLICATION NUMBER: GB 9408602  
; FILING DATE: 29-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WILSON, MARY J.  
; REGISTRATION NUMBER: 32,955  
; REFERENCE/DOCKET NUMBER: 550-32  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; TELEFAX: (703) 816-4100  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 76 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

## US-09-291-038-5

Query Match 100.0%; Score 73; DB 2; Length 76;  
Best Local Similarity 100.0%; Pred. No. 5.3e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ISVORLASVRRITSSK 16  
| | | | | | | | | | | | | | | | | |  
Db 20 ISVORLASVRRITSSK 35  
; GENERAL INFORMATION:  
; APPLICANT: IMAI, Toshio  
; APPLICANT: YOSHIDA, Tetsuya  
; APPLICANT: YOSHIE, Osamu  
; TITLE OF INVENTION: TYPE CC CHEMOKINE-LIKE PROTEIN  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W.

## RESULT 15

US-09-043-961-31  
; Sequence 31, Application US/09043861  
; Patent No. 6793917  
; GENERAL INFORMATION:  
; APPLICANT: IMAI, Toshio  
; APPLICANT: YOSHIDA, Tetsuya  
; APPLICANT: YOSHIE, Osamu  
; TITLE OF INVENTION: TYPE CC CHEMOKINE-LIKE PROTEIN  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W.

CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/043,861  
FILING DATE: 27-MAR-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP96/02801  
FILING DATE: 27-SEP-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 56044/1996  
FILING DATE: 13-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 249457/1995  
FILING DATE: 27-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Wegner, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 74129/432  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5393  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 76 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein

## US-09-043-861-31

Query Match 100.0%; Score 73; DB 2; Length 76;  
Best Local Similarity 100.0%; Pred. No. 5.3e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ISVORLASVRRITSSK 16  
| | | | | | | | | | | | | | | | | |  
Db 20 ISVORLASVRRITSSK 35  
; GENERAL INFORMATION:  
; APPLICANT: Daly, Thomas J.  
; APPLICANT: Larosa, Gregory J.  
; TITLE OF INVENTION: Chemokine-Like Proteins and Methods of  
; TITLE OF INVENTION: Use  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/330,163  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 530

## US-08-330-163-12

US-08-330-163-12  
; Sequence 12, Application US/08330163  
; Patent No. 5656724  
; GENERAL INFORMATION:  
; APPLICANT: Daly, Thomas J.  
; APPLICANT: Larosa, Gregory J.  
; TITLE OF INVENTION: Chemokine-Like Proteins and Methods of  
; TITLE OF INVENTION: Use  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/330,163  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 530

## RESULT 16

US-08-330-163-12  
; Sequence 12, Application US/08330163  
; Patent No. 5656724  
; GENERAL INFORMATION:  
; APPLICANT: Daly, Thomas J.  
; APPLICANT: Larosa, Gregory J.  
; TITLE OF INVENTION: Chemokine-Like Proteins and Methods of  
; TITLE OF INVENTION: Use  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/330,163  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, J. Peter  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 00231/080001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 78 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-330-163-12

Query Match 100.0%; Score 73; DB 1; Length 78;  
Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
|||||

Db 22 ISVQRLASYRRITSSK 37

## RESULT 17

US-08-482-111-12  
Sequence 12, Application US/08482111  
Patent No. 5789539

GENERAL INFORMATION:  
APPLICANT: Daly, Thomas J.  
APPLICANT: Larosa, Gregory J.  
TITLE OF INVENTION: Chemokine-Like Proteins and Methods of Use  
TITLE OF INVENTION: Use  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,111  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, J. Peter  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 00231/080001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906

INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 78 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-482-111-12

Query Match 100.0%; Score 73; DB 1; Length 78;  
Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
|||||

Db 22 ISVQRLASYRRITSSK 37

## RESULT 18

US-09-567-225-14  
Sequence 14, Application US/09567225  
Patent No. 6713052

GENERAL INFORMATION:  
APPLICANT: White, John R.  
APPLICANT: Pelus, Louis  
APPLICANT: Li, Haodong  
APPLICANT: Kreider, Brent L.  
TITLE OF INVENTION: No. 6713052el Chemokine for Mobilizing Stem Cells  
FILE REFERENCE: 1488.1550004  
CURRENT APPLICATION NUMBER: US/09/567,225  
CURRENT FILING DATE: 2000-10-09  
PRIOR APPLICATION NUMBER: US 09/225,501  
PRIOR FILING DATE: 1999-01-06  
PRIOR APPLICATION NUMBER: US 60/006,051  
PRIOR FILING DATE: 1995-10-24  
PRIOR APPLICATION NUMBER: US 08/740,033  
PRIOR FILING DATE: 1996-10-23  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 14  
LENGTH: 78  
TYPE: PRT  
ORGANISM: MCP-1  
US-09-567-225-14

Query Match 100.0%; Score 73; DB 2; Length 78;  
Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
|||||

Db 22 ISVQRLASYRRITSSK 37

## RESULT 19

PCT-US95-00605-1

Sequence 1, Application PC/TUS9500605  
GENERAL INFORMATION:  
APPLICANT: Lyle, Leon  
APPLICANT: Thomas-Miller, Beth  
TITLE OF INVENTION: THERAPEUTIC TREATMENT FOR INHIBITING  
TITLE OF INVENTION: VASCULAR RESTENOSIS  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Mallinckrodt Medical, Inc.  
STREET: 675 McDonnell Boulevard, P.O. Box 5840  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63134

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/00605  
FILING DATE: 13-JAN-1995  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/182,917  
FILING DATE: 14-JAN-1994  
APPLICATION NUMBER: US 07/965,678  
FILING DATE: 22-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Vacca, Rita D.  
REGISTRATION NUMBER: 33,624  
REFERENCE/DOCKET NUMBER: 0783.2

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 314-895-7215  
TELEFAX: 314-895-2156  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 78 amino acids  
TYPE: amino acid  
TOPOLOGY: circular  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 5..22  
PCT-US95-00605-1

Query Match 100.0%; Score 73; DB 4; Length 78;  
Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16  
|||||  
Db 22 ISVORLASYYRITSSK 37

## RESULT 20

US-08-127-499A-35  
Sequence 35, Application US/08127499A  
Patent No. 5510264  
GENERAL INFORMATION:  
APPLICANT: VAN ALSTYNE, Diane  
APPLICANT: SHARMA, Lawrence Rajendra  
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED  
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/127,499A  
FILING DATE: 28-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 51916/102/INBI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown

US-08-127-499A-35  
Query Match 100.0%; Score 73; DB 1; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16  
|||||  
Db 43 ISVORLASYYRITSSK 58

## RESULT 21

US-08-482-847-35  
Sequence 35, Application US/08482847  
Patent No. 5556757  
GENERAL INFORMATION:  
APPLICANT: VAN ALSTYNE, Diane  
APPLICANT: SHARMA, Lawrence Rajendra  
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR  
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR  
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,847  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/127,499  
FILING DATE: 28-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 51916/104/INBI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown

US-08-482-847-35  
Query Match 100.0%; Score 73; DB 1; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16  
|||||  
Db 43 ISVORLASYYRITSSK 58

## RESULT 22

US-08-347-492B-8  
Sequence 8, Application US/08347492B  
Patent No. 5602008  
GENERAL INFORMATION:  
APPLICANT: Wilde, Craig G.  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Bandman, Olga  
APPLICANT: Seilhamer, Jeffrey J.  
TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR  
TITLE OF INVENTION: PRODUCTION AND USES  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto

```
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,492B
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/303,241
; FILING DATE: 07-SEP-1994
; APPLICATION NUMBER: 08/320,011
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0024
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: GI 487124
; US-08-347-492B-8

Query Match 100.0%; Score 73; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISVQRLASYRRITSSK 58

RESULT 23
US-08-480-449-19
; Sequence 19, Application US/08480449
; Patent No. 5688927
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,449
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gasp, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 27866/32779

; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,492B
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/303,241
; FILING DATE: 07-SEP-1994
; APPLICATION NUMBER: 08/320,011
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0024
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: GI 487124
; US-08-347-492B-8

Query Match 100.0%; Score 73; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISVQRLASYRRITSSK 58

RESULT 24
US-08-479-126B-5
; Sequence 5, Application US/08479126B
; Patent No. 5866373
; GENERAL INFORMATION:
; APPLICANT: LI, HAODONG
; APPLICANT: RUBEN, STEVEN M
; APPLICANT: SUTTON, GRANGER G III
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN MONOCYTE
; NUMBER OF SEQUENCES: 6
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,126B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,425
; FILING DATE: 21-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05384
; FILING DATE: 16-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: STREFF, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0340001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-479-126B-5
```

Query Match 100.0%; Score 73; DB 1; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16  
Db 43 ISVORLASYYRRTSSK 58  
|||||

## RESULT 25

US-08-421-144A-5  
; Sequence 5, Application US/08421144A  
; Patent No. 5874211  
; GENERAL INFORMATION:  
; APPLICANT: BANDMAN, OLGA  
; APPLICANT: COLEMAN, ROGER  
; APPLICANT: STUART, SUSAN G.  
; TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/421.144A  
; FILING DATE: 13-APR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Luther, Barbara J.  
; REGISTRATION NUMBER: 33954  
; REFERENCE/DOCKET NUMBER: PF-0031 US  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-852-0195  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 99 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-421-144A-5

Query Match 100.0%; Score 73; DB 1; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16  
Db 43 ISVORLASYYRRTSSK 58  
|||||

## RESULT 26

US-08-726-830A-5  
; Sequence 5, Application US/08726830A  
; Patent No. 5880263  
; GENERAL INFORMATION:  
; APPLICANT: LI, HAODONG  
; APPLICANT: RUBEN, STEVEN M  
; APPLICANT: SUTTON, GRANGER G III  
; TITLE OF INVENTION: MONOCYTE CHEMOTACTIC PROTEIN-4  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, SUITE 600

; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726.830A  
; FILING DATE: 08-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/479,126  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/424,425  
; FILING DATE: 21-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/05384  
; FILING DATE: 16-MAY-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0340002

; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 99 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-726-830A-5

Query Match 100.0%; Score 73; DB 1; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16  
Db 43 ISVORLASYYRRTSSK 58  
|||||

## RESULT 27

US-08-660-542-19  
; Sequence 19, Application US/08660542  
; Patent No. 5932703  
; GENERAL INFORMATION:  
; APPLICANT: Godiska, Ronald  
; APPLICANT: Gray, Patrick W.  
; TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE AND CHEMOKINE  
; TITLE OF INVENTION: ANALOGS  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/660,542  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:

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; INFORMATION FOR SEQ ID NO: 24:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-927-391-24

```

Query Match 100.0%; Score 73; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
|||||  
Db 43 ISVQRLASYRRITSSK 58

## RESULT 30

US-08-995-156A-5  
; Sequence 5, Application US/08995156A  
; Patent No. 6028169  
; GENERAL INFORMATION:  
; APPLICANT: KREIDER, BRENT L.  
; APPLICANT: RUBEN, STEVEN M.  
; APPLICANT: OLSEN, HENRIK S.  
; TITLE OF INVENTION: CHEMOKINE BETA-6 ANTAGONISTS  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/995.156A  
; FILING DATE: Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/042,269  
; FILING DATE: 31-MAR-1997  
; NAME: STEFFE, ERIC K  
; ATTORNEY/AGENT INFORMATION:  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0340004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 99 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-995-156A-5

Query Match 100.0%; Score 73; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
|||||  
Db 43 ISVQRLASYRRITSSK 58

## RESULT 31

US-09-044-856A-5  
; Sequence 5, Application US/09044856A  
; Patent No. 6075124  
; GENERAL INFORMATION:  
; APPLICANT: LI, HAODONG  
; APPLICANT: RUBEN, STEVEN M  
; APPLICANT: SUTTON, GRANGER G III  
; TITLE OF INVENTION: HUMAN CHEMOTACTIC PROTEIN  
; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/044,856A  
; FILING DATE: HEREWITH  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/726,830  
; FILING DATE: 08-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/479,126  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/424,425  
; FILING DATE: 21-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/05384  
; FILING DATE: 16-MAY-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0340006  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 99 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-044-856A-5

Query Match 100.0%; Score 73; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
|||||  
Db 43 ISVQRLASYRRITSSK 58

## RESULT 32

US-09-044-855A-5  
; Sequence 5, Application US/09044855A  
; Patent No. 6100389  
; GENERAL INFORMATION:  
; APPLICANT: LI, HAODONG  
; APPLICANT: RUBEN, STEVEN M  
; APPLICANT: SUTTON, GRANGER G III  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A HUMAN CHEMOTACTIC  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/044,855A  
FILING DATE: HEREWITH  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/479,126  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/424,425  
FILING DATE: 21-APR-1995  
APPLICATION NUMBER: PCT/US94/05384  
FILING DATE: 16-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.0340005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-044-855A-5

Query Match 100.0%; Score 73; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16  
|||||  
Db 43 ISVORLASYYRITSSK 58

RESULT 33  
US-08-679-493A-152  
Sequence 152, Application US/08679493A  
Patent No. 6303295  
GENERAL INFORMATION:  
APPLICANT: Taylor, Ethan W.  
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS  
FILE REFERENCE: 55-95  
CURRENT APPLICATION NUMBER: US/08/679,493A  
CURRENT FILING DATE: 1996-07-12  
PRIOR APPLICATION NUMBER: 60/001203  
PRIOR FILING DATE: 1995-07-14  
PRIOR APPLICATION NUMBER: 60/003,112  
PRIOR FILING DATE: 1995-09-01  
NUMBER OF SEQ ID NOS: 216  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 152  
LENGTH: 99  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-679-493A-152

Query Match 100.0%; Score 73; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16  
|||||  
Db 43 ISVORLASYYRITSSK 58

RESULT 34  
US-08-479-603-19  
Sequence 19, Application US/08479603

Patent No. 6320023  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
APPLICANT: Gray, Patrick W.  
TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/479,603  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 27866/32780  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: "Hu MCP-1"  
US-08-479-603-19

Query Match 100.0%; Score 73; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16  
|||||  
Db 43 ISVORLASYYRITSSK 58

RESULT 35  
US-09-419-281-5  
Sequence 5, Application US/09419281  
Patent No. 6379926  
GENERAL INFORMATION:  
APPLICANT: KREIDER, BRENT L.  
RUBEN, STEVEN M.  
OLSEN, HENRIK S.  
TITLE OF INVENTION: CHEMOKINE BETA-6 ANTAGONISTS  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30



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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/419,281
; FILING DATE: 15-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,156
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0340004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-419-281-5

Query Match 100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
Db 43 ISVORLASYYRRTSSK 58

RESULT 36
US-09-366-887A-10
; Sequence 10, Application US/09366887A
; Patent No. 6403782
; GENERAL INFORMATION:
; APPLICANT: LUSTER, ANDREW D.
; APPLICANT: LEDER, PHILIP
; APPLICANT: ROTHENBERG, MARC
; APPLICANT: GARCIA, EDUARDO
; TITLE OF INVENTION: BOTAXIN: AN EOSINOPHIL CHEMOATTRACTANT
; FILE REFERENCE: 00383/025002
; CURRENT APPLICATION NUMBER: US/09/366,887A
; CURRENT FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 60/000,449
; PRIOR FILING DATE: 1995-06-22
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1995-09-01
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1998-06-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-366-887A-10

Query Match 100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
Db 43 ISVORLASYYRRTSSK 58

RESULT 37
US-08-939-107-19
; Sequence 19, Application US/08939107
; Patent No. 6498015
; GENERAL INFORMATION:
```

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;
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Raport, Carol J.
; TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE (MDC) AND
; TITLE OF INVENTION: CHEMOKINE ANALOGS AND ASSAY TO IDENTIFY MODULATORS OF MDC ACT
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,107
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/558,658
; FILING DATE: 16-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,620
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 27866/33318
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "Hu MCP-1"
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..76
US-08-939-107-19

Query Match 100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
Db 43 ISVORLASYYRRTSSK 58

RESULT 38
US-09-545-894-5
; Sequence 5, Application US/09545894
; Patent No. 6673915
; GENERAL INFORMATION:
; APPLICANT: Luster, Andrew D.
; Garcia-Zepeda, Eduardo A.
; Sarafi, Mindy N.
; TITLE OF INVENTION: MCP-4 AND MCP-5: NOVEL CHEMOKINES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
```

;; CITY: Boston  
;; STATE: MA  
;; COUNTRY: USA  
;; ZIP: 02110  
;;  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; FILING DATE: 07-Apr-2000  
;; CLASSIFICATION: <unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/940,687  
;; FILING DATE: 30-SEP-1997  
;; APPLICATION NUMBER: 60/027,128  
;; FILING DATE: 30-SEP-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Bieker-Brady, Kristina  
;; REGISTRATION NUMBER: 39,109  
;; REFERENCE/DOCKET NUMBER: 00786/293002  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-428-0200  
;; TELEFAX: 617-428-7045  
;; TELEX: <Unknown>  
;;  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 99 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: unknown  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-545-894-5  
  
Query Match 100.0%; Score 73; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 ISVORLASYYRITSSK 16  
Db 43 ISVORLASYYRITSSK 58  
|||||  
  
RESULT 39  
US-09-834-795A-28  
; Sequence 28, Application US/09834795A  
; Patent No. 6723518  
; GENERAL INFORMATION:  
; APPLICANT: Lawrence, Papsidero  
; APPLICANT: Lvn, Dyster  
; APPLICANT: Jana, Frustaci  
; TITLE OF INVENTION: Detection and Treatment of Breast Cancer  
; FILE REFERENCE: 3380/11127-US3  
; CURRENT APPLICATION NUMBER: US/09/834,795A  
; CURRENT FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 09/146,580  
; PRIOR FILING DATE: 1998-09-03  
; PRIOR APPLICATION NUMBER: 60/071,899  
; PRIOR FILING DATE: 1998-01-20  
; PRIOR APPLICATION NUMBER: 60/092,155  
; PRIOR FILING DATE: 1998-07-09  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 28  
; LENGTH: 99  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-834-795A-28  
  
Query Match 100.0%; Score 73; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 ISVORLASYYRITSSK 16  
Db 43 ISVORLASYYRITSSK 58  
|||||  
  
RESULT 40  
US-09-067-447B-19  
; Sequence 19, Application US/09067447B  
; Patent No. 6737513  
; GENERAL INFORMATION:  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Chantry, David H.  
; TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE (MDC) AND  
; TITLE OF INVENTION: CHEMOKINE ANALOGS AND ASSAY TO IDENTIFY MODULATORS OF MDC  
; TITLE OF INVENTION: ACTIVITY  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/067,447B  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/939,107  
; FILING DATE: 26-SEPT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/660,542  
; FILING DATE: 7-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/558,658  
; FILING DATE: 16-NOV-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/479,620  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gass, David A.  
; REGISTRATION NUMBER: 38,153  
; REFERENCE/DOCKET NUMBER: 27866/34404  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 99 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: "Hu MCP-1"  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..76  
US-09-067-447B-19  
  
Query Match 100.0%; Score 73; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ISVORLASYYRITSSK 16
      |||||
Db      43 ISVORLASYYRITSSK 58

RESULT 41
US-09-517-204-10
; Sequence 10, Application US/09517204
; Patent No. 6780973
; GENERAL INFORMATION:
; APPLICANT: LUSTER, ANDREW D.
; APPLICANT: LEDER, PHILIP
; APPLICANT: ROTHENBERG, MARC
; APPLICANT: GARCIA, EDUARDO
; TITLE OF INVENTION: EOTAXIN: AN EOSINOPHIL CHEMOATTRACTANT
; FILE REFERENCE: 00383/025002
; CURRENT APPLICATION NUMBER: US/09/517,204
; CURRENT FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 08/366,887
; PRIOR FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 60/000,449
; PRIOR FILING DATE: 1995-06-22
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1995-09-01
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1998-06-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-517-204-10

Query Match      100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVORLASYYRITSSK 16
      |||||
Db      43 ISVORLASYYRITSSK 58

RESULT 42
US-08-437-306-2
; Sequence 2, Application US/08437306
; Patent No. 6787645
; GENERAL INFORMATION:
; APPLICANT: Rollins, Barrett J.
; APPLICANT: Stiles, Charles D.
; APPLICANT: Wong, Gordon G.
; TITLE OF INVENTION: No. 6787645el Human Cytokine
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millicia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,306
; FILING DATE: 09-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,931
; FILING DATE: 13-APR-1994

Qy      1 ISVORLASYYRITSSK 16
      |||||
Db      43 ISVORLASYYRITSSK 58

RESULT 43
US-08-479-620-19
; Sequence 19, Application US/08479620
; Patent No. 6790947
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,620
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 27866/32628
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-437-306-2

Query Match      100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVORLASYYRITSSK 16
      |||||
Db      43 ISVORLASYYRITSSK 58

PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/003,136
FILING DATE: 12-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,515
FILING DATE: 16-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/351,008
FILING DATE: 12-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: DFCI-196A22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-437-306-2
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; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "Hu MCP-1"
US-08-479-620-19

Query Match      100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISVQRLASYRRITSSK 58

RESULT 44
US-10-054-967-5
; Sequence 5, Application US/10054967
; Patent No. 6815420
; GENERAL INFORMATION:
; APPLICANT: KREIDER, BRENT L.
; RUBEN, STEVEN M.
; OLSEN, HENRIK S.
; TITLE OF INVENTION: CHEMOKINE BETA-6 ANTAGONISTS
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/054,967
; FILING DATE: 25-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,156
; FILING DATE: 19-DEC-1997
; APPLICATION NUMBER: 60/042,269
; FILING DATE: 31-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0340004
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-054-967-5

Query Match      100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISVQRLASYRRITSSK 58

RESULT 45
US-10-141-965-5
; Sequence 5, Application US/10141965
```

```
; Patent No. 6867006
; GENERAL INFORMATION:
; APPLICANT: LI, HAODONG
; RUBEN, STEVEN M
; SUTTON, GRANGER G III
; TITLE OF INVENTION: HUMAN CHEMOTACTIC PROTEIN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/141,965
; FILING DATE: 10-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/453,416
; FILING DATE: 03-DEC-1999
; APPLICATION NUMBER: US 09/044,855
; FILING DATE: 20-MAR-1998
; APPLICATION NUMBER: US 08/479,126
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/424,425
; FILING DATE: 21-APR-1995
; APPLICATION NUMBER: PCT/US94/05384
; FILING DATE: 16-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.034000C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-141-965-5

Query Match      100.0%; Score 73; DB 2; Length 99;
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISVQRLASYRRITSSK 58

RESULT 46
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; Sequence 5, Application PC/TUS9610087
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Monocyte Chemotactic Protein-4
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10087
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; FILING DATE: 07-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/479,126
; FILING DATE: 07-JUN-1995
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10087-5

Query Match 100.0%; Score 73; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISVQRLASYRRITSSK 58

RESULT 47
5212073-2
; Patent No. 5212073
; APPLICANT: ROLLINS, BARRETT;STILES, CHARLES;WONG, GORDON G.
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMAN JE CYTOKINE
; NUMBER OF SEQUENCES: 1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/351,008
; FILING DATE:12-MAY-1989
; SEQ ID NO:2:
; LENGTH: 99
5212073-2

Query Match 100.0%; Score 73; DB 6; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISVQRLASYRRITSSK 58

RESULT 48
US-09-133-521-5
; Sequence 5, Application US/09133521
; Patent No. 6281200
; GENERAL INFORMATION:
; APPLICANT: Fife, Kenneth H.
; APPLICANT: Krathwohl, Mitchell D.
; APPLICANT: Hromas, Robert
; APPLICANT: Brown, Darron R.
; APPLICANT: Broxmeyer, Hal E.
; TITLE OF INVENTION: FUNCTIONAL CHARACTERIZATION OF THE C-C CHEMOKINE-LIKE
; TITLE OF INVENTION: MOLECULES ENODED BY MOLLUSCUM CONTAGIOSUM VIRUS TYPES 1
; TITLE OF INVENTION: AND 2
; FILE REFERENCE: INDY:034
; CURRENT APPLICATION NUMBER: US/09/133,521
; CURRENT FILING DATE: 1998-08-18
; EARLIER APPLICATION NUMBER: 60/055,532
; EARLIER FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-133-521-5

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Best Local Similarity 75.0%; Pred. No. 0.001;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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Db 43 ISMQLANRYRRVTSSK 58

RESULT 49
US-09-366-887A-20
; Sequence 20, Application US/09366887A
; Patent No. 6403782
; GENERAL INFORMATION:
; APPLICANT: LUSTER, ANDREW D.
; APPLICANT: LEDER, PHILIP
; APPLICANT: ROTHENBERG, MARC
; APPLICANT: GARCIA, EDUARDO
; TITLE OF INVENTION: BOTAXIN: AN EOSINOPHIL CHEMOATTRACTANT
; FILE REFERENCE: 00383/025002
; CURRENT APPLICATION NUMBER: US/09/366,887A
; CURRENT FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 60/000,449
; PRIOR FILING DATE: 1995-06-22
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1995-09-01
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1998-06-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-366-887A-20

Query Match 76.7%; Score 56; DB 2; Length 37;
Best Local Similarity 75.0%; Pred. No. 0.0029;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Db 16 IPLQLLESYRRITSGK 31

RESULT 50
US-09-517-204-20
; Sequence 20, Application US/09517204
; Patent No. 6780973
; GENERAL INFORMATION:
; APPLICANT: LUSTER, ANDREW D.
; APPLICANT: LEDER, PHILIP
; APPLICANT: ROTHENBERG, MARC
; APPLICANT: GARCIA, EDUARDO
; TITLE OF INVENTION: BOTAXIN: AN EOSINOPHIL CHEMOATTRACTANT
; FILE REFERENCE: 00383/025002
; CURRENT APPLICATION NUMBER: US/09/517,204
; CURRENT FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 08/366,887
; PRIOR FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 60/000,449
; PRIOR FILING DATE: 1995-06-22
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1995-09-01
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1998-06-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-517-204-20

Query Match 76.7%; Score 56; DB 2; Length 37;
Best Local Similarity 75.0%; Pred. No. 0.0029;
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Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16

Db 16 IPLQRLASYRRITSGK 31

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OM protein - protein search, using sw model

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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29	73	100.0	35	4	US-10-243-795-1370	GENERAL INFORMATI
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38	73	100.0	69	4	US-10-276-971-2	Sequence 2, Appli
39	73	100.0	76	3	US-09-195-457-5	Sequence 5, Appli
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101	59	80.8	23	5	US-10-983-453-12	Sequence 12, Appl	174	47	64.4	137	4	US-10-335-394-2	Sequence 2, Appl
102	58	79.5	23	4	US-10-082-815-5	Sequence 5, Appl	175	47	64.4	151	4	US-10-335-394-7	Sequence 7, Appl
103	58	79.5	23	4	US-10-983-453-5	Sequence 5, Appl	176	47	64.4	325	3	US-09-792-793A-74	Sequence 74, Appl
104	56	76.7	74	3	US-09-792-793A-13	Sequence 13, Appl	177	47	64.4	325	3	US-10-375-209A-74	Sequence 74, Appl
105	56	76.7	74	4	US-10-125-451-20	Sequence 20, Appl	178	47	64.4	327	4	US-09-792-793A-75	Sequence 75, Appl
106	56	76.7	74	4	US-10-263-139-20	Sequence 20, Appl	179	47	64.4	327	4	US-10-375-209A-75	Sequence 75, Appl
107	56	76.7	74	4	US-10-375-209A-13	Sequence 13, Appl	180	47	64.4	332	3	US-09-792-793A-76	Sequence 76, Appl
108	56	76.7	74	4	US-10-646-770-20	Sequence 20, Appl	181	47	64.4	332	4	US-10-375-209A-76	Sequence 76, Appl
109	56	76.7	74	4	US-10-332-038A-3	Sequence 3, Appl	182	47	64.4	348	4	US-10-335-394-16	Sequence 16, Appl
110	56	76.7	74	4	US-10-668-733-8	Sequence 8, Appl	183	47	64.4	359	4	US-10-335-394-14	Sequence 14, Appl
111	56	76.7	74	4	US-10-668-733-11	Sequence 11, Appl	184	47	64.4	361	4	US-10-335-394-14	Sequence 14, Appl
112	56	76.7	74	4	US-10-668-733-15	Sequence 15, Appl	185	47	64.4	471	5	US-10-415-431-1	Sequence 1, Appl
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117	56	76.7	97	3	US-09-834-795A-26	Sequence 26, Appl	190	46	63.0	70	4	US-10-646-770-17	Sequence 17, Appl
118	56	76.7	97	3	US-09-834-794A-26	Sequence 26, Appl	191	45	61.6	97	3	US-09-886-119A-21	Sequence 21, Appl
119	56	76.7	97	4	US-10-057-275-2	Sequence 2, Appl	192	45	61.6	97	4	US-10-376-564-21	Sequence 21, Appl
120	56	76.7	97	4	US-10-057-275-5	Sequence 5, Appl	193	45	61.6	156	4	US-10-335-394-4	Sequence 4, Appl
121	56	76.7	97	4	US-10-114-893-52	Sequence 52, Appl	194	45	61.6	171	4	US-10-335-394-9	Sequence 9, Appl
122	56	76.7	97	4	US-10-289-454-242	Sequence 242, App	195	44	60.3	71	3	US-09-537-859-3	Sequence 3, Appl
123	56	76.7	97	4	US-10-050-902-242	Sequence 242, App	196	44	60.3	71	3	US-09-537-859-4	Sequence 4, Appl
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131	56	76.7	330	4	US-10-375-209A-82	Sequence 82, Appl	204	44	60.3	76	4	US-10-398-457-37	Sequence 37, Appl
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139	52	71.2	82	5	US-10-332-039A-7	Sequence 7, Appl	212	44	60.3	77	5	US-10-847-824-24	Sequence 24, Appl
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141	52	71.2	132	4	US-10-449-831A-212	Sequence 212, App	214	44	60.3	94	4	US-10-001-221A-6	Sequence 6, Appl
142	49	67.1	148	2	US-08-927-939-26	Sequence 26, Appl	215	44	60.3	95	4	US-10-216-774-2198	Sequence 2198, Ap
143	49	67.1	148	4	US-10-764-649-20	Sequence 20, Appl	216	44	60.3	99	3	US-09-886-319A-30	Sequence 30, Appl
144	47	64.4	67	3	US-09-195-457-7	Sequence 7, Appl	217	44	60.3	99	3	US-09-537-859-1	Sequence 1, Appl
145	47	64.4	70	5	US-10-622-134-7	Sequence 7, Appl	218	44	60.3	99	3	US-09-537-859-2	Sequence 2, Appl
146	47	64.4	76	3	US-09-792-793A-22	Sequence 22, Appl	219	44	60.3	99	4	US-10-376-564-30	Sequence 30, Appl
147	47	64.4	76	4	US-10-125-451-19	Sequence 19, Appl	220	44	60.3	99	5	US-10-723-860-2828	Sequence 2828, Ap
148	47	64.4	76	4	US-10-263-139-19	Sequence 19, Appl	221	44	60.3	99	6	US-11-123-089-1	Sequence 1, Appl
149	47	64.4	76	4	US-10-375-209A-22	Sequence 22, Appl	222	44	60.3	99	6	US-11-123-089-2	Sequence 2, Appl
150	47	64.4	76	4	US-10-646-770-19	Sequence 19, Appl	223	44	60.3	109	4	US-09-886-319A-71	Sequence 71, Appl
151	47	64.4	76	4	US-10-332-038A-6	Sequence 6, Appl	224	44	60.3	109	4	US-10-376-564-71	Sequence 71, Appl
152	47	64.4	76	5	US-10-839-017-11	Sequence 11, Appl	225	44	60.3	109	4	US-10-376-564-71	Sequence 71, Appl
153	47	64.4	76	5	US-10-332-039A-6	Sequence 6, Appl	226	44	60.3	109	4	US-10-247-671-169	Sequence 169, App
154	47	64.4	77	3	US-09-792-793A-86	Sequence 86, Appl	227	44	60.3	109	4	US-10-170-385-479	Sequence 479, App
155	47	64.4	77	4	US-10-375-209A-86	Sequence 86, Appl	228	43	58.9	15	2	US-08-927-939-3	Sequence 3, Appl
156	47	64.4	82	4	US-10-803-960-15	Sequence 15, Appl	229	42	57.5	14	4	US-10-082-815-18	Sequence 18, Appl
157	47	64.4	99	2	US-08-927-939-18	Sequence 18, Appl	230	42	57.5	14	5	US-10-983-453-18	Sequence 18, Appl
158	47	64.4	99	3	US-09-834-795A-27	Sequence 27, Appl	231	42	57.5	352	5	US-10-450-763-34016	Sequence 34016, A
159	47	64.4	99	3	US-09-886-319A-22	Sequence 22, Appl	232	41	56.2	18	4	US-10-082-815-17	Sequence 17, Appl
160	47	64.4	99	3	US-09-834-794A-27	Sequence 27, Appl	233	41	56.2	18	4	US-10-082-815-21	Sequence 21, Appl
161	47	64.4	99	4	US-10-125-451-18	Sequence 18, Appl	234	41	56.2	18	5	US-10-983-453-21	Sequence 21, Appl
162	47	64.4	99	4	US-10-263-139-18	Sequence 18, Appl	235	41	56.2	71	3	US-09-195-457-8	Sequence 8, Appl
163	47	64.4	99	4	US-10-376-564-22	Sequence 22, Appl	236	41	56.2	71	5	US-10-622-134-8	Sequence 8, Appl
164	47	64.4	99	4	US-10-170-385-463	Sequence 463, App	237	41	56.2	71	5	US-10-450-763-48926	Sequence 48926, A
165	47	64.4	99	4	US-10-646-770-18	Sequence 18, Appl	238	41	56.2	931	5	US-10-450-763-48928	Sequence 48928, A
166	47	64.4	99	5	US-10-847-824-27	Sequence 27, Appl	239	41	56.2	1908	5	US-10-450-763-48928	Sequence 48928, A
167	47	64.4	99	5	US-10-491-997-144	Sequence 144, App	240	40	54.8	271	4	US-10-424-599-181775	Sequence 181775, A
168	47	64.4	99	5	US-10-287-436A-429	Sequence 429, App	241	39	53.4	186	4	US-10-424-599-257636	Sequence 257636, A
169	47	64.4	99	5	US-10-287-436A-1130	Sequence 1130, App	242	39	53.4	425	4	US-10-424-599-150005	Sequence 150005, A
170	47	64.4	109	4	US-10-818-952-18	Sequence 18, Appl	243	39	53.4	434	4	US-10-424-599-181777	Sequence 181777, A
171	47	64.4	109	4	US-10-057-275-11	Sequence 11, Appl	244	39	53.4	2111	4	US-10-437-963-186073	Sequence 186073, A
172	47	64.4	109	4	US-10-033-067-3	Sequence 3, Appl	245	39	53.4	2498	4	US-10-437-963-186071	Sequence 186071, A
173	47	64.4	109	5	US-10-220-335-311	Sequence 311, App	246	38	52.1	14	4	US-10-082-815-20	Sequence 20, Appl

247	38	52.1	14	5	US-10-983-453-20	Sequence 20, Appl	320	36	49.3	1003	5	US-10-450-763-53380	Sequence 53380, A
248	38	52.1	53	4	US-10-437-963-156780	Sequence 156780,	321	36	49.3	1022	4	US-10-282-122A-55642	Sequence 55642, A
249	38	52.1	82	4	US-10-424-599-231797	Sequence 231797,	322	36	49.3	1134	4	US-10-282-122A-73247	Sequence 73247, A
250	38	52.1	96	4	US-10-425-115-191161	Sequence 191161,	323	36	49.3	1148	3	US-09-815-242-10134	Sequence 10134, A
251	38	52.1	148	4	US-10-767-701-61944	Sequence 61944, A	324	36	49.3	1148	3	US-09-815-242-10134	Sequence 10134, A
252	38	52.1	179	4	US-10-425-114-43854	Sequence 43854, A	325	36	49.3	1148	3	US-10-282-122A-56525	Sequence 56525, A
253	38	52.1	181	4	US-10-425-115-336200	Sequence 336200,	326	36	49.3	1148	4	US-10-282-122A-59749	Sequence 59749, A
254	38	52.1	200	4	US-10-425-115-336197	Sequence 336197,	327	36	49.3	1148	4	US-10-282-122A-75898	Sequence 75898, A
255	38	52.1	223	4	US-10-017-161-1930	Sequence 1930, Ap	328	36	49.3	1166	4	US-10-282-122A-68505	Sequence 68505, A
256	38	52.1	223	4	US-10-292-798-1582	Sequence 1582, Ap	329	36	49.3	1172	3	US-09-822-268A-2	Sequence 2, Appl
257	38	52.1	266	4	US-10-424-599-248825	Sequence 248825,	330	36	49.3	1172	4	US-10-391-777-2	Sequence 2, Appl
258	38	52.1	311	3	US-09-908-006A-43	Sequence 43, Appl	331	36	49.3	1204	5	US-10-787-726-3	Sequence 3, Appl
259	38	52.1	493	4	US-10-424-599-217880	Sequence 217880,	332	36	49.3	1235	3	US-09-921-159-2	Sequence 2, Appl
260	38	52.1	1026	4	US-10-332-426-6	Sequence 6, Appl	333	36	49.3	1237	5	US-10-343-903-24	Sequence 24, Appl
261	38	52.1	1327	4	US-10-437-963-153470	Sequence 153470,	334	36	49.3	1262	5	US-10-450-763-51033	Sequence 51033, A
262	37	50.7	14	4	US-10-082-815-19	Sequence 19, Appl	335	36	49.3	1326	5	US-10-732-923-1617	Sequence 1617, Ap
263	37	50.7	14	5	US-10-983-453-19	Sequence 19, Appl	336	36	49.3	1330	5	US-10-732-923-1599	Sequence 1599, Ap
264	37	50.7	68	4	US-10-425-115-210351	Sequence 210351,	337	36	49.3	1390	5	US-10-732-923-1596	Sequence 1596, Ap
265	37	50.7	195	4	US-10-767-701-59645	Sequence 59645, A	338	36	49.3	1397	5	US-10-732-923-1597	Sequence 1597, Ap
266	37	50.7	197	4	US-10-282-122A-57389	Sequence 57389, A	339	36	49.3	1413	5	US-10-732-923-1598	Sequence 1598, Ap
267	37	50.7	325	4	US-10-424-599-261253	Sequence 261253,	340	36	49.3	1507	5	US-10-450-763-60702	Sequence 60702, A
268	37	50.7	379	4	US-10-125-692-13	Sequence 13, Appl	341	36	49.3	1585	5	US-10-450-763-36434	Sequence 36434, A
269	37	50.7	379	5	US-10-991-347-13	Sequence 13, Appl	342	36	49.3	1585	5	US-10-450-763-41174	Sequence 41174, A
270	37	50.7	436	5	US-10-946-647-1421	Sequence 1421, Ap	343	36	49.3	1598	5	US-10-450-763-36977	Sequence 36977, A
271	37	50.7	476	4	US-10-425-114-40674	Sequence 40674, A	344	36	49.3	1598	5	US-10-450-763-40014	Sequence 40014, A
272	37	50.7	550	4	US-10-125-692-22	Sequence 22, Appl	345	36	49.3	1647	5	US-10-450-763-34360	Sequence 34360, A
273	37	50.7	550	5	US-10-991-347-22	Sequence 22, Appl	346	36	49.3	4292	4	US-10-080-334-273	Sequence 273, App
274	37	50.7	554	4	US-10-125-692-21	Sequence 21, Appl	347	36	49.3	4299	4	US-10-450-763-47419	Sequence 47419, A
275	37	50.7	554	5	US-10-991-347-21	Sequence 21, Appl	348	36	49.3	4299	4	US-10-080-334-90	Sequence 90, Appl
276	37	50.7	585	5	US-10-946-647-1409	Sequence 1409, Ap	349	36	49.3	4302	4	US-10-080-334-271	Sequence 271, App
277	37	50.7	1078	5	US-10-450-763-52313	Sequence 52313, A	350	36	49.3	4302	4	US-10-080-334-272	Sequence 272, App
278	37	50.7	1265	4	US-10-032-585-7168	Sequence 7168, Ap	351	36	49.3	4302	5	US-10-411-915-171	Sequence 171, App
279	37	50.7	1309	5	US-10-450-763-60725	Sequence 60725, A	352	36	49.3	4303	3	US-09-904-968A-2	Sequence 2, Appl
280	37	50.7	1443	4	US-10-369-493-4119	Sequence 4119, Ap	353	36	49.3	4303	4	US-10-080-334-274	Sequence 274, App
281	36	49.3	44	3	US-09-864-761-46231	Sequence 46231, A	354	36	49.3	4725	5	US-10-450-763-54196	Sequence 54196, A
282	36	49.3	50	4	US-10-424-599-246658	Sequence 246658,	355	36	49.3	4977	5	US-10-450-763-47416	Sequence 47416, A
283	36	49.3	51	4	US-10-425-115-248299	Sequence 248299,	356	36	49.3	6685	3	US-10-450-763-53389	Sequence 53389, A
284	36	49.3	52	4	US-10-424-599-185860	Sequence 185860,	357	35.5	48.6	37	3	US-09-864-761-39501	Sequence 39501, A
285	36	49.3	63	4	US-10-425-115-258463	Sequence 258463,	358	35.5	48.6	75	3	US-09-792-793A-23	Sequence 23, Appl
286	36	49.3	62	4	US-10-424-599-184922	Sequence 184922,	359	35.5	48.6	75	4	US-10-375-209A-23	Sequence 7, Appl
287	36	49.3	93	4	US-10-424-599-254538	Sequence 254538,	360	35.5	48.6	82	4	US-10-803-960-7	Sequence 7, Appl
288	36	49.3	118	3	US-09-731-872-432	Sequence 432, App	361	35.5	48.6	98	2	US-08-927-939-50	Sequence 50, Appl
289	36	49.3	118	3	US-09-876-997-432	Sequence 432, App	362	35.5	48.6	98	2	US-08-927-939-83	Sequence 83, Appl
290	36	49.3	118	5	US-10-643-836-432	Sequence 432, App	363	35.5	48.6	98	3	US-09-261-201A-4	Sequence 4, Appl
291	36	49.3	131	5	US-10-450-763-47322	Sequence 47322, A	364	35.5	48.6	98	3	US-09-834-795A-25	Sequence 25, Appl
292	36	49.3	155	4	US-10-424-599-211127	Sequence 211127,	365	35.5	48.6	98	3	US-09-872-611A-2	Sequence 2, Appl
293	36	49.3	158	4	US-10-425-114-62150	Sequence 62150, A	366	35.5	48.6	98	3	US-09-834-794A-25	Sequence 25, Appl
294	36	49.3	159	4	US-10-425-114-70777	Sequence 70777, A	367	35.5	48.6	98	4	US-10-164-621-4	Sequence 4, Appl
295	36	49.3	209	4	US-10-029-386-32426	Sequence 32426, A	368	35.5	48.6	98	4	US-10-125-451-4	Sequence 4, Appl
296	36	49.3	217	5	US-10-739-930-6395	Sequence 6395, Ap	369	35.5	48.6	98	4	US-10-283-439-4	Sequence 4, Appl
297	36	49.3	266	4	US-10-425-115-279025	Sequence 279025,	370	35.5	48.6	98	4	US-10-295-027-1221	Sequence 4, Appl
298	36	49.3	281	4	US-10-425-114-38770	Sequence 38770, A	371	35.5	48.6	98	4	US-10-646-770-4	Sequence 4, Appl
299	36	49.3	327	4	US-10-424-599-180549	Sequence 180549,	372	35.5	48.6	98	5	US-10-723-860-3704	Sequence 3704, Ap
300	36	49.3	331	4	US-10-267-502-377	Sequence 377, App	373	35.5	48.6	98	5	US-10-893-995-4	Sequence 4, Appl
301	36	49.3	331	6	US-11-097-143-6393	Sequence 6393, Ap	374	35.5	48.6	98	5	US-10-847-824-25	Sequence 25, Appl
302	36	49.3	345	4	US-10-282-122A-76642	Sequence 76642, A	375	35.5	48.6	98	5	US-10-756-149-5640	Sequence 5640, Ap
303	36	49.3	355	4	US-10-072-012-773	Sequence 773, App	376	35.5	48.6	106	5	US-10-450-763-43931	Sequence 43931, A
304	36	49.3	386	4	US-10-437-963-202924	Sequence 202924,	377	35	47.9	18	4	US-10-082-815-22	Sequence 22, Appl
305	36	49.3	387	4	US-10-424-599-181776	Sequence 181776,	378	35	47.9	18	5	US-10-983-453-22	Sequence 22, Appl
306	36	49.3	394	4	US-10-125-632-14	Sequence 14, Appl	379	35	47.9	77	4	US-10-437-963-153709	Sequence 153709, A
307	36	49.3	394	5	US-10-991-347-14	Sequence 14, Appl	380	35	47.9	83	4	US-10-282-122A-67661	Sequence 67661, A
308	36	49.3	447	5	US-10-450-763-60705	Sequence 60705, A	381	35	47.9	102	4	US-10-425-115-216653	Sequence 216653, A
309	36	49.3	462	4	US-10-072-012-770	Sequence 770, App	382	35	47.9	121	3	US-09-864-408A-7048	Sequence 7048, Ap
310	36	49.3	481	4	US-10-425-115-271756	Sequence 271756,	383	35	47.9	124	4	US-10-437-963-107961	Sequence 107961, A
311	36	49.3	496	4	US-10-072-012-771	Sequence 771, App	384	35	47.9	127	4	US-10-424-599-217879	Sequence 217879, A
312	36	49.3	496	4	US-10-408-765A-2147	Sequence 2147, Ap	385	35	47.9	128	4	US-10-437-963-174540	Sequence 174540, A
313	36	49.3	521	4	US-10-072-012-769	Sequence 769, App	386	35	47.9	141	4	US-10-231-417-604	Sequence 604, App
314	36	49.3	531	5	US-10-739-930-10720	Sequence 10720, A	387	35	47.9	146	4	US-10-425-114-42380	Sequence 42380, A
315	36	49.3	643	4	US-10-276-774-1441	Sequence 1441, Ap	388	35	47.9	205	5	US-10-732-923-10951	Sequence 10951, A
316	36	49.3	664	5	US-10-450-763-34631	Sequence 34631, A	389	35	47.9	209	4	US-10-369-493-18838	Sequence 18838, A
317	36	49.3	664	5	US-10-450-763-35909	Sequence 35909, A	390	35	47.9	219	6	US-11-097-143-34719	Sequence 34719, A
318	36	49.3	789	4	US-10-282-122A-51312	Sequence 51312,	391	35	47.9	239	4	US-10-424-599-214810	Sequence 214810, A
319	36	49.3	905	5	US-10-450-763-35567	Sequence 35567, A	392	35	47.9	260	4	US-10-425-114-53710	Sequence 53710, A

393	35	47.9	283	4	US-10-369-493-4179	Sequence 4179, Ap	466	34	46.6	182	4	US-10-424-599-219775	Sequence 219775, A
394	35	47.9	287	4	US-10-125-692-32	Sequence 32, Appl	467	34	46.6	186	4	US-10-767-701-39759	Sequence 39759, A
395	35	47.9	287	5	US-10-991-347-32	Sequence 32, Appl	468	34	46.6	194	4	US-10-038-854-356	Sequence 356, App
396	35	47.9	334	6	US-11-097-143-39003	Sequence 39003, A	469	34	46.6	195	4	US-10-425-115-332905	Sequence 332905, A
397	35	47.9	343	4	US-10-032-585-7164	Sequence 7164, Ap	470	34	46.6	200	4	US-10-425-115-302416	Sequence 302416, A
398	35	47.9	347	5	US-10-732-923-20583	Sequence 20583, A	471	34	46.6	207	4	US-10-437-963-127493	Sequence 127493, A
399	35	47.9	347	5	US-10-732-923-20585	Sequence 20585, A	472	34	46.6	208	4	US-10-282-122A-63442	Sequence 63442, A
400	35	47.9	355	5	US-10-495-342-2	Sequence 2, Appl1	473	34	46.6	208	4	US-10-437-963-178719	Sequence 178719, A
401	35	47.9	358	4	US-10-425-114-56843	Sequence 56843, A	474	34	46.6	212	4	US-10-425-115-214278	Sequence 214278, A
402	35	47.9	367	4	US-10-125-692-17	Sequence 17, Appl	475	34	46.6	216	4	US-10-424-599-277860	Sequence 277860, A
403	35	47.9	367	5	US-10-991-347-17	Sequence 17, Appl	476	34	46.6	239	4	US-10-424-599-199074	Sequence 199074, A
404	35	47.9	367	5	US-10-437-963-201660	Sequence 201660, A	477	34	46.6	246	4	US-10-282-122A-77648	Sequence 77648, A
405	35	47.9	446	4	US-10-108-260A-4090	Sequence 4090, Ap	478	34	46.6	250	3	US-09-952-572-8	Sequence 8, Appl1
406	35	47.9	466	4	US-10-072-012-772	Sequence 772, App	479	34	46.6	271	4	US-10-236-031B-16	Sequence 16, Appl
407	35	47.9	469	4	US-10-408-765A-213	Sequence 213, App	480	34	46.6	271	4	US-10-425-114-52132	Sequence 52132, A
408	35	47.9	469	5	US-10-733-969A-70	Sequence 70, Appl	481	34	46.6	271	5	US-10-754-473-7	Sequence 7, Appl1
409	35	47.9	469	5	US-10-923-035-34	Sequence 34, Appl	482	34	46.6	279	4	US-10-038-854-16	Sequence 16, Appl
410	35	47.9	469	5	US-10-495-409A-2	Sequence 2, Appl1	483	34	46.6	280	4	US-10-243-552-905	Sequence 905, App
411	35	47.9	479	4	US-10-408-765A-1279	Sequence 1279, Ap	484	34	46.6	280	5	US-10-450-763-47733	Sequence 47733, A
412	35	47.9	473	4	US-10-369-493-3209	Sequence 2209, Ap	485	34	46.6	311	4	US-10-425-115-214267	Sequence 214267, A
413	35	47.9	473	5	US-10-732-923-11744	Sequence 11744, A	486	34	46.6	326	4	US-10-437-963-199721	Sequence 199721, A
414	35	47.9	490	5	US-10-450-763-38137	Sequence 38137, A	487	34	46.6	335	4	US-10-282-122A-55715	Sequence 55715, A
415	35	47.9	490	5	US-10-450-763-38843	Sequence 38843, A	488	34	46.6	342	4	US-10-243-552-467	Sequence 467, App
416	35	47.9	505	4	US-10-282-122A-61197	Sequence 61197, A	489	34	46.6	343	4	US-10-156-761-8868	Sequence 8868, Ap
417	35	47.9	507	4	US-10-369-493-3579	Sequence 3579, Ap	490	34	46.6	349	4	US-10-282-122A-67075	Sequence 67075, A
418	35	47.9	515	4	US-10-425-114-56951	Sequence 56951, A	491	34	46.6	350	3	US-09-929-955-4	Sequence 955, A
419	35	47.9	515	4	US-10-425-115-221558	Sequence 221558, A	492	34	46.6	350	4	US-10-104-966-4	Sequence 4, Appl1
420	35	47.9	522	4	US-10-425-115-221560	Sequence 221560, A	493	34	46.6	350	4	US-10-104-966-4	Sequence 4, Appl1
421	35	47.9	540	4	US-10-437-963-135231	Sequence 135231, A	494	34	46.6	350	5	US-10-817-591-4	Sequence 4, Appl1
422	35	47.9	545	4	US-10-424-599-211220	Sequence 211220, A	495	34	46.6	351	4	US-10-125-692-20	Sequence 20, Appl
423	35	47.9	550	4	US-10-425-114-37544	Sequence 37544, A	496	34	46.6	351	5	US-10-991-347-20	Sequence 20, Appl
424	35	47.9	552	4	US-10-425-114-56077	Sequence 56077, A	497	34	46.6	355	4	US-10-282-122A-51316	Sequence 51316, A
425	35	47.9	646	4	US-10-243-552-982	Sequence 982, App	498	34	46.6	363	4	US-10-128-590-97	Sequence 97, Appl
426	35	47.9	646	5	US-10-450-763-35613	Sequence 35613, A	499	34	46.6	363	4	US-10-128-590-97	Sequence 97, Appl
427	35	47.9	702	5	US-10-450-763-48708	Sequence 48708, A	500	34	46.6	365	4	US-10-125-692-16	Sequence 16, Appl
428	35	47.9	716	5	US-10-450-763-56239	Sequence 56239, A	501	34	46.6	365	5	US-10-991-347-16	Sequence 16, Appl
429	35	47.9	730	4	US-10-282-122A-57869	Sequence 57869, A	502	34	46.6	384	4	US-10-156-761-9100	Sequence 9100, Ap
430	35	47.9	749	5	US-10-450-763-36138	Sequence 36138, A	503	34	46.6	391	4	US-10-282-122A-50985	Sequence 50985, A
431	35	47.9	808	4	US-10-655-799-38	Sequence 38, Appl	504	34	46.6	421	4	US-10-365-620-70	Sequence 70, Appl
432	35	47.9	811	5	US-10-450-763-59793	Sequence 59793, A	505	34	46.6	421	5	US-10-912-969-72	Sequence 72, Appl
433	35	47.9	924	5	US-10-450-763-55525	Sequence 55525, A	506	34	46.6	431	4	US-10-437-963-202135	Sequence 202135, A
434	35	47.9	1301	4	US-10-437-963-124381	Sequence 124381, A	507	34	46.6	440	5	US-10-450-763-56214	Sequence 56214, A
435	35	47.9	1315	4	US-10-437-963-150897	Sequence 150897, A	508	34	46.6	468	4	US-10-425-115-212787	Sequence 212787, A
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437	35	47.9	1717	5	US-10-450-763-51031	Sequence 51031, A	510	34	46.6	473	4	US-10-408-765A-2491	Sequence 2491, Ap
438	35	47.9	1781	4	US-10-437-963-106977	Sequence 106977, A	511	34	46.6	477	4	US-10-424-599-246486	Sequence 246486, A
439	34.5	47.3	431	4	US-10-369-493-1174	Sequence 11774, Ap	512	34	46.6	487	5	US-10-946-847-1372	Sequence 1372, Ap
440	34	46.6	30	4	US-10-296-734-466	Sequence 466, App	513	34	46.6	488	4	US-10-127-032-99	Sequence 99, Appl
441	34	46.6	30	4	US-10-296-734-468	Sequence 468, App	514	34	46.6	490	4	US-10-125-692-19	Sequence 19, Appl
442	34	46.6	40	4	US-10-425-115-255091	Sequence 255091, A	515	34	46.6	490	4	US-10-767-701-45642	Sequence 45642, A
443	34	46.6	40	4	US-10-425-115-345648	Sequence 345648, A	516	34	46.6	490	5	US-10-991-347-19	Sequence 19, Appl
444	34	46.6	83	4	US-10-282-122A-51395	Sequence 51395, A	517	34	46.6	493	5	US-10-946-847-1401	Sequence 1401, Ap
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446	34	46.6	89	4	US-10-425-115-347133	Sequence 347133, A	519	34	46.6	504	5	US-10-946-847-1399	Sequence 1399, Ap
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448	34	46.6	94	4	US-10-425-115-307564	Sequence 307564, A	521	34	46.6	506	5	US-10-991-347-18	Sequence 18, Appl
449	34	46.6	97	4	US-10-289-454-245	Sequence 245, App	522	34	46.6	506	5	US-10-946-847-1371	Sequence 1371, Ap
450	34	46.6	97	4	US-10-050-902-245	Sequence 245, App	523	34	46.6	576	4	US-10-424-599-173221	Sequence 173221, A
451	34	46.6	97	4	US-10-050-898-245	Sequence 245, App	524	34	46.6	584	4	US-10-424-599-264739	Sequence 264739, A
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453	34	46.6	99	5	US-10-991-347-47	Sequence 47, Appl	526	34	46.6	606	4	US-10-425-115-288564	Sequence 288564, A
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457	34	46.6	113	4	US-10-424-599-159125	Sequence 159125, A	530	34	46.6	613	5	US-10-365-620-74	Sequence 74, Appl
458	34	46.6	126	4	US-10-437-963-140201	Sequence 140201, A	531	34	46.6	614	5	US-10-912-969-76	Sequence 76, Appl
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460	34	46.6	146	4	US-10-425-114-41320	Sequence 41320, A	533	34	46.6	623	4	US-10-335-977-5268	Sequence 5268, Ap
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463	34	46.6	165	4	US-10-104-047-2538	Sequence 2538, Ap	536	34	46.6	645	5	US-10-912-969-74	Sequence 47, Appl
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551	34	46.6	942	4	US-10-425-115-245611	Sequence 245611,	624	33	45.2	164	4	US-10-425-115-355308	Sequence 355308, A
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566	34	46.6	1449	5	US-10-732-923-1694	Sequence 1694, Ap	639	33	45.2	245	5	US-10-472-928-2858	Sequence 2858, Ap
567	34	46.6	1463	4	US-10-437-963-174679	Sequence 174679,	640	33	45.2	254	5	US-10-617-320-3222	Sequence 3222, Ap
568	34	46.6	1935	6	US-11-097-143-6366	Sequence 6366, Ap	641	33	45.2	258	5	US-10-732-923-14336	Sequence 14336, A
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576	34	46.6	3011	3	US-09-995-937-20	Sequence 20, Appl	649	33	45.2	271	5	US-10-450-763-39956	Sequence 39956, A
577	34	46.6	3011	3	US-09-917-563-20	Sequence 20, Appl	650	33	45.2	285	3	US-09-898-570-41	Sequence 41, Appl
578	34	46.6	3011	4	US-10-104-966-1	Sequence 1, Appl	651	33	45.2	285	3	US-09-839-446-41	Sequence 42, Appl
579	34	46.6	3011	4	US-10-259-275-20	Sequence 20, Appl	652	33	45.2	285	3	US-09-839-446-42	Sequence 42, Appl
580	34	46.6	3011	4	US-10-184-150-3	Sequence 3, Appl	653	33	45.2	285	3	US-09-839-446-42	Sequence 42, Appl
581	34	46.6	3011	4	US-10-328-997-3	Sequence 3, Appl	654	33	45.2	287	4	US-10-085-188-6	Sequence 6, Appl
582	34	46.6	3011	4	US-10-189-359-14	Sequence 14, Appl	655	33	45.2	287	4	US-10-085-188-6	Sequence 6, Appl
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586	34	46.6	3011	5	US-11-006-313-20	Sequence 20, Appl	659	33	45.2	304	4	US-10-425-115-315906	Sequence 315906, A
587	34	46.6	3012	3	US-09-238-076-2	Sequence 2, Appl	660	33	45.2	309	4	US-10-101-464A-602	Sequence 602, App
588	34	46.6	3012	3	US-09-995-937-2	Sequence 2, Appl	661	33	45.2	309	5	US-10-864-252-602	Sequence 602, App
589	34	46.6	3012	3	US-09-917-563-2	Sequence 2, Appl	662	33	45.2	313	5	US-10-774-355A-2542	Sequence 2542, Ap
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593	34	46.6	13695	4	US-10-084-846A-3	Sequence 3, Appl	666	33	45.2	339	4	US-10-369-493-21596	Sequence 21596, A
594	33.5	45.9	652	6	US-11-097-143-2655	Sequence 2655, Ap	667	33	45.2	351	4	US-10-425-115-205881	Sequence 205881, A
595	33.5	45.9	652	6	US-11-097-143-23436	Sequence 23436, A	668	33	45.2	351	5	US-10-739-930-7374	Sequence 7374, Ap
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605	33	45.2	61	4	US-10-424-599-162826	Sequence 162826,	678	33	45.2	463	4	US-10-437-963-174802	Sequence 174802, A
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608	33	45.2	69	4	US-10-437-963-166253	Sequence 166253,	681	33	45.2	500	4	US-10-471-950-17	Sequence 17, Appl
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686	33	45.2	548	4	US-10-072-012-512	Sequence 512, App	759	32	43.8	43	4	US-10-321-857-40	Sequence 40, Appl
687	33	45.2	552	4	US-10-032-585-7097	Sequence 7097, Ap	760	32	43.8	43	4	US-10-318-675-38	Sequence 38, Appl
688	33	45.2	552	5	US-10-882-104-84	Sequence 84, Appl	761	32	43.8	43	4	US-10-318-675-40	Sequence 40, Appl
689	33	45.2	555	4	US-10-437-963-166762	Sequence 166762,	762	32	43.8	43	5	US-10-654-637-49	Sequence 49, Appl
690	33	45.2	624	4	US-10-369-493-6941	Sequence 6941, Ap	763	32	43.8	43	5	US-10-654-637-51	Sequence 51, Appl
691	33	45.2	627	6	US-11-030-965-2	Sequence 2, Appll	764	32	43.8	48	4	US-10-424-599-225632	Sequence 225632,
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697	33	45.2	714	5	US-10-983-198-42	Sequence 42, Appl	770	32	43.8	59	4	US-10-282-122A-60160	Sequence 60160, A
698	33	45.2	753	5	US-10-983-198-42	Sequence 42, Appl	771	32	43.8	61	3	US-09-912-020-357	Sequence 357, App
699	33	45.2	819	6	US-11-097-143-40590	Sequence 40590, A	772	32	43.8	61	4	US-10-282-122A-42597	Sequence 42597, A
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702	33	45.2	878	4	US-10-032-585-7515	Sequence 7515, Ap	775	32	43.8	61	4	US-10-282-122A-75943	Sequence 75943, A
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707	33	45.2	1033	4	US-10-282-122A-63149	Sequence 63149, A	780	32	43.8	65	4	US-10-424-599-167454	Sequence 167454,
708	33	45.2	1053	4	US-10-156-761-13567	Sequence 13567, A	781	32	43.8	68	3	US-09-764-891-3403	Sequence 3403, Ap
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RESULT 4  
US-10-983-453-3  
; Sequence 3, Application US/10983453  
; Publication No. US20050221347A1  
; GENERAL INFORMATION:  
; APPLICANT: Sworin, Michael  
; APPLICANT: Jensen, James C.  
; TITLE OF INVENTION: Inhibitors of Binding Between Proteins  
; TITLE OF INVENTION: and Macromolecular Ligands  
; FILE REFERENCE: 2791.1003-008  
; CURRENT APPLICATION NUMBER: US/10/983,453  
; CURRENT FILING DATE: 2004-11-08  
; PRIOR APPLICATION NUMBER: 10/082,815  
; PRIOR FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: PCT/US00/23346  
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; LENGTH: 24  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-983-453-3

Query Match 100.0%; Score 73; DB 5; Length 24;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5  
US-10-082-815-4  
; Sequence 4, Application US/10082815  
; Publication No. US20020182650A1  
; GENERAL INFORMATION:  
; APPLICANT: Jensen, James C.  
; APPLICANT: Sworin, Michael  
; TITLE OF INVENTION: INHIBITORS OF BINDING BETWEEN PROTEINS  
; TITLE OF INVENTION: AND MACROMOLECULAR LIGANDS  
; FILE REFERENCE: 2791.1003-007  
; CURRENT APPLICATION NUMBER: US/10/082,815  
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; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 26  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Disulfide cyclized fragments of Monocyte  
; OTHER INFORMATION: Chemottractant protein-1  
; OTHER INFORMATION: Disulfide bond between cysteines at positions 2  
; OTHER INFORMATION: and 26  
US-10-082-815-4

Query Match 100.0%; Score 73; DB 4; Length 26;

Best Local Similarity 100.0%; Pred. No. 3.6e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ISVQRLASYRRITSSK 16  
| | | | | | | | | | | | | | | | | |  
Db 10 ISVQRLASYRRITSSK 25  
RESULT 6  
US-10-243-795-1375  
; GENERAL INFORMATION:  
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.  
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES  
; FILE REFERENCE: 59296.00003  
; CURRENT APPLICATION NUMBER: US/10/243,795  
; CURRENT FILING DATE: 2002-09-13  
; NUMBER OF SEQ ID NOS: 1640  
; SOFTWARE: PatentIn version 3.2  
; FEATURE:  
; OTHER INFORMATION: c-term may be amidated  
US-10-243-795-1375

Query Match 100.0%; Score 73; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3.6e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
| | | | | | | | | | | | | | | | | |  
Db 10 ISVQRLASYRRITSSK 25

RESULT 7  
US-10-243-795-1411  
; GENERAL INFORMATION:  
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.  
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES  
; FILE REFERENCE: 59296.00003  
; CURRENT APPLICATION NUMBER: US/10/243,795  
; CURRENT FILING DATE: 2002-09-13  
; NUMBER OF SEQ ID NOS: 1640  
; SOFTWARE: PatentIn version 3.2  
; FEATURE:  
; OTHER INFORMATION: c-term may be amidated  
US-10-243-795-1411

Query Match 100.0%; Score 73; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3.6e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
| | | | | | | | | | | | | | | | | |  
Db 10 ISVQRLASYRRITSSK 25

RESULT 8  
US-10-243-795-1412  
; GENERAL INFORMATION:  
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.  
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES  
; FILE REFERENCE: 59296.00003  
; CURRENT APPLICATION NUMBER: US/10/243,795  
; CURRENT FILING DATE: 2002-09-13  
; NUMBER OF SEQ ID NOS: 1640  
; SOFTWARE: PatentIn version 3.2  
; FEATURE:  
; OTHER INFORMATION: c-term may be amidated  
US-10-243-795-1412

Query Match 100.0%; Score 73; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3.6e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16



```
Db      10 ISVQRLASYRRITSSK 25
|||||
RESULT 9
US-10-983-453-4
; Sequence 4, Application US/10983453
; Publication No. US20050221347A1
; GENERAL INFORMATION:
; APPLICANT: Swolin, Michael
; TITLE OF INVENTION: Inhibitors of Binding Between Proteins
; TITLE OF INVENTION: and Macromolecular Ligands
; FILE REFERENCE: 2791.1003-008
; CURRENT APPLICATION NUMBER: US/10/983,453
; CURRENT FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: 10/082,815
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/23346
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/150,230
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/150,318
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/152,421
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-983-453-4

Query Match      100.0%; Score 73; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
|||||
Db      10 ISVQRLASYRRITSSK 25

RESULT 10
US-10-243-795-1351
; Sequence 1351, Application US/10243795
; Publication No. US20040197303A1
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1351
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1351

Query Match      100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
|||||
Db      20 ISVQRLASYRRITSSK 35

RESULT 11
US-10-243-795-1352
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1352

Query Match      100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
|||||
Db      20 ISVQRLASYRRITSSK 35

RESULT 12
US-10-243-795-1353
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1353

Query Match      100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
|||||
Db      20 ISVQRLASYRRITSSK 35

RESULT 13
US-10-243-795-1354
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1354

Query Match      100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
|||||
Db      20 ISVQRLASYRRITSSK 35

RESULT 14
US-10-243-795-1355
; GENERAL INFORMATION:
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; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1355

Query Match          100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
   |||||
Db 20 ISVQRLASYRRITSSK 35

RESULT 15
US-10-243-795-1356
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1356

Query Match          100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
   |||||
Db 20 ISVQRLASYRRITSSK 35

RESULT 16
US-10-243-795-1357
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1357

Query Match          100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
   |||||
Db 20 ISVQRLASYRRITSSK 35

RESULT 17
US-10-243-795-1358
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
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; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1358

Query Match          100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
   |||||
Db 20 ISVQRLASYRRITSSK 35

RESULT 18
US-10-243-795-1359
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1359

Query Match          100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
   |||||
Db 20 ISVQRLASYRRITSSK 35

RESULT 19
US-10-243-795-1360
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1360

Query Match          100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
   |||||
Db 20 ISVQRLASYRRITSSK 35

RESULT 20
US-10-243-795-1361
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
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; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1361

Query Match      100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
      |||||
Db      20 ISVQRLASYRRITSSK 35

RESULT 21
US-10-243-795-1362
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1362

Query Match      100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
      |||||
Db      20 ISVQRLASYRRITSSK 35

RESULT 22
US-10-243-795-1363
; Sequence 1363, Application US/10243795
; Publication No. US20040197303A1
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1363
; LENGTH: 35
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1363

Query Match      100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
      |||||
Db      20 ISVQRLASYRRITSSK 35

RESULT 23
US-10-243-795-1364
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
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; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1364

Query Match      100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
      |||||
Db      20 ISVQRLASYRRITSSK 35

RESULT 24
US-10-243-795-1365
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1365

Query Match      100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
      |||||
Db      20 ISVQRLASYRRITSSK 35

RESULT 25
US-10-243-795-1366
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1366

Query Match      100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
      |||||
Db      20 ISVQRLASYRRITSSK 35

RESULT 26
US-10-243-795-1367
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
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; OTHER INFORMATION: c-term may be amidated  
US-10-243-795-1367

Query Match 100.0%; Score 73; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16  
| | | | | | | | | | | | | | | | | |  
Db 20 ISVORLASYYRRTSSK 35

RESULT 27  
US-10-243-795-1368  
; GENERAL INFORMATION:  
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.  
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES  
; FILE REFERENCE: 59296.00003  
; CURRENT APPLICATION NUMBER: US/10/243,795  
; CURRENT FILING DATE: 2002-09-13  
; NUMBER OF SEQ ID NOS: 1640  
; SOFTWARE: PatentIn version 3.2  
; FEATURE:  
; OTHER INFORMATION: c-term may be amidated  
US-10-243-795-1368

Query Match 100.0%; Score 73; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16  
| | | | | | | | | | | | | | | | | |  
Db 20 ISVORLASYYRRTSSK 35

RESULT 28  
US-10-243-795-1369  
; GENERAL INFORMATION:  
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.  
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES  
; FILE REFERENCE: 59296.00003  
; CURRENT APPLICATION NUMBER: US/10/243,795  
; CURRENT FILING DATE: 2002-09-13  
; NUMBER OF SEQ ID NOS: 1640  
; SOFTWARE: PatentIn version 3.2  
; FEATURE:  
; OTHER INFORMATION: c-term may be amidated  
US-10-243-795-1369

Query Match 100.0%; Score 73; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16  
| | | | | | | | | | | | | | | | | |  
Db 20 ISVORLASYYRRTSSK 35

RESULT 29  
US-10-243-795-1370  
; GENERAL INFORMATION:  
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.  
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES  
; FILE REFERENCE: 59296.00003  
; CURRENT APPLICATION NUMBER: US/10/243,795  
; CURRENT FILING DATE: 2002-09-13  
; NUMBER OF SEQ ID NOS: 1640  
; SOFTWARE: PatentIn version 3.2  
; FEATURE:  
; OTHER INFORMATION: c-term may be amidated  
US-10-243-795-1370

Query Match 100.0%; Score 73; DB 4; Length 35;

Best Local Similarity 100.0%; Pred. No. 5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16  
| | | | | | | | | | | | | | | | | |  
Db 20 ISVORLASYYRRTSSK 35

RESULT 30  
US-10-243-795-1371  
; GENERAL INFORMATION:  
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.  
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES  
; FILE REFERENCE: 59296.00003  
; CURRENT APPLICATION NUMBER: US/10/243,795  
; CURRENT FILING DATE: 2002-09-13  
; NUMBER OF SEQ ID NOS: 1640  
; SOFTWARE: PatentIn version 3.2  
; FEATURE:  
; OTHER INFORMATION: c-term may be amidated  
US-10-243-795-1371

Query Match 100.0%; Score 73; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16  
| | | | | | | | | | | | | | | | | |  
Db 20 ISVORLASYYRRTSSK 35

RESULT 31  
US-10-243-795-1372  
; GENERAL INFORMATION:  
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.  
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES  
; FILE REFERENCE: 59296.00003  
; CURRENT APPLICATION NUMBER: US/10/243,795  
; CURRENT FILING DATE: 2002-09-13  
; NUMBER OF SEQ ID NOS: 1640  
; SOFTWARE: PatentIn version 3.2  
; FEATURE:  
; OTHER INFORMATION: c-term may be amidated  
US-10-243-795-1372

Query Match 100.0%; Score 73; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16  
| | | | | | | | | | | | | | | | | |  
Db 20 ISVORLASYYRRTSSK 35

RESULT 32  
US-10-243-795-1373  
; GENERAL INFORMATION:  
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.  
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES  
; FILE REFERENCE: 59296.00003  
; CURRENT APPLICATION NUMBER: US/10/243,795  
; CURRENT FILING DATE: 2002-09-13  
; NUMBER OF SEQ ID NOS: 1640  
; SOFTWARE: PatentIn version 3.2  
; FEATURE:  
; OTHER INFORMATION: c-term may be amidated  
US-10-243-795-1373

Query Match 100.0%; Score 73; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16

Db 20 ISVORLASYYRITSSK 35  
|||||

## RESULT 33

US-10-243-795-1374  
; GENERAL INFORMATION:  
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.  
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES  
; FILE REFERENCE: 59296.00003  
; CURRENT APPLICATION NUMBER: US/10/243,795  
; CURRENT FILING DATE: 2002-09-13  
; NUMBER OF SEQ ID NOS: 1640  
; SOFTWARE: PatentIn version 3.2  
; FEATURE:  
; OTHER INFORMATION: c-term may be amidated  
US-10-243-795-1374

Query Match 100.0%; Score 73; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16  
|||||  
Db 20 ISVORLASYYRITSSK 35  
|||||

## RESULT 34

US-10-243-795-1413  
; GENERAL INFORMATION:  
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.  
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES  
; FILE REFERENCE: 59296.00003  
; CURRENT APPLICATION NUMBER: US/10/243,795  
; CURRENT FILING DATE: 2002-09-13  
; NUMBER OF SEQ ID NOS: 1640  
; SOFTWARE: PatentIn version 3.2  
; FEATURE:  
; OTHER INFORMATION: c-term may be amidated  
US-10-243-795-1413

Query Match 100.0%; Score 73; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16  
|||||  
Db 20 ISVORLASYYRITSSK 35  
|||||

## RESULT 35

US-10-243-795-1378  
; GENERAL INFORMATION:  
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.  
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES  
; FILE REFERENCE: 59296.00003  
; CURRENT APPLICATION NUMBER: US/10/243,795  
; CURRENT FILING DATE: 2002-09-13  
; NUMBER OF SEQ ID NOS: 1640  
; SOFTWARE: PatentIn version 3.2  
; FEATURE:  
; OTHER INFORMATION: c-term may be amidated  
US-10-243-795-1378

Query Match 100.0%; Score 73; DB 4; Length 41;  
Best Local Similarity 100.0%; Pred. No. 6e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16  
|||||  
Db 8 ISVORLASYYRITSSK 23  
|||||

## RESULT 36

US-10-243-795-1416  
; GENERAL INFORMATION:  
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.  
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES  
; FILE REFERENCE: 59296.00003  
; CURRENT APPLICATION NUMBER: US/10/243,795  
; CURRENT FILING DATE: 2002-09-13  
; NUMBER OF SEQ ID NOS: 1640  
; SOFTWARE: PatentIn version 3.2  
; FEATURE:  
; OTHER INFORMATION: c-term may be amidated  
US-10-243-795-1416

Query Match 100.0%; Score 73; DB 4; Length 41;  
Best Local Similarity 100.0%; Pred. No. 6e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16  
|||||  
Db 8 ISVORLASYYRITSSK 23  
|||||

## RESULT 37

US-10-339-778-4  
; Sequence 4, Application US/10339778  
; Publication No. US20030129214A1  
; GENERAL INFORMATION:  
; APPLICANT: Bornstein, P.  
; TITLE OF INVENTION: METHODS OF ENHANCING THE BIOCOMPATIBILITY OF AN IMPLANTABLE MEDIC  
; FILE REFERENCE: UWOTL-1-20275  
; CURRENT APPLICATION NUMBER: US/10/339,778  
; CURRENT FILING DATE: 2003-01-09  
; PRIOR APPLICATION NUMBER: US 60/347,560  
; PRIOR FILING DATE: 2002-01-10  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 69  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(69)  
; OTHER INFORMATION: MCP-1 truncation  
US-10-339-778-4

Query Match 100.0%; Score 73; DB 4; Length 69;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16  
|||||  
Db 13 ISVORLASYYRITSSK 28  
|||||

## RESULT 38

US-10-276-971-2  
; Sequence 2, Application US/10276971  
; Publication No. US20030162737A1  
; GENERAL INFORMATION:  
; APPLICANT: Egashira Kensuke  
; APPLICANT: Yoshikazu Yonemitsu  
; APPLICANT: Katsuo Sueishi  
; APPLICANT: Yasuhiro Ikeda  
; APPLICANT: Yoshiyuki Inada  
; TITLE OF INVENTION: Preventatives and Remedies for Pulmonary Hypertension  
; FILE REFERENCE: 2733 USOP  
; CURRENT APPLICATION NUMBER: US/10/276,971  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 4

; SEQ ID NO 2  
; LENGTH: 69  
; TYPE: PRT  
; ORGANISM: Human  
US-10-276-971-2

Query Match 100.0%; Score 73; DB 4; Length 69;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
| | | | | | | | | | | | | | | | | |  
Db 13 ISVQRLASYRRITSSK 28

## RESULT 39

US-09-195-457-5  
; Sequence 5, Application US/09195457  
; Patent No. US20020081623A1  
; GENERAL INFORMATION:  
; APPLICANT: WILLIAMS, TIMOTHY J.  
; APPLICANT: JOSE, PETER J.  
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.  
; APPLICANT: HSUAN, JOHN J.  
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE  
; FILE REFERENCE: 550-33  
; CURRENT APPLICATION NUMBER: US/09/195,457  
; CURRENT FILING DATE: 1998-11-18  
; PRIOR APPLICATION NUMBER: 08/470,323  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: PCT/GB94/02006  
; PRIOR FILING DATE: 1994-09-14  
; PRIOR APPLICATION NUMBER: GB 9318984.3  
; PRIOR FILING DATE: 1993-09-14  
; PRIOR APPLICATION NUMBER: GB 94086902.2  
; PRIOR FILING DATE: 1994-04-29  
; NUMBER OF SEQ ID NOS: 11  
; SEQ ID NO 5  
; LENGTH: 76  
; TYPE: PRT  
; ORGANISM: human  
US-09-195-457-5

Query Match 100.0%; Score 73; DB 3; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
| | | | | | | | | | | | | | | | | |  
Db 20 ISVQRLASYRRITSSK 35

## RESULT 40

US-09-792-793A-20  
; Sequence 20, Application US/09792793A  
; Patent No. US20020168370A1  
; GENERAL INFORMATION:  
; APPLICANT: McDonald, John R.  
; APPLICANT: Coggin, Philip  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS  
; FILE REFERENCE: 25020-601D  
; CURRENT APPLICATION NUMBER: US/09/792,793A  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 76  
; TYPE: PRT  
; ORGANISM: homo sapien  
; FEATURE:  
; OTHER INFORMATION: Human Chemokine Polypeptide: MCP-1  
US-09-792-793A-20

Query Match 100.0%; Score 73; DB 3; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
| | | | | | | | | | | | | | | | | |  
Db 20 ISVQRLASYRRITSSK 35

## RESULT 41

US-10-339-778-3  
; Sequence 3, Application US/10339778  
; Publication No. US20030129214A1  
; GENERAL INFORMATION:  
; APPLICANT: Bornstein, P.  
; APPLICANT: Kyriakides, T.  
; TITLE OF INVENTION: METHODS OF ENHANCING THE BIOCOMPATIBILITY OF AN IMPLANTABLE MEDIC  
; TITLE OF INVENTION: DEVICE  
; FILE REFERENCE: UWOTL-1-20275  
; CURRENT APPLICATION NUMBER: US/10/339,778  
; CURRENT FILING DATE: 2003-01-09  
; PRIOR APPLICATION NUMBER: US 60/347,560  
; PRIOR FILING DATE: 2002-01-10  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 76  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-339-778-3

Query Match 100.0%; Score 73; DB 4; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
| | | | | | | | | | | | | | | | | |  
Db 20 ISVQRLASYRRITSSK 35

## RESULT 42

US-10-276-971-1  
; Sequence 1, Application US/10276971  
; Publication No. US20030162737A1  
; GENERAL INFORMATION:  
; APPLICANT: Egashira Kensuke  
; APPLICANT: Yoshikazu Yonemitsu  
; APPLICANT: Katsuo Sueishi  
; APPLICANT: Yasuhiro Ikeda  
; APPLICANT: Yoshiyuki Inada  
; TITLE OF INVENTION: Preventatives and Remedies for Pulmonary Hypertension  
; FILE REFERENCE: 2733 US0P  
; CURRENT APPLICATION NUMBER: US/10/276,971  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 4  
; SEQ ID NO 1  
; LENGTH: 76  
; TYPE: PRT  
; ORGANISM: Human  
US-10-276-971-1

Query Match 100.0%; Score 73; DB 4; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16  
| | | | | | | | | | | | | | | | | |  
Db 20 ISVQRLASYRRITSSK 35

## RESULT 43

US-10-375-209A-20

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; Sequence 20, Application US/10375209A
; Publication No. US20030215421A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggin, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601E
; CURRENT APPLICATION NUMBER: US/10/375,209A
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 76
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; OTHER INFORMATION: Human Chemokine Polypeptide: MCP-1
US-10-375-209A-20

Query Match 100.0%; Score 73; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQLASYYRRTTSK 16
| | | | | | | | | | | | | | | |
Db 20 ISVQLASYYRRTTSK 35
| | | | | | | | | | | | | | | |

RESULT 44
US-10-332-038A-5
; Sequence 5, Application US/10332038A
; Publication No. US2004007835A1
; GENERAL INFORMATION:
; APPLICANT: Gryphon Therapeutics, Inc.
; APPLICANT: Offord, Robin
; APPLICANT: Gaertner, Hubert
; APPLICANT: Hartley, Oliver
; TITLE OF INVENTION: Chemokine Receptor Modulators, Production and Use
; FILE REFERENCE: 03504.271
; CURRENT APPLICATION NUMBER: US/10/332,038A
; CURRENT FILING DATE: 2003-05-06
; PRIOR FILING DATE: 2003-05-06
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-332-038A-5

Query Match 100.0%; Score 73; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQLASYYRRTTSK 16
| | | | | | | | | | | | | | | |
Db 20 ISVQLASYYRRTTSK 35
| | | | | | | | | | | | | | | |

RESULT 45
US-10-668-733-7
; Sequence 7, Application US/10668733
; Publication No. US20040138422A1
; GENERAL INFORMATION:
; APPLICANT: Demotz et al.
; TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS
; FILE REFERENCE: 29964/3872A
; CURRENT APPLICATION NUMBER: US/10/668,733
; CURRENT FILING DATE: 2003-09-23
; PRIOR FILING DATE: 2002-09-23
```

```
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: misc feature
; LOCATION: (75)..(75)
; OTHER INFORMATION: The Lysine at position 75 is biotinylated
US-10-668-733-7

Query Match 100.0%; Score 73; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQLASYYRRTTSK 16
| | | | | | | | | | | | | | | |
Db 20 ISVQLASYYRRTTSK 35
| | | | | | | | | | | | | | | |

RESULT 46
US-10-668-733-14
; Sequence 14, Application US/10668733
; Publication No. US20040138422A1
; GENERAL INFORMATION:
; APPLICANT: Demotz et al.
; TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS
; FILE REFERENCE: 29964/3872A
; CURRENT APPLICATION NUMBER: US/10/668,733
; CURRENT FILING DATE: 2003-09-23
; PRIOR FILING DATE: 2003-09-23
; PRIOR FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-668-733-14

Query Match 100.0%; Score 73; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQLASYYRRTTSK 16
| | | | | | | | | | | | | | | |
Db 20 ISVQLASYYRRTTSK 35
| | | | | | | | | | | | | | | |

RESULT 47
US-10-393-804A-1
; Sequence 1, Application US/10393804A
; Publication No. US20040185450A1
; GENERAL INFORMATION:
; APPLICANT: Heavner, George
; APPLICANT: Das, Anuk
; TITLE OF INVENTION: MCP-1 MUTANT PROTEINS, ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0290NP
; CURRENT APPLICATION NUMBER: US/10/393,804A
; CURRENT FILING DATE: 2003-03-21
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-10-393-804A-1

Query Match 100.0%; Score 73; DB 4; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASVRRITSSK 16  
|||||  
Db 20 ISVQRLASYRRITSSK 35

RESULT 48

US-10-243-795-7  
; Sequence 7, Application US/10243795  
; Publication No. US20040197303A1  
; GENERAL INFORMATION:  
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.  
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES  
; FILE REFERENCE: 59296.00003  
; CURRENT APPLICATION NUMBER: US/10/243,795  
; CURRENT FILING DATE: 2002-09-13  
; NUMBER OF SEQ ID NOS: 1640  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 76  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

US-10-243-795-7

Query Match 100.0%; Score 73; DB 4; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASVRRITSSK 16  
|||||  
Db 20 ISVQRLASYRRITSSK 35

RESULT 49

US-10-872-198-102  
; Sequence 102, Application US/10872198  
; Publication No. US20050002897A1  
; GENERAL INFORMATION:  
; APPLICANT: Ulrich HAUPTS  
; APPLICANT: Andre KOLTERMANN  
; APPLICANT: Andreas SCHEIDIG  
; APPLICANT: Christian VOETSMIEIER  
; APPLICANT: Ulrich Kettling  
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF  
; FILE REFERENCE: 04156.0002U4  
; CURRENT APPLICATION NUMBER: US/10/872,198  
; CURRENT FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 60/543,518  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/524,960  
; PRIOR FILING DATE: 2003-11-25  
; PRIOR APPLICATION NUMBER: EP 04003058  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: EP 03025871  
; PRIOR FILING DATE: 2003-11-11  
; PRIOR APPLICATION NUMBER: EP 03025851  
; PRIOR FILING DATE: 2003-11-10  
; PRIOR APPLICATION NUMBER: EP 03013819  
; PRIOR FILING DATE: 2003-06-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 102  
; LENGTH: 76  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-872-198-102

Query Match 100.0%; Score 73; DB 5; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASVRRITSSK 16  
|||||  
Db 20 ISVQRLASYRRITSSK 35

RESULT 50

US-10-839-017-8  
; Sequence 8, Application US/10839017  
; Publication No. US20050058635A1  
; GENERAL INFORMATION:  
; APPLICANT: DEMUTH, HANS-ULRICH  
; APPLICANT: HOFFMANN, TORSTEN  
; APPLICANT: NIESTROJ, ANDRE J.  
; APPLICANT: SCHILLING, STEPHAN  
; TITLE OF INVENTION: USE OF EFFECTORS OF GLUTAMINYL CYCLASE  
; FILE REFERENCE: 20488-53  
; CURRENT APPLICATION NUMBER: US/10/839,017  
; CURRENT FILING DATE: 2004-05-05  
; PRIOR APPLICATION NUMBER: 60/468,043  
; PRIOR FILING DATE: 2003-05-05  
; PRIOR APPLICATION NUMBER: 60/512,038  
; PRIOR FILING DATE: 2003-10-15  
; PRIOR APPLICATION NUMBER: 60/468,014  
; PRIOR FILING DATE: 2003-05-05  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 8  
; LENGTH: 76  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-839-017-8

Query Match 100.0%; Score 73; DB 5; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASVRRITSSK 16  
|||||  
Db 20 ISVQRLASYRRITSSK 35

Search completed: February 6, 2006, 14:33:50  
Job time : 189 secs



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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:42:04 ; Search time 21.9909 Seconds  
(without alignments)  
1518.479 Million cell updates/sec

Title: US-10-644-277-149

Perfect score: 405

Sequence: 1 QPDALNAPVTCCYNFTNRKI.....QKWQDSMDHLDKQTQTPKT 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_21.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004as.\*

9: Geneseqp2005as.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	405	100.0	76	2	AAR28660 MCF. 3/20
2	405	100.0	76	2	AAR87680 Monocyte
3	405	100.0	76	3	AAY69030 Amino aci
4	405	100.0	76	5	AAO20010 Human che
5	405	100.0	76	5	AAO14143 Human MCP
6	405	100.0	76	5	AAM53048 Human mon
7	405	100.0	76	7	ADC89673 Human mat
8	405	100.0	76	7	ADD14998 Human mon
9	405	100.0	76	7	ADE80852 huMCP1 ch
10	405	100.0	76	7	ADE06777 Human MCP
11	405	100.0	76	8	ADK52443 Human MCP
12	405	100.0	76	8	ADM70376 Human MCP
13	405	100.0	76	8	ADS19898 Modified
14	405	100.0	76	8	ADS19905 Human che
15	405	100.0	76	8	ADS75929 Monocyte
16	405	100.0	76	8	ADR70694 Macrophag
17	405	100.0	76	8	ADR70705 Macrophag
18	405	100.0	76	8	ADR70702 Macrophag
19	405	100.0	76	8	ADR70703 Macrophag
20	405	100.0	76	8	ADR70691 Human mac
21	405	100.0	76	8	ADR70696 Macrophag
22	405	100.0	76	8	ADR70704 Macrophag
23	405	100.0	76	8	ADR70695 Macrophag
24	405	100.0	76	8	ADR70700 Macrophag

25	405	100.0	76	8	ADR70693 Macrophag
26	405	100.0	76	8	ADR70698 Macrophag
27	405	100.0	76	8	ADR70706 Macrophag
28	405	100.0	76	8	ADR70697 Macrophag
29	405	100.0	76	8	ADR70699 Macrophag
30	405	100.0	76	8	ADR70701 Macrophag
31	405	100.0	76	8	ADU24450 Novel glu
32	405	100.0	76	8	ADU46724 CCL2, sub
33	405	100.0	76	9	ADV90272 Proteasee-
34	405	100.0	76	9	ADV91968 Human mat
35	405	100.0	76	9	ADZ58557 Mature hu
36	405	100.0	76	9	ADZ71380 N-termina
37	405	100.0	76	9	AEA16549 Human mon
38	405	100.0	76	9	AE92582 Glutaminyl
39	405	100.0	98	8	ADJ36261 Self-coal
40	405	100.0	99	1	AAP95387 Human mon
41	405	100.0	99	2	AAR28663 MCF. 3/20
42	405	100.0	99	2	AAR73914 Human mon
43	405	100.0	99	2	AAR70800 Chemoattr
44	405	100.0	99	2	AAW40174 Macrophag
45	405	100.0	99	2	AAY26176 Monocyte

#### ALIGNMENTS

##### RESULT 1

AAR28660

ID AAR28660 standard; protein; 76 AA.

XX AC AAR28660;

XX DT 25-MAR-2003 (revised)

DT 24-MAR-1993 (first entry)

XX DE MCF.

XX KW Plasmid; monocyte chemotactic factor; MCF; translation; termination;

KW terminator; initiation; ribosome binding site; RBS; promoter; tryptophan;

XX KW repressor.

XX OS Synthetic.

XX PN WO9219737-A1.

XX PD 12-NOV-1992.

XX PF 27-APR-1992; 92WO-JP000550.

XX PR 09-MAY-1991; 91JP-00135950.

XX PA (DAIN ) DAINIPPON PHARM CO LTD.

XX PI Yamagishi J, Matsuo N, Fukui T, Yamada M;

XX DR WPI; 1992-398864/48.

XX DR N-PSDB; AAQ30745, AAQ30746.

XX PT Prodn. of polypeptide(s) having monocyte chemotactic activity - using

XX PT expression plasmids with E. coli elements and specific E.coli strains.

XX PS Claim 1; Page 48 + Page 36; 56pp; English.

XX CC An expression plasmid, pHM483, for producing MCF(76) consisting of 76

XX CC amino acids was constructed. The prod. can be used for e.g. treating

XX CC bacterial infectious diseases. (Updated on 25-MAR-2003 to correct PN

XX CC field.)

XX SQ Sequence 76 AA;

Query Match 100.0%; Score 405; DB 2; Length 76;

Best Local Similarity 100.0%; Pred. No. 1.3e-42;

Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
QY 61 QDSMDHLDKQTPTPKT 76
DB 61 QDSMDHLDKQTPTPKT 76

RESULT 2
AAR87680
ID AAR87680 standard; protein; 76 AA.
XX
AC AAR87680;
XX
DT 05-MAR-1996 (first entry)
DE Monocyte chemotactic activating factor for use as wound remedy.
XX monocyte chemotactic activating factor; MCAF; wound remedy.
XX Homo sapiens.
XX
XX WO9507710-A1.
XX
XX 23-MAR-1995.
XX
XX 13-SEP-1994; 94WO-JP001512.
XX
XX 13-SEP-1993; 93JP-00227385.
XX (TORA ) TORAY IND INC.
XX Matsushima K, Naruto M;
XX WPI; 1995-131181/17.
XX Wound treatment using monocyte chemotactic factor - has potent
PT therapeutic effect on skin wounds and ulcers.
XX Disclosure; Page 12; 22pp; Japanese.
XX The invention relates to a new remedy for curing wounds which, instead of
CC comprising a growth factor, comprises a monocyte chemotactic activating
CC factor (MCAF) or its variants or derivatives. The factor has potent
CC effect on skin wounds and ulcers. The present sequence is human MCAF, the
CC activity of which is exemplified as the new remedy
XX
SQ Sequence 76 AA;
Query Match 100.0%; Score 405; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
QY 61 QDSMDHLDKQTPTPKT 76
DB 61 QDSMDHLDKQTPTPKT 76

RESULT 3
AAY69030
ID AAY69030 standard; protein; 76 AA.
XX
AC AAY69030;
XX
DT 30-MAY-2000 (first entry)
DE Amino acid sequence of chemokine receptor ligand MCP-1.
```

```
XX Chemokine receptor; ligand; inflammatory response; immune effector cell;
KW secondary tissue damage; central nervous system injury; MCP-1;
KW CNS inflammatory disease; neurodegenerative disorder; heart disease;
KW inflammatory eye disease; inflammatory bowel disease;
KW inflammatory joint disease; inflammatory kidney; renal disease;
KW inflammatory lung disease; inflammatory nasal disease;
KW inflammatory thyroid disease; thyroiditis; cytokine-regulated cancer.
XX
OS Homo sapiens.
XX
XX WO200004926-A2.
XX
XX 03-FEB-2000.
XX
XX 21-JUL-1999; 99WO-CA000659.
XX
XX 22-JUL-1998; 98US-00120523.
XX (OSPR-) OSPREY PHARM LTD.
XX
XX McDonald JR, Coggins PJ;
XX WPI; 2000-182542/16.
XX
XX A new therapeutic agent comprising a conjugate for treating secondary
PT tissue damage and other disease conditions like Alzheimer's disease,
PT stroke, Parkinson's disease and atherosclerosis.
XX
XX Disclosure; Page 60; 204pp; English.
XX
XX The present sequence represents a chemokine receptor ligand. The present
CC ligand can be incorporated into the conjugates of the invention. The
CC specification describes a conjugate, comprising a targeted agent and a
CC chemokine receptor ligand. The conjugate binds to a chemokine receptor
CC resulting in internalisation of the targeted agent in cells bearing the
CC receptor. The conjugates are used for formulating a medicament or for
CC treating disorders associated with inflammatory responses resulting from
CC activation, proliferation and migration of immune effector cells. The
CC disorders or disease states comprise secondary tissue damage such as
CC central nervous system (CNS) injury, CNS inflammatory diseases,
CC neurodegenerative disorders, heart disease, inflammatory eye diseases,
CC inflammatory bowel diseases, inflammatory joint diseases, inflammatory
CC kidney or renal diseases, inflammatory lung diseases, inflammatory nasal
CC diseases, inflammatory thyroid disease such as thyroiditis, or cytokine-
CC regulated cancers
XX
SQ Sequence 76 AA;
Query Match 100.0%; Score 405; DB 3; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 1 QPDAINAPVTCVNFNTRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
QY 61 QDSMDHLDKQTPTPKT 76
DB 61 QDSMDHLDKQTPTPKT 76

RESULT 4
AAO20010
ID AAO20010 standard; protein; 76 AA.
XX
XX AAO20010;
XX
DT 11-JUN-2002 (first entry)
DE Human chemokine MCP-1 protein.
XX
XX Human; chemokine; anti-HIV; antiasthmatic; antiarthritic; antirheumatic;
```

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XX Preventives and remedies for pulmonary hypertension containing mutant of  
 PT MCP-1 antagonistic inhibitory type or its salt, encoded DNA or  
 PT neutralization antibody.

XX Disclosure; Page 31; 39pp; Japanese.

XX The invention relates to preventives and remedies for pulmonary  
 CC hypertension, comprising an antagonistic inhibitory mutant of monocyte  
 CC chemoattractant protein-1 (MCP-1), DNA encoding the mutant MCP-1, or a  
 CC neutralising antibody against MCP-1. MCP-1 is a member of the C-C  
 CC chemokine family. The preventives and remedies have hypotensive activity  
 CC and can be used in the prevention and treatment of pulmonary hypertension  
 CC particularly pulmonary primary hypertension. The present sequence  
 CC represents wild-type human MCP-1

XX Sequence 76 AA;

Query Match 100.0%; Score 405; DB 5; Length 76;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-42;  
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60  
 DB 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60  
 QY 61 QDSMDHLDKQTQTPKT 76  
 DB 61 QDSMDHLDKQTQTPKT 76

RESULT 7  
 ADC89673

ID ADC89673 standard; protein; 76 AA.

AC ADC89673;

DT 01-JAN-2004 (first entry)

DE Human mature MCP-1 SEQ ID NO:4.

XX human; MCP-1; monocyte chemoattractant protein; MCP; immunosuppressive;  
 KW antiinflammatory; cytostatic; antimicrobial; vasotropic; gene therapy;  
 KW MCP-2; MCP-3; MCP-4; Eotaxin; leukocyte migration; leukocyte activation;  
 KW vascular disorder; cancer; inflammatory; autoimmune disease; infection.

XX Synthetic.

OS Homo sapiens.

XX WO2003084993-A1.

XX 16-OCT-2003.

XX 09-APR-2003; 2003WO-EP050097.

XX 10-APR-2002; 2002US-0371442P.

XX (ISTP ) ARS APPLIED RES SYSTEMS HOLDING NV.

XX Proudfoot A, Kosco-Vilbois M, Handel T;

XX WPI; 2003-804294/75.

XX New antagonists of MCP proteins, useful in preparing a composition for  
 PT treating or preventing diseases related to excessive leukocyte migration  
 PT and activation e.g. vascular, inflammatory or autoimmune disease, cancer  
 PT or infection.

XX Example 3; SEQ ID NO 4; 63pp; English.

XX The invention relates to novel antagonists of MCP proteins comprising  
 CC mutants of MCP proteins in which the following combinations of residues,  
 CC numbered on the sequence of human mature MCP-1, are substituted to

CC Alanine, Glycine, Serine, Threonine, Proline, Aspartic Acid, Asparagine,  
 CC Glutamic Acid or Glutamine: 18 and/or 19; 18 and/or 19, together with 58; 18  
 CC and/or 19, together with 66; 18 and/or 19, together with 58 and 66; and  
 CC 18 and/or 19, together with 24, 44, 49 and/or 75. A protein of the  
 CC invention has immunosuppressive, antiinflammatory, cytostatic,  
 CC antimicrobial, and vasotropic activity. The protein may have a use in  
 CC MCP-2, human MCP-3, human MCP-4 or human Eotaxin. The MCP antagonists are  
 CC useful in preparing a composition for treating or preventing diseases  
 CC related to excessive leukocyte migration and activation, e.g., vascular  
 CC disorders, cancer, inflammatory or autoimmune disease or infection. The  
 CC present sequence is used in the exemplification of the invention.

XX Sequence 76 AA;

Query Match 100.0%; Score 405; DB 7; Length 76;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-42;  
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60  
 DB 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76

DB 61 QDSMDHLDKQTQTPKT 76

RESULT 8  
 ADD14998

ID ADD14998 standard; protein; 76 AA.

AC ADD14998;

XX 15-JAN-2004 (first entry)

XX Human monocyte chemoattractant protein-1 (MCP-1) mature protein.

XX antiinflammatory; MCP-1 Antagonist; biocompatibility; medical device;  
 KW monocyte chemoattractant protein 1; MCP-1; MCP-1 antagonist;  
 KW chronic inflammation; fibrous encapsulation; human.

XX Homo sapiens.

XX US2003129214-A1.

XX 10-JUL-2003.

XX 09-JAN-2003; 2003US-00339778.

XX 10-JAN-2002; 2002US-0347560P.

XX (UNIW ) UNIV WASHINGTON.

XX Bornstein P, Kyriakides T;

XX WPI; 2003-787133/74.

XX N-PSDB; ADD14996.

XX Enhancing biocompatibility of a medical device implanted in a portion of  
 PT a living body by contacting the portion of the body that is in contact  
 PT with the implanted device with monocyte chemoattractant protein 1 (MCP-1)  
 PT antagonist.

XX Disclosure; SEQ ID NO 3; 18pp; English.

XX The invention describes a method of enhancing (M1) the biocompatibility  
 CC of a medical device implanted within a portion of a living body  
 CC comprising contacting a portion of the living body in contact with the  
 CC device with a monocyte chemoattractant protein 1 (MCP-1) antagonist to  
 CC inhibit chronic inflammation induced by the presence of the medical  
 CC device or fibrous encapsulation of the medical device. The method is  
 CC useful for enhancing the biocompatibility of a medical device implanted

CC in a portion of a living body by inhibiting chronic inflammation or  
CC formation of fibrous capsules around the device. This is the amino acid  
CC sequence of human monocyte chemoattractant protein-1 (MCP-1) mature  
CC protein.  
XX

SQ Sequence 76 AA;

Query Match 100.0%; Score 405; DB 7; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.3e-42;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNFKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60  
DB 1 QPDAINAPVTCYNTNFKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

QY 61 QDSMDHLDKQTPTPKT 76

DB 61 QDSMDHLDKQTPTPKT 76

RESULT 9

ADE80852  
ID ADE80852 standard; peptide; 76 AA.

XX AC ADE80852;

DT 29-JAN-2004 (first entry)

XX huMCP1 chemokine.

XX Nuclear targeting peptide; nuclear targeting domain; ESKine; PESKY;  
XX chemokine; cancer; cytostatic; huMCP1; chemokine.

XX Unidentified.

XX WO2003082920-A1.

XX 09-OCT-2003.

XX 02-APR-2003; 2003WO-GB001472.

XX 02-APR-2002; 2002GB-00007624.

XX (CANC-) CANCER RES TECHNOLOGY LTD.

XX Graham G;

XX WPI; 2003-788341/74.

XX New nuclear targeting peptide comprising a nuclear targeting domain  
PT isolated from a chemokine, useful for preparing a medicament for treating  
PT cancer, particularly Burkitt's lymphoma or nasopharyngeal carcinoma.

XX Disclosure; Fig 11; 66pp; English.

XX The present invention relates to a nuclear targeting peptide (ADE80826)  
CC comprising a nuclear targeting domain isolated from the C-terminal  
CC sequence of the ESKine and PESKY chemokines. The nuclear targeting domain  
CC allows the protein to translocate to the cell nucleus. The nuclear  
CC targeting peptide is useful in preparing a medicament for treating  
CC cancer, particularly Burkitt's lymphoma or nasopharyngeal carcinoma. The  
CC present sequence is a chemokine sequence, used in a sequence alignment in  
CC the invention.  
XX

SQ Sequence 76 AA;

Query Match 100.0%; Score 405; DB 7; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.3e-42;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNFKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

DB 1 QPDAINAPVTCYNTNFKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

QY 61 QDSMDHLDKQTPTPKT 76  
DB 61 QDSMDHLDKQTPTPKT 76

RESULT 10

ADE06777  
ID ADE06777 standard; protein; 76 AA.

XX AC ADE06777;

DT 29-JAN-2004 (first entry)

XX Human MCP-1 SEQ ID NO:1.

XX human; MCP-1; monocyte chemoattractant protein-1; immunosuppressive;  
XX cardiant; neuroprotective; antimicrobial; cytostatic; gene therapy;  
XX immune disorder; cardiovascular disorder; neurological disorder;  
XX infectious disorder; malignant disorder.

XX Homo sapiens.

XX WO2003083059-A2.

XX 09-OCT-2003.

XX 24-MAR-2003; 2003WO-US009056.

XX 26-MAR-2002; 2002US-0367932P.

XX (CENZ ) CENTOCOR INC.

XX Heavner GA, Das A;

XX WPI; 2003-804039/75.

XX New monocyte chemoattractant protein-1 (MCP-1) mutein nucleic acid,  
PT useful for diagnosing or treating a MCP-1 mutein-related condition, e.g.  
PT immune, cardiovascular, neurologic or infectious or malignant disorders.

XX Claim 1; SEQ ID NO 1; 81pp; English.

XX The invention relates to a novel monocyte chemoattractant protein-1 (MCP-  
CC 1) mutant nucleic acid. A protein of the invention has immunosuppressive,  
CC cardiant, neuroprotective, antimicrobial, and cytostatic activity. A  
CC polynucleotide of the invention may have a use in gene therapy. The  
CC protein, nucleic acid, composition and method are useful for diagnosing  
CC or treating a MCP-1 mutein-related condition, e.g. immune,  
CC cardiovascular, neurologic or infectious or malignant disorders. The  
CC present sequence represents human MCP-1.

XX Sequence 76 AA;

Query Match 100.0%; Score 405; DB 7; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.3e-42;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNFKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

DB 1 QPDAINAPVTCYNTNFKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

QY 61 QDSMDHLDKQTPTPKT 76

DB 61 QDSMDHLDKQTPTPKT 76

RESULT 11

ADK52443  
ID ADK52443 standard; protein; 76 AA.

XX AC ADK52443;

XX



Dd	1	QPDAINAPVTCCYNFTNRKISVORLASYYRRITSSKCPKEAVIFKTIVAKEICADPQKQKW	60
Qy	61	QDSMDHLDKQTQTPKT	76
Dd	61	QDSMDHLDKQTQTPKT	76
RESULT 13			
ADS19898	ID	ADS19898 standard; protein; 76 AA.	
XX	AC	ADS19898;	
XX	AC	ADS19898;	
DT	18-NOV-2004	(first entry)	
XX	XX	Modified human chemokine CCL2/MCP-1 polypeptide SEQ ID NO: 7.	
DE	XX	human; chemokine; CCL2; receptor-binding; labeled chemokine;	
KW	XX	chemokine receptor assay; MCP-1.	
KW	XX	chemokine receptor assay; MCP-1.	
XX	XX	Homo sapiens.	
OS	OS	Synthetic.	
XX	XX	XX	
FH	Key	Location/Qualifiers	
FT	Modified-site	75	
FT		/note= "biotinylated"	
XX	XX	WO2004026893-A2.	
XX	XX	01-APR-2004.	
PD	XX	23-SEP-2003; 2003WO-EP010698.	
PF	XX	23-SEP-2002; 2002US-0412866P.	
PR	XX	(RMFD-) RMF DICTAGENE SA.	
XX	XX	Demotz S, Moulon C, Strong A, Vizzavona J, Cousin P, Raymond C;	
PI	PI	Roggero M;	
XX	XX	WPI; 2004-295377/27.	
XX	XX	Producing detectably labeled chemokines retaining the receptor-binding	
PT	PT	specificity of unlabeled chemokines comprises introducing by chemical	
PT	PT	synthesizes a modified moiety at selected amino acid positions in the	
PT	PT	chemokines.	
XX	XX	Example 3; Page 46; 53pp; English.	
PS	XX	The present invention relates to a method of producing a detectably	
CC	CC	labeled polypeptide retaining the receptor-binding specificity of the	
CC	CC	unlabeled polypeptide, which comprises introducing by chemical synthesis	
CC	CC	a modified moiety at one or more selected amino acid positions in the	
CC	CC	polypeptide. The methods are useful for detecting chemokine receptors or	
CC	CC	for producing labeled chemokines having improved chemokine biological	
CC	CC	activity. The labeled chemokine molecules may be used in a variety of	
CC	CC	therapeutic and diagnostic applications, including in chemokine receptor	
CC	CC	assays or high-throughput screening assays. The present sequence is a	
CC	CC	modified peptide as described in the invention.	
XX	XX	Sequence 76 AA;	
XX	XX	Query Match 100.0%; Score 405; DB 8; Length 76;	
XX	XX	Best Local Similarity 100.0%; Pred No. 1.3e-42;	
XX	XX	Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	QPDAINAPVTCCYNFTNRKISVORLASYYRRITSSKCPKEAVIFKTIVAKEICADPQKQKW	60
Dd	1	QPDAINAPVTCCYNFTNRKISVORLASYYRRITSSKCPKEAVIFKTIVAKEICADPQKQKW	60
Qy	61	QDSMDHLDKQTQTPKT	76
Dd	61	QDSMDHLDKQTQTPKT	76



DE Monocyte chemoattractant protein 1 C-terminal fragment.  
XX cytosolic; prostate cancer; monocyte chemoattractant protein-1; MCP-1.  
KW Homo sapiens.  
OS  
XX  
PN WO2004080273-A2.  
XX  
PD 23-SEP-2004.  
XX  
XX 14-MAR-2004; 2004WO-IL000240.  
XX  
XX 12-MAR-2003; 2003US-0453514P.  
PR 12-MAR-2003; 2003US-0453515P.  
PR 28-NOV-2003; 2003US-0525135P.  
PR 05-JAN-2004; 2004US-0534111P.  
XX  
XX (RAPP-) RAPPAPORT FAMILY INST RES IN MEDICAL SCI.  
PA  
XX Karin N;  
PI  
XX WPI; 2004-690440/67.  
DR N-PSDB; ADS75928.  
XX  
XX Treating prostate cancer, involves administering agent capable of  
PT reducing activity and/or expression of monocyte chemoattractant protein-1  
PT or its effector to subject, thus treating prostate cancer in subject.  
XX  
XX Example; SEQ ID NO 8; 78pp; English.  
XX  
XX The invention relates to a method of treating (M1) prostate cancer, by  
CC administering an agent capable of reducing activity and/or expression of  
CC monocyte chemoattractant protein-1 (MCP-1) or its effector to a subject,  
CC thus treating the prostate cancer in the subject. (M1) is useful for  
CC treating prostate cancer. An antibody (I) to MCP-1 is useful for  
CC manufacturing a medicament for the treatment of prostate cancer. This  
CC sequence corresponds to the C-terminal fragment of the MCP-1 protein.  
XX  
SQ Sequence 76 AA;  
Query Match 100.0%; Score 405; DB 8; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.3e-42;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QPDAINAPVTCYNTNRKISVQRLASYRRTSSKCPKEAVIFKTIIVAKEICADPKQKWV 60  
Db 1 QPDAINAPVTCYNTNRKISVQRLASYRRTSSKCPKEAVIFKTIIVAKEICADPKQKWV 60  
Qy 61 QDSMDHLDKQTPTKT 76  
Db 61 QDSMDHLDKQTPTKT 76  
Search completed: February 3, 2006, 09:50:53  
Job time : 23.9909 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 6, 2006, 14:30:54 ; Search time 16 Seconds  
(Without alignments)  
11.718 Million cell updates/sec

Title: US-10-644-277-149\_COPY\_20\_35

Perfect score: 73

Sequence: 1 ISVORLASVRRITSSK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 88029

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:\*

1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB pep.\*

2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep.\*

3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep.\*

4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB pep.\*

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8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	100.0	65	7	US-11-043-788-9
2	73	100.0	99	7	US-11-043-788-8
3	56	76.7	74	6	US-10-509-232-1
4	56	76.7	97	6	US-10-995-561-900
5	46	63.0	73	6	US-10-329-472-7
6	38	52.1	44	6	US-10-957-887B-309
7	38	52.1	818	6	US-10-501-675-9
8	37	50.7	550	7	US-11-052-554A-200
9	36	49.3	1680	6	US-10-517-939-362
10	35	47.9	495	6	US-10-821-234-1154
11	35	47.9	808	7	US-11-110-082-38
12	34	46.6	3011	6	US-10-985-205-3
13	34	46.6	3194	7	US-10-052-554A-90
14	33	45.2	317	6	US-10-497-135-8
15	33	45.2	318	6	US-10-497-135-7
16	33	45.2	500	6	US-10-517-151-4
17	33	45.2	548	7	US-11-152-697-3
18	33	45.2	2828	7	US-11-080-931-54
19	33	45.2	2828	7	US-11-186-284-49
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102	30	41.1	459	6	US-10-512-376-6	Sequence 6, Appli	175	29	39.7	1247	6	US-10-055-877-10	Sequence 10, Appl
103	30	41.1	473	7	US-11-124-368A-325	Sequence 325, App	176	29	39.7	1508	7	US-11-043-889-47	Sequence 47, Appl
104	30	41.1	474	7	US-11-043-889-16	Sequence 16, Appl	177	29	39.7	3003	6	US-10-453-372-1080	Sequence 1080, Ap
105	30	41.1	481	6	US-10-512-376-5	Sequence 5, Appli	178	29	39.7	3361	6	US-10-453-372-1082	Sequence 1082, Ap
106	30	41.1	485	6	US-11-052-554A-36	Sequence 36, Appl	179	29	39.7	4655	6	US-10-995-561-556	Sequence 556, App
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109	30	41.1	593	7	US-11-169-041-239	Sequence 239, App	182	28	38.4	108	6	US-10-793-626-1636	Sequence 1636, Ap
110	30	41.1	669	6	US-10-878-556A-87	Sequence 87, Appl	183	28	38.4	175	6	US-11-098-662-124	Sequence 124, App
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113	30	41.1	980	6	US-10-995-561-771	Sequence 773, App	186	28	38.4	176	7	US-11-098-662-134	Sequence 134, App
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121	29.5	40.4	922	6	US-10-517-939-38	Sequence 38, Appl	194	28	38.4	181	7	US-11-098-662-50	Sequence 50, Appl
122	29.5	40.4	1473	7	US-11-019-711-112	Sequence 112, App	195	28	38.4	181	7	US-11-098-662-54	Sequence 54, Appl
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125	29	39.7	125	7	US-11-082-389-46	Sequence 46, Appl	198	28	38.4	181	7	US-11-098-662-66	Sequence 66, Appl
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127	29	39.7	210	6	US-10-467-657-698	Sequence 698, App	200	28	38.4	181	7	US-11-098-662-74	Sequence 74, Appl
128	29	39.7	250	6	US-10-821-234-987	Sequence 987, App	201	28	38.4	181	7	US-11-098-662-78	Sequence 78, Appl
129	29	39.7	261	6	US-10-055-877-164	Sequence 164, App	202	28	38.4	181	7	US-11-098-662-82	Sequence 82, Appl
130	29	39.7	261	6	US-10-055-877-165	Sequence 165, App	203	28	38.4	182	7	US-11-098-662-84	Sequence 84, Appl
131	29	39.7	262	6	US-10-055-877-16	Sequence 16, Appl	204	28	38.4	182	7	US-11-098-662-88	Sequence 88, Appl
132	29	39.7	262	6	US-10-055-877-18	Sequence 18, Appl	205	28	38.4	182	7	US-11-098-662-44	Sequence 44, Appl
133	29	39.7	272	6	US-10-793-626-3198	Sequence 3198, Ap	206	28	38.4	182	7	US-11-098-662-48	Sequence 48, Appl
134	29	39.7	299	6	US-10-858-730-17	Sequence 17, Appl	207	28	38.4	182	7	US-11-098-662-52	Sequence 52, Appl
135	29	39.7	312	7	US-11-217-562-4	Sequence 4, Appli	208	28	38.4	182	7	US-11-098-662-56	Sequence 56, Appl
136	29	39.7	318	6	US-10-055-877-222	Sequence 222, App	209	28	38.4	182	7	US-11-098-662-60	Sequence 60, Appl
137	29	39.7	318	6	US-10-055-877-326	Sequence 326, App	210	28	38.4	182	7	US-11-098-662-64	Sequence 64, Appl
138	29	39.7	325	6	US-10-888-730-14	Sequence 14, Appl	211	28	38.4	182	7	US-11-098-662-68	Sequence 68, Appl
139	29	39.7	362	6	US-10-467-657-2872	Sequence 2872, Ap	212	28	38.4	182	7	US-11-098-662-72	Sequence 72, Appl
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149	29	39.7	459	7	US-11-112-882-23	Sequence 23, App	222	28	38.4	185	6	US-10-467-657-3296	Sequence 3296, Ap
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152	29	39.7	476	6	US-11-055-822-942	Sequence 942, App	225	28	38.4	200	7	US-11-098-662-20	Sequence 20, Appl
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155	29	39.7	525	7	US-11-112-882-27	Sequence 27, Appl	228	28	38.4	251	6	US-10-821-234-998	Sequence 162, App
156	29	39.7	633	6	US-10-453-372-1072	Sequence 1072, Ap	229	28	38.4	262	6	US-10-055-877-162	Sequence 30, Appl
157	29	39.7	633	6	US-10-453-372-1078	Sequence 1078, Ap	230	28	38.4	291	7	US-11-078-735-30	Sequence 24, Appl
158	29	39.7	642	6	US-10-131-826A-370	Sequence 370, App	231	28	38.4	291	7	US-11-050-346-24	Sequence 167, App
159	29	39.7	745	6	US-10-532-153-15	Sequence 15, Appl	232	28	38.4	312	7	US-11-156-084-167	Sequence 359, App
160	29	39.7	778	6	US-10-821-234-1276	Sequence 1276, Ap	233	28	38.4	312	7	US-11-156-084-359	Sequence 415, App
161	29	39.7	790	6	US-10-763-712A-75	Sequence 75, Appl	234	28	38.4	330	6	US-10-485-517-415	Sequence 33, Appl
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169	29	39.7	1188	7	US-11-115-639-43	Sequence 43, Appl	242	28	38.4	385	6	US-10-714-887-220	Sequence 220, App
170	29	39.7	1194	7	US-11-000-463-249	Sequence 249, App	243	28	38.4	388	6	US-10-995-561-838	Sequence 838, App
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246	28	38.4	456	6	US-10-763-712A-44	Sequence 44, Appl	319	27	37.0	146	7	US-11-176-830-673	Sequence 673, App
247	28	38.4	456	6	US-10-966-483-34	Sequence 34, Appl	320	27	37.0	146	7	US-11-176-830-674	Sequence 674, App
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250	28	38.4	479	6	US-11-021-441-20	Sequence 20, Appl	323	27	37.0	146	7	US-11-176-830-677	Sequence 677, App
251	28	38.4	480	6	US-10-878-556A-198	Sequence 198, Appl	324	27	37.0	146	7	US-11-176-830-678	Sequence 678, App
252	28	38.4	480	6	US-10-521-162-40	Sequence 40, Appl	325	27	37.0	146	7	US-11-176-830-679	Sequence 679, App
253	28	38.4	484	7	US-11-078-735-43	Sequence 43, Appl	326	27	37.0	146	7	US-11-176-830-680	Sequence 680, App
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256	28	38.4	490	6	US-11-021-441-26	Sequence 26, Appl	329	27	37.0	146	7	US-11-176-830-683	Sequence 683, App
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262	28	38.4	531	6	US-11-010-239-32	Sequence 32, Appl	335	27	37.0	185	6	US-10-453-372-846	Sequence 846, App
263	28	38.4	532	6	US-10-821-234-1071	Sequence 1071, Ap	336	27	37.0	185	6	US-10-821-234-1384	Sequence 1384, Ap
264	28	38.4	541	7	US-11-024-959-463	Sequence 463, App	337	27	37.0	197	6	US-10-714-887-98	Sequence 98, Appl
265	28	38.4	542	7	US-11-074-176-30	Sequence 30, Appl	338	27	37.0	199	7	US-11-052-554A-84	Sequence 84, Appl
266	28	38.4	551	7	US-11-143-984A-32	Sequence 32, Appl	339	27	37.0	212	7	US-11-214-199-4	Sequence 4, Appli
267	28	38.4	687	6	US-10-821-234-1197	Sequence 1197, Ap	340	27	37.0	212	7	US-11-214-199-12	Sequence 12, Appl
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272	28	38.4	775	6	US-10-795-201-1	Sequence 1, Appli	345	27	37.0	232	6	US-10-714-887-90	Sequence 90, Appl
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274	28	38.4	864	7	US-11-050-346-10	Sequence 10, Appl	347	27	37.0	233	6	US-10-714-887-100	Sequence 100, App
275	28	38.4	864	7	US-11-103-077-29	Sequence 29, Appl	348	27	37.0	233	7	US-11-179-977-20	Sequence 20, Appl
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278	28	38.4	976	6	US-10-966-483-2	Sequence 2, Appli	351	27	37.0	252	6	US-10-763-712A-114	Sequence 114, App
279	28	38.4	976	7	US-11-233-796-2	Sequence 2, Appli	352	27	37.0	252	7	US-11-166-412-229	Sequence 229, App
280	28	38.4	1035	6	US-10-966-483-20	Sequence 20, Appl	353	27	37.0	254	7	US-11-067-323-430	Sequence 430, App
281	28	38.4	1035	7	US-11-021-441-4	Sequence 4, Appli	354	27	37.0	254	7	US-11-067-323-432	Sequence 432, App
282	28	38.4	1206	6	US-10-770-726-47	Sequence 47, Appl	355	27	37.0	273	7	US-11-113-424-74	Sequence 74, Appl
283	28	38.4	1206	6	US-10-763-712A-18	Sequence 18, Appl	356	27	37.0	273	7	US-11-113-424-75	Sequence 2086, Ap
284	28	38.4	1206	6	US-10-763-712A-99	Sequence 99, Appl	357	27	37.0	277	6	US-10-793-626-2086	Sequence 2086, Ap
285	28	38.4	1213	7	US-11-074-176-256	Sequence 256, App	358	27	37.0	283	6	US-10-453-372-850	Sequence 850, App
286	28	38.4	1343	7	US-11-115-639-37	Sequence 37, Appl	359	27	37.0	289	6	US-10-467-657-2452	Sequence 2452, Ap
287	28	38.4	1343	7	US-11-115-639-38	Sequence 38, Appl	360	27	37.0	289	6	US-10-453-372-836	Sequence 836, App
288	28	38.4	1343	7	US-11-115-639-39	Sequence 39, Appl	361	27	37.0	290	6	US-10-453-372-842	Sequence 842, App
289	28	38.4	1343	7	US-11-115-639-40	Sequence 40, Appl	362	27	37.0	290	6	US-10-453-372-848	Sequence 848, App
290	28	38.4	1343	7	US-11-115-639-41	Sequence 41, Appl	363	27	37.0	290	7	US-11-113-424-77	Sequence 77, Appl
291	28	38.4	1344	7	US-11-091-643-20	Sequence 20, Appl	364	27	37.0	290	7	US-11-113-424-78	Sequence 78, Appl
292	28	38.4	1504	7	US-11-019-711-98	Sequence 98, Appl	365	27	37.0	295	6	US-10-453-372-840	Sequence 840, App
293	28	38.4	1532	6	US-10-821-234-914	Sequence 914, App	366	27	37.0	312	7	US-11-008-570-42	Sequence 42, Appl
294	28	38.4	1565	6	US-10-467-657-2704	Sequence 2704, Ap	367	27	37.0	313	7	US-11-166-412-228	Sequence 228, App
295	28	38.4	1572	7	US-11-143-980-46	Sequence 46, Appl	368	27	37.0	326	6	US-10-873-528-33	Sequence 33, Appl
296	28	38.4	1881	7	US-11-040-472-8	Sequence 8, Appli	369	27	37.0	348	6	US-10-467-657-8350	Sequence 8350, Ap
297	28	38.4	1905	6	US-10-877-346-44	Sequence 44, Appl	370	27	37.0	375	7	US-11-196-976-2	Sequence 2, Appli
298	27	37.0	43	6	US-10-957-887B-68	Sequence 68, Appl	371	27	37.0	394	6	US-10-821-234-1194	Sequence 1194, Ap
299	27	37.0	45	6	US-10-957-887B-297	Sequence 297, App	372	27	37.0	397	6	US-10-858-730-29	Sequence 29, Appl
300	27	37.0	49	6	US-10-467-657-3762	Sequence 297, App	373	27	37.0	397	7	US-11-192-219-47	Sequence 47, Appl
301	27	37.0	62	6	US-10-995-561-707	Sequence 707, App	374	27	37.0	405	6	US-10-467-657-4964	Sequence 4964, Ap
302	27	37.0	92	5	US-09-978-360A-776	Sequence 776, App	375	27	37.0	421	6	US-10-793-626-144	Sequence 144, App
303	27	37.0	95	6	US-10-467-657-6530	Sequence 6530, Ap	376	27	37.0	430	7	US-11-126-313-35	Sequence 35, Appl
304	27	37.0	110	5	US-09-978-360A-616	Sequence 616, App	377	27	37.0	430	7	US-11-126-313-36	Sequence 36, Appl
305	27	37.0	117	6	US-10-821-234-1362	Sequence 1362, Ap	378	27	37.0	445	6	US-10-793-626-1294	Sequence 1294, Ap
306	27	37.0	138	6	US-10-467-657-2928	Sequence 2928, Ap	379	27	37.0	453	6	US-10-793-626-804	Sequence 804, App
307	27	37.0	146	6	US-10-519-390-19	Sequence 19, Appl	380	27	37.0	460	7	US-11-076-163-5	Sequence 5, Appli
308	27	37.0	146	7	US-11-176-830-211	Sequence 211, App	381	27	37.0	460	6	US-11-166-412-68	Sequence 68, Appl
309	27	37.0	146	7	US-11-176-830-653	Sequence 653, App	382	27	37.0	461	6	US-10-858-730-62	Sequence 62, Appl
310	27	37.0	146	7	US-11-176-830-664	Sequence 664, App	383	27	37.0	465	7	US-11-186-284-197	Sequence 197, App
311	27	37.0	146	7	US-11-176-830-665	Sequence 665, App	384	27	37.0	473	6	US-10-467-657-298	Sequence 298, App
312	27	37.0	146	7	US-11-176-830-666	Sequence 666, App	385	27	37.0	473	6	US-10-467-657-6328	Sequence 6328, Ap
313	27	37.0	146	7	US-11-176-830-667	Sequence 667, App	386	27	37.0	482	6	US-10-793-626-24	Sequence 24, Appl
314	27	37.0	146	7	US-11-176-830-668	Sequence 668, App	387	27	37.0	487	7	US-11-124-368A-308	Sequence 308, App
315	27	37.0	146	7	US-11-176-830-669	Sequence 669, App	388	27	37.0	487	6	US-11-124-368A-309	Sequence 309, App
316	27	37.0	146	7	US-11-176-830-670	Sequence 670, App	389	27	37.0	514	6	US-10-878-556A-32	Sequence 32, Appl
317	27	37.0	146	7	US-11-176-830-671	Sequence 671, App	390	27	37.0	526	7	US-11-124-368A-310	Sequence 310, App

391	27	37.0	537	7	US-11-129-442-47	Sequence 47, Appl	464	26	35.6	184	6	US-10-620-787-13	Sequence 13, Appl
392	27	37.0	545	7	US-11-065-943-63	Sequence 63, Appl	465	26	35.6	184	6	US-10-620-787-14	Sequence 14, Appl
393	27	37.0	546	6	US-10-467-657-6000	Sequence 6000, Ap	466	26	35.6	199	6	US-10-467-657-8058	Sequence 8058, Ap
394	27	37.0	549	6	US-10-467-657-4612	Sequence 4612, Ap	467	26	35.6	211	7	US-11-124-368A-175	Sequence 175, App
395	27	37.0	549	6	US-10-467-657-7190	Sequence 7190, Ap	468	26	35.6	211	7	US-11-124-368A-176	Sequence 176, App
396	27	37.0	549	6	US-10-467-657-7190	Sequence 7190, Ap	468	26	35.6	211	7	US-11-124-368A-176	Sequence 176, App
397	27	37.0	559	6	US-10-521-162-4	Sequence 4, Appli	469	26	35.6	226	6	US-10-821-234-1033	Sequence 1033, Ap
398	27	37.0	579	6	US-10-821-234-1352	Sequence 1352, Ap	470	26	35.6	229	6	US-10-793-626-62	Sequence 62, Appl
399	27	37.0	637	6	US-10-821-234-961	Sequence 961, App	471	26	35.6	229	6	US-10-821-234-894	Sequence 894, App
400	27	37.0	637	7	US-11-154-324-4	Sequence 4, Appli	472	26	35.6	232	6	US-11-052-554A-186	Sequence 186, App
401	27	37.0	641	7	US-11-094-519A-29	Sequence 29, Appl	473	26	35.6	246	6	US-10-131-826A-244	Sequence 244, App
402	27	37.0	712	6	US-10-521-162-12	Sequence 12, Appl	474	26	35.6	247	7	US-11-113-424-76	Sequence 76, Appl
403	27	37.0	720	6	US-10-063-703-38	Sequence 38, Appl	475	26	35.6	254	7	US-11-067-323-724	Sequence 724, App
404	27	37.0	720	6	US-11-102-240-38	Sequence 38, Appl	476	26	35.6	254	7	US-11-067-323-1013	Sequence 1013, Ap
405	27	37.0	737	6	US-10-467-657-3452	Sequence 3452, Ap	477	26	35.6	263	7	US-11-082-389-66	Sequence 66, Appl
406	27	37.0	748	6	US-10-821-234-888	Sequence 888, App	478	26	35.6	264	6	US-10-873-528-70	Sequence 70, Appl
407	27	37.0	751	7	US-11-114-906-8	Sequence 8, Appli	479	26	35.6	264	7	US-11-055-822-550	Sequence 550, App
408	27	37.0	764	7	US-11-114-906-6	Sequence 6, Appli	480	26	35.6	264	7	US-11-055-822-596	Sequence 596, App
409	27	37.0	768	7	US-11-144-630-12	Sequence 12, Appl	481	26	35.6	265	6	US-10-793-626-1976	Sequence 1976, Ap
410	27	37.0	769	6	US-10-485-517-401	Sequence 401, App	482	26	35.6	266	6	US-10-467-657-5258	Sequence 5258, Ap
411	27	37.0	838	7	US-11-114-906-40	Sequence 40, Appl	483	26	35.6	266	6	US-10-467-657-5258	Sequence 5258, Ap
412	27	37.0	851	7	US-11-114-906-38	Sequence 38, Appl	484	26	35.6	280	7	US-10-793-626-2344	Sequence 2344, Ap
413	27	37.0	862	7	US-11-182-016-35	Sequence 35, Appl	485	26	35.6	302	7	US-11-170-653-66	Sequence 66, Appl
414	27	37.0	864	7	US-11-114-906-4	Sequence 4, Appli	486	26	35.6	302	7	US-11-112-882-2	Sequence 2, Appli
415	27	37.0	870	7	US-11-114-906-2	Sequence 2, Appli	487	26	35.6	308	7	US-11-156-084-304	Sequence 304, App
416	27	37.0	943	7	US-11-024-959-487	Sequence 487, App	488	26	35.6	312	7	US-11-008-570-41	Sequence 41, Appl
417	27	37.0	951	7	US-11-114-906-36	Sequence 36, Appl	489	26	35.6	313	6	US-10-723-207-4	Sequence 4, Appli
418	27	37.0	953	7	US-11-037-243-66	Sequence 66, Appl	490	26	35.6	313	7	US-11-095-093-2	Sequence 2, Appli
419	27	37.0	957	7	US-11-114-906-34	Sequence 34, Appl	491	26	35.6	318	7	US-11-127-877-38	Sequence 38, Appl
420	27	37.0	1075	7	US-11-089-551A-23	Sequence 23, Appl	492	26	35.6	320	7	US-11-012-522-11	Sequence 11, Appl
421	27	37.0	1138	6	US-10-509-422-4	Sequence 4, Appli	493	26	35.6	324	6	US-11-012-522-17	Sequence 17, Appl
422	27	37.0	1168	6	US-10-509-422-2	Sequence 2, Appli	494	26	35.6	324	6	US-11-229-371-121	Sequence 121, App
423	27	37.0	1300	7	US-11-052-554A-125	Sequence 125, App	495	26	35.6	329	6	US-11-012-522-17	Sequence 17, Appl
424	27	37.0	1436	6	US-10-453-372-1094	Sequence 1094, Ap	496	26	35.6	335	7	US-10-467-657-3774	Sequence 3774, Ap
425	27	37.0	1588	7	US-11-052-554A-280	Sequence 280, App	497	26	35.6	338	6	US-11-055-822-132	Sequence 132, App
426	27	37.0	1593	6	US-10-453-372-1092	Sequence 1092, Ap	498	26	35.6	343	6	US-11-055-822-132	Sequence 132, App
427	27	37.0	1627	7	US-11-052-554A-124	Sequence 124, Appl	499	26	35.6	348	6	US-10-454-437-436	Sequence 436, App
428	27	37.0	1728	7	US-11-019-711-72	Sequence 72, Appl	500	26	35.6	359	6	US-10-454-437-436	Sequence 182, App
429	27	37.0	1873	7	US-11-126-313-29	Sequence 29, Appl	501	26	35.6	359	6	US-10-055-877-159	Sequence 159, App
430	27	37.0	2221	7	US-11-126-313-30	Sequence 30, Appl	502	26	35.6	360	7	US-11-129-143-58	Sequence 58, Appl
431	27	37.0	2591	6	US-10-453-372-718	Sequence 718, App	503	26	35.6	361	7	US-11-082-389-64	Sequence 64, Appl
432	27	37.0	2602	6	US-10-453-372-716	Sequence 716, App	504	26	35.6	362	7	US-11-013-247A-7	Sequence 7, Appli
433	27	37.0	2617	6	US-10-453-372-666	Sequence 666, App	505	26	35.6	362	7	US-11-052-554A-77	Sequence 77, Appl
434	27	37.0	2617	6	US-10-453-372-732	Sequence 732, App	506	26	35.6	362	7	US-11-052-554A-204	Sequence 204, App
435	27	37.0	2617	6	US-10-453-372-734	Sequence 734, App	507	26	35.6	363	7	US-11-186-807-4	Sequence 4, Appli
436	27	37.0	2617	6	US-10-453-372-736	Sequence 736, App	508	26	35.6	363	7	US-11-013-247A-6	Sequence 6, Appli
437	27	37.0	2617	6	US-10-453-372-738	Sequence 738, App	509	26	35.6	364	6	US-10-467-657-4118	Sequence 4118, Ap
438	27	37.0	2617	6	US-10-453-372-740	Sequence 740, App	510	26	35.6	393	6	US-10-467-657-1038	Sequence 1038, Ap
439	27	37.0	2617	6	US-10-453-372-742	Sequence 742, App	511	26	35.6	413	6	US-11-052-554A-308	Sequence 308, App
440	27	37.0	2617	6	US-10-453-372-744	Sequence 744, App	512	26	35.6	422	6	US-10-873-528-77	Sequence 77, Appl
441	27	37.0	2617	6	US-10-453-372-746	Sequence 746, App	513	26	35.6	422	7	US-11-156-084-40	Sequence 40, Appl
442	27	37.0	2617	6	US-10-453-372-748	Sequence 748, App	514	26	35.6	426	7	US-11-171-531-1	Sequence 1, Appli
443	27	37.0	2617	6	US-10-453-372-750	Sequence 750, App	515	26	35.6	429	7	US-11-127-877-51	Sequence 51, Appl
444	26.5	36.3	381	7	US-11-113-424-190	Sequence 48, Appl	516	26	35.6	447	7	US-11-156-084-43	Sequence 43, Appl
445	26.5	36.3	381	6	US-10-689-742-172	Sequence 190, App	517	26	35.6	448	7	US-11-013-247A-5	Sequence 5, Appli
446	26.5	36.3	713	6	US-10-467-657-1012	Sequence 1012, Ap	518	26	35.6	455	6	US-10-714-887-212	Sequence 212, App
447	26.5	36.3	713	7	US-11-190-799-4	Sequence 4, Appli	519	26	35.6	459	7	US-11-156-084-247	Sequence 247, App
448	26	35.6	20	6	US-10-485-788A-568	Sequence 568, App	520	26	35.6	461	6	US-10-131-826A-454	Sequence 454, App
449	26	35.6	29	7	US-11-196-670-51	Sequence 51, Appl	521	26	35.6	463	6	US-10-501-411A-341	Sequence 341, App
450	26	35.6	40	6	US-10-957-887B-271	Sequence 271, App	522	26	35.6	463	7	US-11-156-084-32	Sequence 32, Appl
451	26	35.6	74	6	US-10-467-657-1976	Sequence 1976, Ap	523	26	35.6	463	7	US-11-156-084-41	Sequence 41, Appl
452	26	35.6	100	7	US-11-127-877-567	Sequence 567, App	524	26	35.6	463	7	US-11-156-084-242	Sequence 242, App
453	26	35.6	110	6	US-10-793-626-200	Sequence 200, App	525	26	35.6	465	7	US-11-169-041-173	Sequence 173, App
454	26	35.6	114	6	US-10-467-657-124	Sequence 124, App	526	26	35.6	466	7	US-11-127-877-50	Sequence 50, Appl
455	26	35.6	114	6	US-10-467-657-1414	Sequence 1414, Ap	527	26	35.6	466	7	US-11-156-084-42	Sequence 42, Appl
456	26	35.6	114	6	US-10-467-657-3162	Sequence 3162, Ap	528	26	35.6	472	6	US-10-467-657-86	Sequence 86, Appl
457	26	35.6	114	6	US-10-467-657-3754	Sequence 3754, Ap	529	26	35.6	472	6	US-10-467-657-6324	Sequence 6324, Ap
458	26	35.6	114	6	US-10-467-657-8674	Sequence 8674, Ap	530	26	35.6	483	6	US-10-714-887-4	Sequence 4, Appli
459	26	35.6	119	7	US-11-084-508-23	Sequence 23, Appl	531	26	35.6	483	6	US-10-467-657-2894	Sequence 2894, Ap
460	26	35.6	135	7	US-11-019-711-82	Sequence 82, Appl	532	26	35.6	495	6	US-10-770-726-81	Sequence 81, Appl
461	26	35.6	135	7	US-11-019-711-83	Sequence 83, Appl	533	26	35.6	501	7	US-11-013-247A-2	Sequence 2, Appli
462	26	35.6	146	6	US-10-835-615-797	Sequence 797, App	534	26	35.6	502	7	US-11-226-701-4	Sequence 4, Appli
463	26	35.6	154	7	US-11-055-822-894	Sequence 894, App	535	26	35.6	510	7	US-11-052-554A-119	Sequence 119, App
							536	26	35.6	516	7	US-11-045-802-36	Sequence 36, Appl

537	26	35.6	528	6	US-10-793-626-1930	Sequence 1930, Ap	610	26	35.6	3144	7	US-11-055-035-1	Sequence 1, Appli
538	26	35.6	529	7	US-11-013-247A-17	Sequence 17, Appl	611	26	35.6	3333	6	US-10-766-317-4	Sequence 4, Appli
539	26	35.6	540	7	US-11-045-802-35	Sequence 35, Appl	612	26	35.6	4384	6	US-10-821-234-1120	Sequence 1120, Ap
540	26	35.6	562	7	US-11-065-943-24	Sequence 24, Appl	613	25.5	34.9	140	6	US-10-821-234-1347	Sequence 1347, Ap
541	26	35.6	562	7	US-11-166-892-10	Sequence 10, Appl	614	25.5	34.9	331	6	US-10-131-826A-184	Sequence 184, App
542	26	35.6	565	7	US-11-045-802-34	Sequence 34, Appl	615	25.5	34.9	803	6	US-10-513-759-2	Sequence 2, Appli
543	26	35.6	575	6	US-10-467-657-1456	Sequence 1456, Ap	616	25	34.2	6	US-10-895-064-158	Sequence 158, App	
544	26	35.6	579	7	US-11-045-802-32	Sequence 32, Appl	617	25	34.2	14	6	US-10-857-620A-1	Sequence 1, Appli
545	26	35.6	579	7	US-11-045-802-33	Sequence 33, Appl	618	25	34.2	18	6	US-10-485-788A-838	Sequence 838, App
546	26	35.6	581	7	US-11-045-802-30	Sequence 30, Appl	619	25	34.2	18	7	US-11-024-251-9	Sequence 9, Appli
547	26	35.6	583	6	US-10-763-712A-38	Sequence 38, Appl	620	25	34.2	23	7	US-11-060-005-18	Sequence 18, Appl
548	26	35.6	584	7	US-11-045-802-31	Sequence 31, Appl	621	25	34.2	30	7	US-11-145-861-387	Sequence 387, App
549	26	35.6	585	7	US-11-127-877-63	Sequence 63, Appl	622	25	34.2	31	6	US-10-982-727-89	Sequence 89, Appl
550	26	35.6	587	7	US-11-205-109-27	Sequence 27, Appl	623	25	34.2	42	7	US-11-067-425A-77	Sequence 77, Appl
551	26	35.6	592	6	US-10-467-962B-95	Sequence 95, Appl	624	25	34.2	42	7	US-11-067-425A-78	Sequence 78, Appl
552	26	35.6	592	6	US-10-524-647-112	Sequence 112, App	625	25	34.2	42	7	US-11-067-425A-79	Sequence 79, Appl
553	26	35.6	597	6	US-10-055-877-303	Sequence 303, App	626	25	34.2	42	7	US-11-067-425A-80	Sequence 80, Appl
554	26	35.6	597	7	US-11-045-802-28	Sequence 28, Appl	627	25	34.2	43	6	US-10-957-887B-231	Sequence 231, App
555	26	35.6	600	6	US-10-878-556A-43	Sequence 43, Appl	628	25	34.2	44	6	US-10-957-887B-61	Sequence 61, Appl
556	26	35.6	626	6	US-10-467-657-1772	Sequence 1772, Ap	629	25	34.2	45	6	US-10-467-657-7602	Sequence 7602, Ap
557	26	35.6	655	7	US-11-045-802-29	Sequence 29, Appl	630	25	34.2	49	6	US-10-467-657-5052	Sequence 5052, Ap
558	26	35.6	659	6	US-10-467-657-6006	Sequence 6006, Ap	631	25	34.2	50	6	US-10-895-064-2746	Sequence 2746, Ap
559	26	35.6	661	7	US-11-019-711-107	Sequence 107, App	632	25	34.2	60	6	US-10-502-972-11	Sequence 11, Appl
560	26	35.6	692	7	US-11-045-802-26	Sequence 26, Appl	633	25	34.2	98	6	US-10-821-234-1161	Sequence 1161, Ap
561	26	35.6	710	7	US-11-045-802-2	Sequence 2, Appli	634	25	34.2	108	5	US-09-978-360A-440	Sequence 440, App
562	26	35.6	710	7	US-11-045-802-19	Sequence 19, Appl	635	25	34.2	133	6	US-10-467-657-5098	Sequence 5098, Ap
563	26	35.6	710	7	US-11-045-802-20	Sequence 20, Appl	636	25	34.2	133	7	US-11-149-462-5	Sequence 5, Appli
564	26	35.6	710	7	US-11-045-802-21	Sequence 21, Appl	637	25	34.2	135	7	US-11-019-711-56	Sequence 56, Appl
565	26	35.6	710	7	US-11-045-802-22	Sequence 22, Appl	638	25	34.2	135	7	US-11-019-711-84	Sequence 84, Appl
566	26	35.6	710	7	US-11-045-802-23	Sequence 23, Appl	639	25	34.2	153	6	US-10-821-234-1086	Sequence 1086, Ap
567	26	35.6	710	7	US-11-045-802-24	Sequence 24, Appl	640	25	34.2	159	6	US-10-467-657-2736	Sequence 2736, Ap
568	26	35.6	712	6	US-10-995-561-984	Sequence 984, App	641	25	34.2	166	6	US-10-467-657-1080	Sequence 1080, Ap
569	26	35.6	729	7	US-11-130-821-3	Sequence 3, Appli	642	25	34.2	182	6	US-10-661-966-6	Sequence 6, Appli
570	26	35.6	731	7	US-11-130-821-3	Sequence 3, Appli	643	25	34.2	192	7	US-11-175-690-336	Sequence 336, App
571	26	35.6	732	7	US-11-078-189-14	Sequence 14, Appl	644	25	34.2	192	7	US-11-175-690-337	Sequence 337, App
572	26	35.6	763	7	US-10-995-561-985	Sequence 35, Appl	645	25	34.2	205	6	US-10-793-626-240	Sequence 240, App
573	26	35.6	769	6	US-10-995-561-985	Sequence 985, App	646	25	34.2	207	7	US-11-129-104-98	Sequence 98, Appl
574	26	35.6	769	6	US-10-995-561-986	Sequence 986, App	647	25	34.2	209	6	US-10-467-657-6890	Sequence 6890, Ap
575	26	35.6	773	7	US-11-010-239-63	Sequence 63, Appl	648	25	34.2	218	6	US-10-821-234-1595	Sequence 1595, Ap
576	26	35.6	773	7	US-11-143-980-67	Sequence 67, Appl	649	25	34.2	219	6	US-10-793-626-2206	Sequence 2206, Ap
577	26	35.6	816	7	US-11-143-980-67	Sequence 67, Appl	650	25	34.2	220	6	US-10-661-966-5	Sequence 5, Appli
578	26	35.6	828	6	US-10-995-561-983	Sequence 983, App	651	25	34.2	225	6	US-10-793-626-1452	Sequence 1452, Ap
579	26	35.6	834	6	US-10-131-826A-148	Sequence 148, App	652	25	34.2	226	6	US-10-793-626-1734	Sequence 1734, Ap
580	26	35.6	841	6	US-11-052-554A-212	Sequence 212, App	653	25	34.2	226	6	US-10-670-009-6	Sequence 6, Appli
581	26	35.6	841	6	US-10-624-932-6	Sequence 6, Appli	654	25	34.2	229	7	US-11-055-822-798	Sequence 798, App
582	26	35.6	841	6	US-10-624-932-8	Sequence 8, Appli	655	25	34.2	233	6	US-10-878-556A-147	Sequence 147, App
583	26	35.6	847	7	US-11-124-368A-234	Sequence 234, App	656	25	34.2	239	6	US-10-895-064-1311	Sequence 1311, Ap
584	26	35.6	854	6	US-10-511-657-4	Sequence 4, Appli	657	25	34.2	245	6	US-10-467-657-8582	Sequence 8582, Ap
585	26	35.6	892	7	US-11-082-389-396	Sequence 396, App	658	25	34.2	247	6	US-10-510-386-242	Sequence 242, App
586	26	35.6	918	6	US-10-995-561-981	Sequence 981, App	659	25	34.2	249	6	US-10-821-234-1596	Sequence 1596, Ap
587	26	35.6	961	6	US-10-831-997-4	Sequence 4, Appli	660	25	34.2	252	6	US-10-995-561-601	Sequence 601, App
588	26	35.6	970	6	US-10-467-657-5524	Sequence 5524, Ap	661	25	34.2	257	6	US-10-793-626-3244	Sequence 3244, Ap
589	26	35.6	1019	6	US-10-995-561-982	Sequence 982, App	662	25	34.2	257	6	US-10-467-657-720	Sequence 720, App
590	26	35.6	1023	6	US-10-995-561-968	Sequence 968, App	663	25	34.2	257	7	US-11-156-084-290	Sequence 290, App
591	26	35.6	1076	6	US-10-467-657-5708	Sequence 5708, Ap	664	25	34.2	261	7	US-11-169-041-190	Sequence 190, App
592	26	35.6	1165	7	US-11-197-380-6	Sequence 6, Appli	665	25	34.2	262	6	US-10-793-626-876	Sequence 876, App
593	26	35.6	1390	6	US-11-063-343-35	Sequence 35, Appl	666	25	34.2	267	7	US-11-165-067A-3	Sequence 3, Appli
594	26	35.6	1404	6	US-10-995-561-526	Sequence 526, App	667	25	34.2	269	5	US-09-978-360A-529	Sequence 529, App
595	26	35.6	1433	7	US-11-094-519A-40	Sequence 40, Appl	668	25	34.2	277	6	US-10-510-386-96	Sequence 96, Appl
596	26	35.6	1445	7	US-11-169-041-181	Sequence 181, App	669	25	34.2	277	6	US-10-454-437-8	Sequence 8, Appli
597	26	35.6	1463	7	US-11-080-991-22	Sequence 22, Appl	670	25	34.2	277	7	US-11-055-822-608	Sequence 608, App
598	26	35.6	1581	7	US-11-090-439-24	Sequence 24, Appl	671	25	34.2	278	7	US-11-009-658-8	Sequence 8, Appli
599	26	35.6	1581	7	US-11-090-439-26	Sequence 26, Appl	672	25	34.2	281	7	US-11-144-833-14	Sequence 14, Appl
600	26	35.6	1588	6	US-10-995-561-527	Sequence 527, App	673	25	34.2	288	6	US-10-793-626-1118	Sequence 1118, Ap
601	26	35.6	1713	6	US-10-766-317-2	Sequence 2, Appli	674	25	34.2	292	6	US-10-527-500-9	Sequence 9, Appli
602	26	35.6	1724	6	US-10-766-317-6	Sequence 6, Appli	675	25	34.2	293	6	US-10-467-657-6664	Sequence 6664, Ap
603	26	35.6	1992	7	US-11-013-759-3	Sequence 3, Appli	676	25	34.2	296	6	US-10-467-657-2944	Sequence 2944, Ap
604	26	35.6	1992	7	US-11-013-759-13	Sequence 13, Appl	677	25	34.2	300	6	US-10-793-626-1900	Sequence 1900, Ap
605	26	35.6	2047	7	US-11-013-759-4	Sequence 4, Appli	678	25	34.2	302	7	US-11-165-226-127	Sequence 127, App
606	26	35.6	2047	7	US-11-013-759-7	Sequence 7, Appli	679	25	34.2	310	7	US-11-169-041-163	Sequence 163, App
607	26	35.6	2233	6	US-10-873-528-2	Sequence 2, Appli	680	25	34.2	311	6	US-10-793-626-1260	Sequence 1260, Ap
608	26	35.6	2471	7	US-11-050-346-68	Sequence 68, Appl	681	25	34.2	313	6	US-10-995-561-972	Sequence 972, App
609	26	35.6	2902	7	US-11-052-554A-91	Sequence 91, Appl	682	25	34.2	314	7	US-11-008-570-43	Sequence 43, Appl

683	25	34.2	318	6	US-10-467-657-7760	Sequence 7760, Ap	756	25	34.2	542	6	US-10-524-647-12	Sequence 12, Appl
684	25	34.2	318	7	US-11-058-924-8	Sequence 8, Appl	757	25	34.2	542	7	US-11-152-747-6	Sequence 6, Appl
685	25	34.2	323	7	US-11-165-067A-13	Sequence 13, Appl	758	25	34.2	544	7	US-11-166-609-18	Sequence 18, Appl
686	25	34.2	325	6	US-10-793-626-1076	Sequence 1076, Ap	759	25	34.2	546	7	US-11-166-609-2	Sequence 2, Appl
687	25	34.2	327	6	US-10-821-234-884	Sequence 884, App	760	25	34.2	548	7	US-11-114-906-14	Sequence 14, Appl
688	25	34.2	329	7	US-11-194-246-239	Sequence 239, App	761	25	34.2	534	7	US-11-159-902-4	Sequence 4, Appl
689	25	34.2	335	6	US-10-995-561-970	Sequence 970, App	762	25	34.2	564	7	US-11-082-389-78	Sequence 78, Appl
690	25	34.2	335	7	US-11-129-143-106	Sequence 106, App	763	25	34.2	567	6	US-10-503-051-5	Sequence 5, Appl
691	25	34.2	337	6	US-10-485-517-234	Sequence 234, App	764	25	34.2	568	6	US-10-997-247-4	Sequence 47, Appl
692	25	34.2	338	6	US-10-520-820-6	Sequence 6, Appl	765	25	34.2	572	6	US-10-878-556A-47	Sequence 47, Appl
693	25	34.2	345	6	US-10-995-561-971	Sequence 971, App	766	25	34.2	583	6	US-10-793-626-1358	Sequence 1358, Ap
694	25	34.2	346	7	US-11-012-522-13	Sequence 13, Appl	767	25	34.2	585	6	US-10-793-556A-42	Sequence 42, Appl
695	25	34.2	353	6	US-10-875-716-10	Sequence 10, Appl	768	25	34.2	600	6	US-10-606-302-3	Sequence 3, Appl
696	25	34.2	355	6	US-10-503-051-2	Sequence 2, Appl	769	25	34.2	611	6	US-10-467-657-4656	Sequence 4656, Ap
697	25	34.2	366	5	US-09-978-360A-421	Sequence 421, App	770	25	34.2	611	6	US-10-523-912-4	Sequence 4, Appl
698	25	34.2	366	7	US-11-000-463-897	Sequence 897, App	771	25	34.2	621	7	US-10-632-150-56	Sequence 56, Appl
699	25	34.2	368	6	US-10-467-657-4756	Sequence 4756, Ap	772	25	34.2	621	7	US-11-073-450-56	Sequence 56, Appl
700	25	34.2	380	7	US-11-144-833-12	Sequence 12, Appl	773	25	34.2	628	7	US-11-094-519A-28	Sequence 28, Appl
701	25	34.2	380	7	US-11-144-833-13	Sequence 13, Appl	774	25	34.2	631	6	US-10-467-657-5452	Sequence 5452, Ap
702	25	34.2	383	7	US-11-159-516A-2	Sequence 2, Appl	775	25	34.2	631	6	US-10-867-657-7396	Sequence 7396, Ap
703	25	34.2	383	7	US-11-159-516A-29	Sequence 29, Appl	776	25	34.2	631	6	US-10-467-657-7396	Sequence 22, Appl
704	25	34.2	384	6	US-10-467-657-508	Sequence 508, App	777	25	34.2	631	6	US-10-813-646-22	Sequence 44, Appl
705	25	34.2	389	6	US-10-513-118-2	Sequence 2, Appl	778	25	34.2	640	7	US-11-094-519A-44	Sequence 9, Appl
706	25	34.2	398	7	US-11-110-011-4	Sequence 4, Appl	779	25	34.2	640	7	US-11-205-109-9	Sequence 36, Appl
707	25	34.2	400	7	US-11-108-172-1115	Sequence 1115, Ap	780	25	34.2	644	6	US-10-763-712A-36	Sequence 36, Appl
708	25	34.2	400	7	US-11-000-463-425	Sequence 425, App	781	25	34.2	648	6	US-10-793-626-568	Sequence 568, App
709	25	34.2	406	6	US-10-131-826A-82	Sequence 82, Appl	782	25	34.2	648	7	US-10-793-626-568	Sequence 12, Appl
710	25	34.2	406	6	US-10-131-826A-430	Sequence 430, App	783	25	34.2	654	7	US-11-114-906-10	Sequence 10, Appl
711	25	34.2	406	6	US-10-467-657-1048	Sequence 1048, Ap	784	25	34.2	657	7	US-11-114-906-10	Sequence 10, Appl
712	25	34.2	406	6	US-10-878-556A-11	Sequence 11, Appl	785	25	34.2	661	6	US-10-453-372-642	Sequence 48, Appl
713	25	34.2	406	7	US-11-108-841-3	Sequence 3, Appl	786	25	34.2	664	7	US-10-453-372-642	Sequence 642, App
714	25	34.2	406	7	US-11-108-841-3	Sequence 3, Appl	787	25	34.2	685	6	US-10-661-966-3	Sequence 3, Appl
715	25	34.2	410	6	US-10-821-234-912	Sequence 912, App	788	25	34.2	688	7	US-11-165-226-124	Sequence 124, App
716	25	34.2	416	6	US-10-793-626-2	Sequence 2, Appl	789	25	34.2	695	6	US-10-453-372-648	Sequence 648, App
717	25	34.2	422	6	US-10-524-647-122	Sequence 122, App	790	25	34.2	700	6	US-10-995-561-922	Sequence 922, App
718	25	34.2	424	6	US-10-793-626-1046	Sequence 1046, Ap	791	25	34.2	706	6	US-10-995-561-924	Sequence 924, App
719	25	34.2	424	6	US-10-467-657-2678	Sequence 2678, Ap	792	25	34.2	707	6	US-11-024-959-269	Sequence 269, App
720	25	34.2	424	6	US-10-967-457-74	Sequence 74, Appl	793	25	34.2	709	7	US-11-165-067A-9	Sequence 9, Appl
721	25	34.2	429	7	US-11-000-463-302	Sequence 302, App	794	25	34.2	710	7	US-11-089-551A-33	Sequence 33, Appl
722	25	34.2	429	7	US-11-000-463-774	Sequence 774, App	795	25	34.2	736	7	US-11-078-189-11	Sequence 11, Appl
723	25	34.2	429	7	US-11-205-109-32	Sequence 32, Appl	796	25	34.2	736	6	US-10-793-626-1138	Sequence 1138, Ap
724	25	34.2	431	7	US-11-060-920-4	Sequence 4, Appl	797	25	34.2	753	6	US-10-485-517-173	Sequence 173, App
725	25	34.2	432	6	US-10-793-626-2942	Sequence 2942, Ap	798	25	34.2	757	6	US-10-055-877-157	Sequence 157, App
726	25	34.2	434	6	US-10-821-234-1553	Sequence 1553, Ap	799	25	34.2	758	6	US-10-467-962B-12	Sequence 12, Appl
727	25	34.2	440	6	US-10-063-703-134	Sequence 134, App	800	25	34.2	765	6	US-10-661-966-10	Sequence 10, Appl
728	25	34.2	440	7	US-11-062-240-134	Sequence 134, App	801	25	34.2	765	6	US-10-661-966-15	Sequence 15, Appl
729	25	34.2	447	6	US-10-967-521A-14	Sequence 14, Appl	802	25	34.2	765	7	US-11-144-630-69	Sequence 69, Appl
730	25	34.2	451	6	US-10-770-726-79	Sequence 79, Appl	803	25	34.2	774	7	US-11-000-463-459	Sequence 459, App
731	25	34.2	458	6	US-10-878-556A-28	Sequence 28, Appl	804	25	34.2	775	6	US-10-453-372-656	Sequence 656, App
732	25	34.2	460	6	US-10-990-276-1	Sequence 1, Appl	805	25	34.2	776	7	US-11-114-906-24	Sequence 24, Appl
733	25	34.2	468	7	US-11-052-554A-182	Sequence 182, App	806	25	34.2	777	6	US-10-821-234-1658	Sequence 1658, Ap
734	25	34.2	471	6	US-10-336-263A-6	Sequence 6, Appl	807	25	34.2	783	6	US-10-661-966-2	Sequence 2, Appl
735	25	34.2	473	7	US-11-069-642-5	Sequence 5, Appl	808	25	34.2	783	7	US-11-186-284-59	Sequence 59, Appl
736	25	34.2	487	6	US-10-131-826A-528	Sequence 528, App	809	25	34.2	789	7	US-11-114-906-22	Sequence 22, Appl
737	25	34.2	491	6	US-10-793-626-2770	Sequence 2770, Ap	810	25	34.2	792	7	US-11-108-172-1127	Sequence 1127, Ap
738	25	34.2	492	6	US-10-467-962B-51	Sequence 51, Appl	811	25	34.2	793	6	US-10-995-561-925	Sequence 925, App
739	25	34.2	495	6	US-10-873-528-99	Sequence 99, Appl	812	25	34.2	801	7	US-11-175-690-249	Sequence 249, App
740	25	34.2	496	6	US-10-793-626-1386	Sequence 1386, Ap	813	25	34.2	801	7	US-11-175-690-250	Sequence 250, App
741	25	34.2	496	7	US-11-110-082-31	Sequence 31, Appl	814	25	34.2	804	6	US-10-453-372-650	Sequence 650, App
742	25	34.2	500	7	US-11-120-308-138	Sequence 138, App	815	25	34.2	825	6	US-10-453-372-644	Sequence 644, App
743	25	34.2	504	7	US-11-055-822-136	Sequence 136, App	816	25	34.2	833	7	US-11-159-902-2	Sequence 2, Appl
744	25	34.2	510	6	US-10-485-517-320	Sequence 320, App	817	25	34.2	834	6	US-10-453-372-658	Sequence 658, App
745	25	34.2	518	7	US-11-166-609-13	Sequence 13, Appl	818	25	34.2	838	7	US-11-052-554A-40	Sequence 40, Appl
746	25	34.2	519	6	US-10-821-234-1373	Sequence 1373, Ap	819	25	34.2	840	7	US-11-052-554A-40	Sequence 40, Appl
747	25	34.2	520	7	US-11-112-882-26	Sequence 26, Appl	820	25	34.2	844	6	US-10-763-712A-48	Sequence 48, Appl
748	25	34.2	524	7	US-11-054-281-34	Sequence 34, Appl	821	25	34.2	847	6	US-10-453-372-654	Sequence 654, App
749	25	34.2	524	7	US-11-054-281-121	Sequence 121, App	822	25	34.2	857	6	US-10-453-372-652	Sequence 36, Appl
750	25	34.2	526	6	US-10-467-657-6754	Sequence 6754, Ap	823	25	34.2	858	6	US-10-878-556A-36	Sequence 36, Appl
751	25	34.2	527	7	US-11-069-642-21	Sequence 21, Appl	824	25	34.2	863	7	US-11-114-906-30	Sequence 30, Appl
752	25	34.2	529	6	US-10-467-657-3958	Sequence 3958, Ap	825	25	34.2	875	7	US-11-114-906-30	Sequence 30, Appl
753	25	34.2	531	6	US-10-517-937-70	Sequence 70, Appl	826	25	34.2	877	6	US-10-821-234-960	Sequence 960, App
754	25	34.2	535	7	US-11-114-906-16	Sequence 16, Appl	827	25	34.2	889	7	US-11-114-906-20	Sequence 20, Appl
755	25	34.2	538	7	US-11-166-609-21	Sequence 21, Appl	828	25	34.2	895	7	US-11-114-906-18	Sequence 18, Appl



829	25	34.2	905	6	US-10-453-372-638	Sequence 638, App	902	24.5	33.6	302	7	US-11-156-084-351	Sequence 351, App
830	25	34.2	905	6	US-10-453-372-662	Sequence 662, App	903	24.5	33.6	334	6	US-10-895-064-24	Sequence 24, Appl
831	25	34.2	905	6	US-10-453-372-664	Sequence 664, App	904	24.5	33.6	334	6	US-10-895-064-25	Sequence 25, Appl
832	25	34.2	917	7	US-11-169-041-145	Sequence 145, App	905	24.5	33.6	334	6	US-10-895-064-26	Sequence 26, Appl
833	25	34.2	963	6	US-10-995-561-923	Sequence 923, App	906	24.5	33.6	351	7	US-11-067-884-4	Sequence 4, Appl
834	25	34.2	963	6	US-10-453-372-660	Sequence 660, App	907	24.5	33.6	352	7	US-11-052-554A-220	Sequence 220, App
835	25	34.2	976	6	US-11-114-906-28	Sequence 28, Appl	908	24.5	33.6	401	7	US-11-055-832-336	Sequence 336, App
836	25	34.2	976	6	US-11-114-906-26	Sequence 26, Appl	909	24.5	33.6	416	6	US-10-467-657-5060	Sequence 5060, Ap
837	25	34.2	982	7	US-11-114-906-26	Sequence 26, Appl	909	24.5	33.6	416	6	US-10-467-657-5060	Sequence 5060, Ap
838	25	34.2	983	7	US-11-113-424-59	Sequence 59, Appl	910	24.5	33.6	490	6	US-10-467-657-7280	Sequence 7280, Ap
839	25	34.2	984	7	US-11-113-424-60	Sequence 60, Appl	911	24.5	33.6	490	6	US-10-467-657-8158	Sequence 8158, Ap
840	25	34.2	985	7	US-11-113-424-61	Sequence 61, Appl	912	24.5	33.6	862	7	US-11-128-420-11	Sequence 11, Appl
841	25	34.2	986	6	US-10-821-234-1310	Sequence 1310, Ap	913	24.5	33.6	862	7	US-11-007-428-2	Sequence 2, Appl
842	25	34.2	998	6	US-10-510-524-1	Sequence 1, Appl	914	24.5	33.6	862	7	US-11-183-294-16	Sequence 16, Appl
843	25	34.2	1012	6	US-10-453-372-646	Sequence 646, App	915	24.5	33.6	862	7	US-10-312-954-2	Sequence 2, Appl
844	25	34.2	1015	6	US-10-467-657-180	Sequence 180, App	916	24.5	33.6	862	7	US-10-312-954-2	Sequence 2, Appl
845	25	34.2	1015	6	US-10-467-657-180	Sequence 180, App	916	24.5	33.6	862	7	US-10-312-954-2	Sequence 2, Appl
846	25	34.2	1035	7	US-11-113-424-20	Sequence 20, Appl	917	24.5	33.6	1141	6	US-10-995-561-1009	Sequence 1009, Ap
847	25	34.2	1042	7	US-11-037-243-74	Sequence 74, Appl	918	24.5	33.6	1141	6	US-10-995-561-1010	Sequence 1010, Ap
848	25	34.2	1045	7	US-11-113-424-54	Sequence 54, Appl	919	24.5	33.6	1405	6	US-10-995-561-529	Sequence 529, Ap
849	25	34.2	1045	7	US-11-113-424-54	Sequence 54, Appl	920	24.5	33.6	1406	6	US-10-995-561-530	Sequence 530, App
850	25	34.2	1052	7	US-11-113-424-22	Sequence 22, Appl	921	24.5	33.6	1436	6	US-10-995-561-531	Sequence 531, App
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853	25	34.2	1122	7	US-11-191-374-3	Sequence 3, Appl	924	24	32.9	18	7	US-11-033-039-1230	Sequence 1230, Ap
854	25	34.2	1122	7	US-11-191-375-3	Sequence 3, Appl	925	24	32.9	20	6	US-10-982-727-90	Sequence 90, Appl
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875	25	34.2	1548	7	US-11-108-172-1095	Sequence 1095, Ap	946	24	32.9	60	6	US-10-467-657-2482	Sequence 2482, Ap
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883	25	34.2	2326	7	US-11-126-313-37	Sequence 37, Appl	954	24	32.9	60	6	US-10-467-657-2482	Sequence 2482, Ap
884	25	34.2	2333	7	US-11-096-281-13	Sequence 13, Appl	955	24	32.9	60	6	US-10-467-657-2482	Sequence 2482, Ap
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896	25	34.2	3256	7	US-11-124-368A-304	Sequence 304, App	967	24	32.9	60	6	US-10-467-657-2482	Sequence 2482, Ap
897	25	34.2	5024	6	US-10-793-626-2964	Sequence 2964, Ap	968	24	32.9	60	6	US-10-467-657-2482	Sequence 2482, Ap
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982 24 32.9 169 7 US-11-182-208-21 Sequence 21, Appl
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984 24 32.9 177 6 US-10-798-579A-28 Sequence 28, Appl
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992 24 32.9 190 7 US-11-182-016-39 Sequence 39, Appl
993 24 32.9 194 7 US-11-194-246-301 Sequence 301, Ap
994 24 32.9 196 6 US-10-821-234-982 Sequence 982, Ap
995 24 32.9 197 7 US-11-087-749-52 Sequence 52, Appl
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ALIGNMENTS

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; Sequence 9, Application US/11043788
; Publication No. US20060014166A1
; GENERAL INFORMATION:
; APPLICANT: Comugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1006
; CURRENT APPLICATION NUMBER: US/11/043,788
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 506
; SEQ ID NO 9
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-788-9
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Db 43 ISVQRLASYRRITSSK 58
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; Sequence 8, Application US/11043788
; Publication No. US20060014166A1
; GENERAL INFORMATION:
; APPLICANT: Comugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1006
; CURRENT APPLICATION NUMBER: US/11/043,788
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 506
; SEQ ID NO 8
; LENGTH: 99
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-11-043-788-8
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Db 43 ISVQRLASYRRITSSK 58
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; Sequence 1, Application US/10509292
; Publication No. US20050287159A1
; GENERAL INFORMATION:
; APPLICANT: Merckia Pharma LLC
; TITLE OF INVENTION: Methods and Compositions for Treating and Preventing Botaxin
; TITLE OF INVENTION: Mediated Inflammatory Conditions
; FILE REFERENCE: MERPH.001
; CURRENT APPLICATION NUMBER: US/10/509,292
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/367,591
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.2
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RESULT 4
US-10-995-561-900
; Sequence 900, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 97
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; ORGANISM: Homo sapiens
US-10-995-561-900
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US-10-329-472-7
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**Qy**

**1 ISVQLASYRRITSSK 16**

:: | :: : ||

APPLICANT: Curran, Maurice  
; APPLICANT: Healey, Shaun  
; APPLICANT: Hazlewood, Geoff

; APPLICANT: Wu, Di  
; APPLICANT: Blum, David  
; APPLICANT: Esteghlalian, Alireza  
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM  
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM  
; FILE REFERENCE: 564462007901  
; CURRENT APPLICATION NUMBER: US/10/517,939  
; CURRENT FILING DATE: 2004-12-13  
; PRIOR APPLICATION NUMBER: PCT/US03/19153  
; PRIOR FILING DATE: 2003-06-16  
; PRIOR APPLICATION NUMBER: 60/389,299  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 380  
; SOFTWARE: FastSeq for Windows Version 4.0  
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; LENGTH: 1680  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Obtained from an environmental sample.  
; FEATURE:  
; NAME/KEY: SIGNAL  
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US-10-517-939-362

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Db 989 IGVGGGSYRFVASGR 1004

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; Sequence 1154, Application US/10821234  
; Publication No. US200502551141  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: PC\_SEQ\_genes Version 1.0  
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; TYPE: PRT  
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RESULT 11  
US-11-110-082-38  
; Sequence 38, Application US/11110082  
; Publication No. US200502665581  
; GENERAL INFORMATION:  
; APPLICANT: Demmer, Jeroen  
; APPLICANT: Hall, Claire

; APPLICANT: Norris, Michael Geoffrey  
; APPLICANT: Saulebury, Keith Martin  
; TITLE OF INVENTION: Compositions Isolated from Forage  
; TITLE OF INVENTION: Grasses and methods for their use.  
; FILE REFERENCE: 11000.1074UC1  
; CURRENT APPLICATION NUMBER: US/11/110,082  
; CURRENT FILING DATE: 2005-04-19  
; PRIOR APPLICATION NUMBER: 60/563,723  
; PRIOR FILING DATE: 2004-04-20  
; PRIOR APPLICATION NUMBER: 10/655,799  
; PRIOR FILING DATE: 2003-09-05  
; PRIOR APPLICATION NUMBER: 60/408,782  
; PRIOR FILING DATE: 2002-09-05  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 808  
; TYPE: PRT  
; ORGANISM: Festuca arundinacea  
US-11-110-082-38

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RESULT 12  
US-10-985-205-3  
; Sequence 3, Application US/10985205  
; Publication No. US20050266400A1  
; GENERAL INFORMATION:  
; APPLICANT: Dumonceaux, Julie  
; APPLICANT: Cormier, Emmanuel G.  
; APPLICANT: Gardner, Jason P.  
; APPLICANT: Dragic, Tatjana  
; TITLE OF INVENTION: NOVEL SEQUENCES ENCODING HEPATITIS C VIRUS GLYCOPROTEINS  
; FILE REFERENCE: 71242-A/JPW/AJD  
; CURRENT APPLICATION NUMBER: US/10/985,205  
; CURRENT FILING DATE: 2004-11-09  
; PRIOR APPLICATION NUMBER: US 60/519,536  
; PRIOR FILING DATE: 2003-11-12  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 3011  
; TYPE: PRT  
; ORGANISM: Hepatitis C virus  
US-10-985-205-3

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Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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RESULT 13  
US-11-052-554A-90  
; Sequence 90, Application US/11052554A  
; Publication No. US20050288666A1  
; GENERAL INFORMATION:  
; APPLICANT: Sachdeva, et al.  
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE  
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL  
; FILE REFERENCE: 30853/40359A  
; CURRENT APPLICATION NUMBER: US/11/052,554A  
; CURRENT FILING DATE: 2005-02-07

; PRIOR APPLICATION NUMBER: US 60/589,227  
; PRIOR FILING DATE: 2004-07-20  
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004  
; PRIOR FILING DATE: 2004-02-06  
; NUMBER OF SEQ ID NOS: 763  
; SOFTWARE: PatentIn version 3.3  
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; ORGANISM: Helicobacter pylori J99  
US-11-052-554A-90

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Best Local Similarity 87.5%; Pred. No. 4.9e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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| | | | |  
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RESULT 14  
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; Sequence 8, Application US/10497135  
; Publication No. US20050272132A1  
; GENERAL INFORMATION:  
; APPLICANT: Biotech Technology Ltd  
; APPLICANT: Gregory, Matthew A  
; APPLICANT: Gaisner, Sabine  
; APPLICANT: Petkovic, Hrvoje  
; APPLICANT: Moss, Steven  
; TITLE OF INVENTION: Production of Polyketides and Other Natural Products  
; FILE REFERENCE: 4408-P03444US00  
; CURRENT APPLICATION NUMBER: US/10/497,135  
; CURRENT FILING DATE: 2004-05-26  
; PRIOR APPLICATION NUMBER: PCT/GB03/003230  
; PRIOR FILING DATE: 2003-07-16  
; PRIOR APPLICATION NUMBER: GB0216509.0  
; PRIOR FILING DATE: 2002-07-16  
; PRIOR APPLICATION NUMBER: GB0224922.5  
; PRIOR FILING DATE: 2002-10-25  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 317  
; TYPE: PRT  
; ORGANISM: Streptomyces hygroscopicus  
US-10-497-135-8

Query Match 45.2%; Score 33; DB 6; Length 317;  
Best Local Similarity 63.6%; Pred. No. 61;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 QRLASYRRITS 14  
| | | | |  
Db 210 QRLASYRRIT 220

RESULT 15  
US-10-497-135-7  
; Sequence 7, Application US/10497135  
; Publication No. US20050272132A1  
; GENERAL INFORMATION:  
; APPLICANT: Biotech Technology Ltd  
; APPLICANT: Gaisner, Sabine  
; APPLICANT: Petkovic, Hrvoje  
; APPLICANT: Moss, Steven  
; TITLE OF INVENTION: Production of Polyketides and Other Natural Products  
; FILE REFERENCE: 4408-P03444US00  
; CURRENT APPLICATION NUMBER: US/10/497,135  
; CURRENT FILING DATE: 2004-05-26  
; PRIOR APPLICATION NUMBER: PCT/GB03/003230

; PRIOR FILING DATE: 2003-07-16  
; PRIOR APPLICATION NUMBER: GB0216509.0  
; PRIOR FILING DATE: 2002-07-16  
; PRIOR APPLICATION NUMBER: GB0224922.5  
; PRIOR FILING DATE: 2002-10-25  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 318  
; TYPE: PRT  
; ORGANISM: Streptomyces hygroscopicus  
US-10-497-135-7

Query Match 45.2%; Score 33; DB 6; Length 318;  
Best Local Similarity 63.6%; Pred. No. 62;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 QRLASYRRITS 14  
| | | | |  
Db 211 QRLASYRRIT 221

RESULT 16  
US-10-517-151-4  
; Sequence 4, Application US/10517151  
; Publication No. US20060019252A1  
; GENERAL INFORMATION:  
; APPLICANT: Nakamura, Yusuke  
; APPLICANT: Furukawa, Yoichi  
; APPLICANT: Oncotherapy Science, Inc.  
; APPLICANT: The University of Tokyo  
; TITLE OF INVENTION: Genes and Polypeptides Relating to Hepatocellular or  
; FILE REFERENCE: 082379-000400US  
; CURRENT APPLICATION NUMBER: US/10/517,151  
; CURRENT FILING DATE: 2004-12-05  
; PRIOR APPLICATION NUMBER: US 60/386,985  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: WO PCT/JPO3/07070  
; PRIOR FILING DATE: 2003-06-04  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-517-151-4

Query Match 45.2%; Score 33; DB 6; Length 500;  
Best Local Similarity 46.7%; Pred. No. 1e+02;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16  
| | | | |  
Db 328 SSSRLVSHRRVHSGE 342

RESULT 17  
US-11-152-697-3  
; Sequence 3, Application US/11152697  
; Publication No. US2006000367A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL HUMAN KUPFFER CELL RECEPTOR  
; FILE REFERENCE: D0242 NP  
; CURRENT APPLICATION NUMBER: US/11/152,697  
; CURRENT FILING DATE: 2005-06-14  
; PRIOR APPLICATION NUMBER: 60/580,006  
; PRIOR FILING DATE: 2004-06-15  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3

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; LENGTH: 548
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-152-697-3

Query Match      45.2%   Score 33; DB 7; Length 548;
Best Local Similarity 40.0%; Pred.No. 1.1e+02;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy    1 ISVORLASYYRRITSS 15
Db    104 VAIQLRDYEENSS 118
      ::||| |::||
RESULT 18
US-11-080-991-54
; Sequence 54, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Peter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 2828
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-54

Query Match      45.2%   Score 33; DB 7; Length 2828;
Best Local Similarity 46.7%; Pred.No. 6.5e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy    1 ISVORLASYYRRITSS 15
Db    2137 LNVQAAANARITGT 2151
      :|||: |||:
RESULT 19
US-11-186-284-49
; Sequence 49, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPW01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228

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Query Match      43.8%; Score 32; DB 6; Length 43;
Best Local Similarity 40.0%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 ISVQRLASVRRITSS 15
    :||| :| :|||
Db 18 VSVQDIMSWNNLSSS 32

RESULT 22
US-11-156-084-358
; Sequence 358, Application US/11156084
; Publication No. US20060010515A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
; FILE REFERENCE: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156,084
; CURRENT FILING DATE: 2005-08-17
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 358
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Geobacter sulfurreducens PCA
US-11-156-084-358

Query Match      43.8%; Score 32; DB 7; Length 311;
Best Local Similarity 66.7%; Pred. No. 92;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ISVQRLASVYRRI 12
    :||| :|||
Db 202 ISVERDDLYRRI 213

RESULT 23
US-11-217-562-3
; Sequence 3, Application US/11217562
; Publication No. US20060002952A1
; GENERAL INFORMATION:
; APPLICANT: WANG, LI
; APPLICANT: BABIUK, LORNE A.
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: WILLSON, PHILIP
; TITLE OF INVENTION: POSTWEANING MULTISYSTEM WASTING SYNDROME VIRUS FROM
; FILE REFERENCE: 9000-0040
; CURRENT APPLICATION NUMBER: US/11/217,562
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: US/09/209,961
; PRIOR FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: 60/069,233
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069,750
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Porcine Circovirus Type II
US-11-217-562-3

Query Match      43.8%; Score 32; DB 7; Length 314;
Best Local Similarity 87.5%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ASVRRITS 14
    :||| :|||
Db 273 ALYRRITS 280
```

```
RESULT 24
US-10-454-437-140
; Sequence 140, Application US/10454437
; Publication No. US2005027115A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128PCPN
; CURRENT APPLICATION NUMBER: US/10/454,437
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 140
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-140

Query Match      43.8%; Score 32; DB 6; Length 432;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 VQRLASVRRITS 14
    :||| :|||
Db 33 IERLGSVTRTVS 44

RESULT 25
US-11-055-822-184
; Sequence 184, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121PCPN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
```

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; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 184
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-184

Query Match      43.8%; Score 32; DB 7; Length 432;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 VORLASVRRITS 14
   :||| ||| |
Db 33 IERLGSYTRTVS 44

RESULT 26
US-11-127-877-39
; Sequence 39, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-39

Query Match      43.8%; Score 32; DB 7; Length 472;
Best Local Similarity 42.9%; Pred. No. 1.4e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ISVORLASVRRITS 14
   ||| | :||| :
Db 216 ISIHRLPLAYKRIVT 229

RESULT 27
US-11-182-016-33
; Sequence 33, Application US/11182016
; Publication No. US20060019294A1
; GENERAL INFORMATION:
; APPLICANT: SUGEN, INC.
```

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; TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS
; FILE REFERENCE: 038602/0102
; CURRENT APPLICATION NUMBER: US/11/182,016
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US/09/958,359
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Tks 118
US-11-182-016-33

Query Match      43.8%; Score 32; DB 7; Length 496;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SVORLASVRRITSS 15
   | :| :||| :||
Db 294 SARFSSRRFSSS 307

RESULT 28
US-10-467-962B-37
; Sequence 37, Application US/10467962B
; Publication No. US20050246784A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Blau, Astrid
; APPLICANT: Daeschner, Klaus
; APPLICANT: Klein, Mathieu
; TITLE OF INVENTION: Identification of Herbicidally Active Substances
; FILE REFERENCE: 2000_857
; CURRENT APPLICATION NUMBER: US/10/467,962B
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/EP02/01466
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 37
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-467-962B-37

Query Match      43.8%; Score 32; DB 6; Length 566;
Best Local Similarity 60.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 RLASVRRITS 14
   ||| ||| :|
Db 465 RLACYRTLTA 474

RESULT 29
US-10-957-887B-222
; Sequence 222, Application US/10957887B
; Publication No. US20050272677A1
; GENERAL INFORMATION:
; APPLICANT: Friesen, Robert H. E.
; APPLICANT: Leenhouts, Cornelius J.
; APPLICANT: Hektor, Harm
; APPLICANT: van Esch, Johannes H.
; APPLICANT: Heeres, Andre
; TITLE OF INVENTION: DELIVERY OF A SUBSTANCE TO A PRE-DETERMINED SITE
; FILE REFERENCE: 2183-6668US
; CURRENT APPLICATION NUMBER: US/10/957,887B
; CURRENT FILING DATE: 2004-10-04
; PRIOR APPLICATION NUMBER: PCT/NL/00256
; PRIOR FILING DATE: 2003-04-04
```

; NUMBER OF SEQ ID NOS: 309  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 222  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Listeria ivanovii  
US-10-957-887B-222

Query Match 42.5%; Score 31; DB 6; Length 43;  
Best Local Similarity 42.9%; Pred. No. 16;  
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 SVQRLASYRRITSS 15  
||| | | : : : ||  
DB 19 SVQNLMSWNNLSSS 32

RESULT 30  
US-10-957-887B-233  
; Sequence 233, Application US/10957887B  
; Publication No. US20050272677A1  
; GENERAL INFORMATION:  
; APPLICANT: Friesen, Robert H. E.  
; APPLICANT: Leenhouts, Cornelius J.  
; APPLICANT: Hektor, Harm  
; APPLICANT: van Esch, Johannes H.  
; APPLICANT: Heeres, Andre  
; TITLE OF INVENTION: DELIVERY OF A SUBSTANCE TO A PRE-DETERMINED SITE  
; FILE REFERENCE: 2183-6668US  
; CURRENT APPLICATION NUMBER: US/10/957,887B  
; CURRENT FILING DATE: 2004-10-04  
; PRIOR APPLICATION NUMBER: PCT/NL/00256  
; PRIOR FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 309  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 233  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Listeria seeligeri  
US-10-957-887B-233

Query Match 42.5%; Score 31; DB 6; Length 43;  
Best Local Similarity 50.0%; Pred. No. 16;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 SVQRLASYRRITSS 15  
||| | | : : : ||  
DB 19 SVQDLMSWNNLSSS 32

RESULT 31  
US-10-957-887B-236  
; Sequence 236, Application US/10957887B  
; Publication No. US20050272677A1  
; GENERAL INFORMATION:  
; APPLICANT: Friesen, Robert H. E.  
; APPLICANT: Leenhouts, Cornelius J.  
; APPLICANT: Hektor, Harm  
; APPLICANT: van Esch, Johannes H.  
; APPLICANT: Heeres, Andre  
; TITLE OF INVENTION: DELIVERY OF A SUBSTANCE TO A PRE-DETERMINED SITE  
; FILE REFERENCE: 2183-6668US  
; CURRENT APPLICATION NUMBER: US/10/957,887B  
; CURRENT FILING DATE: 2004-10-04  
; PRIOR APPLICATION NUMBER: PCT/NL/00256  
; PRIOR FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 309  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 236  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Listeria welshimeri  
US-10-957-887B-236

Query Match 42.5%; Score 31; DB 6; Length 43;  
Best Local Similarity 50.0%; Pred. No. 16;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 SVQRLASYRRITSS 15  
||| | | : : : ||  
DB 19 SVQDLMSWNNLSSS 32

RESULT 32  
US-10-793-626-894  
; Sequence 894, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 894  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-894

Query Match 42.5%; Score 31; DB 6; Length 110;  
Best Local Similarity 60.0%; Pred. No. 45;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 ASYRRITSSK 16  
||| | | : : : ||  
DB 43 ASFRKSTSSR 52

RESULT 33  
US-11-054-515-1584  
; Sequence 1584, Application US/11054515  
; Publication No. US2005025532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523P3  
; CURRENT APPLICATION NUMBER: US/11/054,515  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.



```
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1584
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1584

Query Match          42.5%; Score 31; DB 7; Length 254;
Best Local Similarity 56.2%; Pred. No. 1.1e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

Qy 1 ISVQRLAS--YRRITS 14
Db 70 ISVRLTSVAYMELTS 85

RESULT 34
US-11-129-143-103
; Sequence 103, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: VELISEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Streptomyces griseolosporeus
US-11-129-143-103

Query Match          42.5%; Score 31; DB 7; Length 334;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ISVQRLASVRRITSS 15
Db 81 VTAQALDGLRLTAS 95

RESULT 35
US-11-196-976-4
; Sequence 4, Application US/11196976
; Publication No. US20050272091A1
; GENERAL INFORMATION:
; APPLICANT: Ruelle, Jean-Louis
; TITLE OF INVENTION: Polynucleotides and Polypeptides BASB033
; TITLE OF INVENTION: from Neisseria Meningitidis and Their Uses
; FILE REFERENCE: BM45331
; CURRENT APPLICATION NUMBER: US/11/196,976
; CURRENT FILING DATE: 2005-08-03
; PRIOR APPLICATION NUMBER: US/10/417,885
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US/09/787,084
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: PCT/EP99/06718
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: GB 9820003.3
; PRIOR FILING DATE: 1998-09-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Neisseria meningitidis

US-11-196-976-4
Query Match          42.5%; Score 31; DB 7; Length 374;
Best Local Similarity 46.7%; Pred. No. 1.7e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SVORLASVRRITSSK 16
Db 33 NVTRLACYDRIFAQA 47

RESULT 36
US-11-103-957-95
; Sequence 95, Application US/11103957
; Publication No. US20050281847A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Verlant, Vincent Georges Christian Louis
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45261
; CURRENT APPLICATION NUMBER: US/11/103,957
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: US/10/467,534
; PRIOR FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/EP02/01356
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103169.9
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-11-103-957-95

Query Match          42.5%; Score 31; DB 7; Length 375;
Best Local Similarity 46.7%; Pred. No. 1.7e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SVORLASVRRITSSK 16
Db 34 NVTRLACYDRIFAQA 48

RESULT 37
US-10-467-657-7076
; Sequence 7076, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7076
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7076

Query Match          42.5%; Score 31; DB 6; Length 386;
Best Local Similarity 46.7%; Pred. No. 1.8e+02;
```

Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16  
:|||||:|:|:  
Db 45 NVTRLACYDRIPAAQ 59

## RESULT 38

US-10-821-234-1463  
; Sequence 1463, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt SEQ\_genes Version 1.0  
; SEQ ID NO 1463  
; LENGTH: 432  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1463

Query Match 42.5%; Score 31; DB 6; Length 432;  
Best Local Similarity 55.6%; Pred. No. 2e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QRLASYRRI 12  
|:|:|:|:  
Db 379 QEIATYRL 387

## RESULT 39

US-11-024-959-287  
; Sequence 287, Application US/11024959  
; Publication No. US20060010516A1  
; GENERAL INFORMATION:  
; APPLICANT: FORSTER, RICHARD L.  
; APPLICANT: CONNETT, MARIE B.  
; APPLICANT: EMERSON, SARAH JANE  
; APPLICANT: GRIGOR, MURRAY ROBERT  
; APPLICANT: HIGGINS, COLLEEN M.  
; APPLICANT: LUND, STEVEN TROY  
; APPLICANT: MAGUSIN, ANDREAS  
; APPLICANT: KODRZYCKI, BOB  
; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS  
; FILE REFERENCE: 044463-0360  
; CURRENT APPLICATION NUMBER: US/11/024,959  
; CURRENT FILING DATE: 2004-12-30  
; PRIOR APPLICATION NUMBER: 60/533,036  
; PRIOR FILING DATE: 2003-12-30  
; NUMBER OF SEQ ID NOS: 782  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 287  
; LENGTH: 465  
; TYPE: PRT  
; ORGANISM: Eucalyptus sp.  
US-11-024-959-287

Query Match 42.5%; Score 31; DB 7; Length 465;  
Best Local Similarity 50.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRI 12  
|:|:|:|:|:  
Db 301 IDVQRLLSFDKV 312

## RESULT 40

US-11-024-959-288  
; Sequence 288, Application US/11024959  
; Publication No. US20060010516A1  
; GENERAL INFORMATION:  
; APPLICANT: FORSTER, RICHARD L.  
; APPLICANT: CONNETT, MARIE B.  
; APPLICANT: EMERSON, SARAH JANE  
; APPLICANT: GRIGOR, MURRAY ROBERT  
; APPLICANT: HIGGINS, COLLEEN M.  
; APPLICANT: LUND, STEVEN TROY  
; APPLICANT: MAGUSIN, ANDREAS  
; APPLICANT: KODRZYCKI, BOB  
; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS  
; FILE REFERENCE: 044463-0360  
; CURRENT APPLICATION NUMBER: US/11/024,959  
; CURRENT FILING DATE: 2004-12-30  
; PRIOR APPLICATION NUMBER: 60/533,036  
; PRIOR FILING DATE: 2003-12-30  
; NUMBER OF SEQ ID NOS: 782  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 288  
; LENGTH: 465  
; TYPE: PRT  
; ORGANISM: Eucalyptus sp.  
US-11-024-959-288

Query Match 42.5%; Score 31; DB 7; Length 465;  
Best Local Similarity 50.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRI 12  
|:|:|:|:|:  
Db 301 IDVQRLLSFDKV 312

## RESULT 41

US-11-065-943-65  
; Sequence 65, Application US/11065943  
; Publication No. US20050250131A1  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, JEAN-LUC  
; APPLICANT: VICHIER-GUERRE, SOPHIE  
; APPLICANT: FERRIS, STEPHANE  
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I  
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,  
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME  
; FILE REFERENCE: 266426USOXCP  
; CURRENT APPLICATION NUMBER: US/11/065,943  
; CURRENT FILING DATE: 2005-02-25  
; PRIOR APPLICATION NUMBER: US 10/787,219  
; PRIOR FILING DATE: 2004-02-27  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 65  
; LENGTH: 545  
; TYPE: PRT  
; ORGANISM: Thermus aquaticus  
US-11-065-943-65

Query Match 42.5%; Score 31; DB 7; Length 545;  
Best Local Similarity 35.7%; Pred. No. 2.6e+02;  
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 VQRLASYRRITSSK 16  
|:|:|:|:|:  
Db 240 VEKILQYRELTKLK 253

## RESULT 42

US-11-065-943-67

; Sequence 67, Application US/11065943  
; Publication No. US20050250131A1  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, JEAN-LUC  
; APPLICANT: VICHIER-GUERRE, SOPHIE  
; APPLICANT: FERRIS, STEPHANE  
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I  
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,  
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME  
; FILE REFERENCE: 266426USOXCIP  
; CURRENT APPLICATION NUMBER: US/11/065,943  
; CURRENT FILING DATE: 2005-02-25  
; PRIOR FILING DATE: 2004-02-27  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 67  
; LENGTH: 545  
; TYPE: PRT  
; ORGANISM: Thermus aquaticus  
US-11-065-943-67

Query Match 42.5%; Score 31; DB 7; Length 545;  
Best Local Similarity 35.7%; Pred. No. 2.6e+02;  
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 VORLASYRRITSSK 16  
|::||:|  
Db 240 VEKILQYRELTKLK 253

RESULT 43  
US-11-065-943-69  
; Sequence 69, Application US/11065943  
; Publication No. US20050250131A1  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, JEAN-LUC  
; APPLICANT: VICHIER-GUERRE, SOPHIE  
; APPLICANT: FERRIS, STEPHANE  
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I  
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,  
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME  
; FILE REFERENCE: 266426USOXCIP  
; CURRENT APPLICATION NUMBER: US/11/065,943  
; CURRENT FILING DATE: 2005-02-25  
; PRIOR FILING DATE: 2004-02-27  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 69  
; LENGTH: 545  
; TYPE: PRT  
; ORGANISM: Thermus aquaticus  
US-11-065-943-69

Query Match 42.5%; Score 31; DB 7; Length 545;  
Best Local Similarity 35.7%; Pred. No. 2.6e+02;  
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 VORLASYRRITSSK 16  
|::||:|  
Db 240 VEKILQYRELTKLK 253

RESULT 44  
US-11-065-943-73  
; Sequence 73, Application US/11065943  
; Publication No. US20050250131A1  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, JEAN-LUC  
; APPLICANT: VICHIER-GUERRE, SOPHIE  
; APPLICANT: FERRIS, STEPHANE  
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I

; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,  
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME  
; FILE REFERENCE: 266426USOXCIP  
; CURRENT APPLICATION NUMBER: US/11/065,943  
; CURRENT FILING DATE: 2005-02-25  
; PRIOR FILING DATE: 2004-02-27  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 73  
; LENGTH: 545  
; TYPE: PRT  
; ORGANISM: Thermus aquaticus  
US-11-065-943-73

Query Match 42.5%; Score 31; DB 7; Length 545;  
Best Local Similarity 35.7%; Pred. No. 2.6e+02;  
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 VORLASYRRITSSK 16  
|::||:|  
Db 240 VEKILQYRELTKLK 253

RESULT 45  
US-11-065-943-75  
; Sequence 75, Application US/11065943  
; Publication No. US20050250131A1  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, JEAN-LUC  
; APPLICANT: VICHIER-GUERRE, SOPHIE  
; APPLICANT: FERRIS, STEPHANE  
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I  
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,  
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME  
; FILE REFERENCE: 266426USOXCIP  
; CURRENT APPLICATION NUMBER: US/11/065,943  
; CURRENT FILING DATE: 2005-02-25  
; PRIOR FILING DATE: 2004-02-27  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 75  
; LENGTH: 545  
; TYPE: PRT  
; ORGANISM: Thermus aquaticus  
US-11-065-943-75

Query Match 42.5%; Score 31; DB 7; Length 545;  
Best Local Similarity 35.7%; Pred. No. 2.6e+02;  
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 VORLASYRRITSSK 16  
|::||:|  
Db 240 VEKILQYRELTKLK 253

RESULT 46  
US-11-065-943-77  
; Sequence 77, Application US/11065943  
; Publication No. US20050250131A1  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, JEAN-LUC  
; APPLICANT: VICHIER-GUERRE, SOPHIE  
; APPLICANT: FERRIS, STEPHANE  
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I  
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,  
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME  
; FILE REFERENCE: 266426USOXCIP  
; CURRENT APPLICATION NUMBER: US/11/065,943  
; CURRENT FILING DATE: 2005-02-25  
; PRIOR FILING DATE: 2004-02-27

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; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-77

Query Match      42.5%; Score 31; DB 7; Length 545;
Best Local Similarity 35.7%; Pred. No. 2.6e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      3 VORLASYRRITSSK 16
Db      240 VEKILQYRELTKLK 253

RESULT 47
US-11-065-943-79
; Sequence 79, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-79

Query Match      42.5%; Score 31; DB 7; Length 545;
Best Local Similarity 35.7%; Pred. No. 2.6e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      3 VORLASYRRITSSK 16
Db      240 VEKILQYRELTKLK 253

RESULT 48
US-11-065-943-81
; Sequence 81, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-81
```

```
Query Match      42.5%; Score 31; DB 7; Length 545;
Best Local Similarity 35.7%; Pred. No. 2.6e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      3 VORLASYRRITSSK 16
Db      240 VEKILQYRELTKLK 253
```

```
RESULT 49
US-11-065-943-83
; Sequence 83, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 83
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-83
```

```
Query Match      42.5%; Score 31; DB 7; Length 545;
Best Local Similarity 35.7%; Pred. No. 2.6e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      3 VORLASYRRITSSK 16
Db      240 VEKILQYRELTKLK 253
```

```
RESULT 50
US-11-065-943-85
; Sequence 85, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 85
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-85
```

```
Query Match      42.5%; Score 31; DB 7; Length 545;
Best Local Similarity 35.7%; Pred. No. 2.6e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      3 VORLASYRRITSSK 16
Db      240 VEKILQYRELTKLK 253
```

Db 240 VEKILQYRELTCLK 253

Search completed: February 6, 2006, 14:34:05  
Job time : 21 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:43:53 ; Search time 5.68063 Seconds  
(without alignment)  
1287.264 Million cell updates/sec

Title: US-10-644-277-149

Perfect score: 405

Sequence: 1 QPDAINAPVTCCYNFTNRKI.....QKWVQDSMDHLKQTQTPKT 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	405	100.0	99	2 A60299	monocyte chemoattr
2	337	83.2	99	2 JC2136	monocyte chemoattr
3	315	77.8	99	1 A39296	monocyte chemoattr
4	315	77.8	99	2 JC2336	monocyte chemoattr
5	314	77.5	125	2 I46857	monocyte chemoattr
6	288	71.1	72	2 A55984	monocyte chemoattr
7	287	70.9	109	2 A54678	monocyte chemoattr
8	270	66.7	97	2 JC4912	eotaxin precursor
9	268	66.2	99	2 JC5295	monocyte chemoattr
10	261	64.4	99	2 JC2417	monocyte chemoattr
11	252	62.2	148	1 A30209	PGPF-inducible JE
12	241	59.5	148	1 S07723	Immediate-early se
13	236	58.3	120	2 I48147	monocyte chemoattr
14	214	52.8	96	2 I48099	eotaxin precursor
15	207	51.1	96	2 JC2478	monocyte chemoattr
16	200	49.4	97	2 A48093	monocyte chemoattr
17	145.5	35.9	93	2 B35673	LD78-beta protein
18	142.5	35.2	92	2 A30574	macrophage inflam
19	135.5	33.5	92	1 A31767	macrophage inflam
20	133.5	33.0	92	2 I46730	immune activation
21	127.5	31.5	92	2 C30552	macrophage inflam
22	123	30.4	92	2 I52322	macrophage inflam
23	119	29.4	92	2 A32393	macrophage inflam
24	108.5	26.8	91	1 A46539	monocyte chemoattr
25	106	26.2	120	2 JE0177	lymphocyte and mon
26	105.5	26.0	91	1 A28815	monocyte chemoattr
27	99.5	24.6	96	2 A37236	I-309 protein prec
28	99.5	24.6	114	1 ETHUL	lymphotactin prec
29	98	24.2	50	2 C60407	monocyte adherence

30	94	23.2	103	2 A53096	interleukin-8 prec
31	93.5	23.1	92	2 S24236	TCA3 protein - mou
32	91.5	22.6	114	1 ETMSL	lymphotactin prec
33	83	20.5	101	2 I48148	Neutrophil attract
34	79	19.5	101	2 S42496	interleukin-8 prec
35	79	19.5	101	2 I46871	interleukin-8 - ra
36	75	18.5	95	2 JN0841	interleukin-8 - do
37	73.5	18.1	116	2 I49555	gene C10 protein -
38	70	17.3	99	2 A37034	interleukin-8 prec
39	66	16.3	2867	2 AG3481	cellobiose-phospho
40	65.5	16.2	143	2 S76162	hypothetical prote
41	65	16.0	282	2 S44825	F54P2.8 protein -
42	64.5	15.9	363	2 T26700	hypothetical prote
43	64	15.8	1019	2 E90037	hypothetical prote
44	64	15.8	1076	2 F96831	hypothetical prote
45	62.5	15.4	853	2 AB2020	hypothetical prote

#### ALIGNMENTS

#### RESULT 1

A60299

monocyte chemoattractant protein 1 precursor - human

N;Alternate names: GDCF-1; glioma-derived monocyte chemotactic factor 1; MCAF; MCP-1; mo

N;Contains: glioma-derived chemotactic factor 2 (GDCF-2)

C;Species: Homo sapiens (man)

C;Date: 20-Feb-1993 #sequence revision 20-Feb-1993 #text change 09-Jul-2004

C;Accession: A35474; A33476; S03339; I51841; A60299; A32300; A32396; A34561; 157488; JCI:

R;Shyu, Y.J.; Li, Y.S.; Kolattukudy, P.E.

Biochem. Biophys. Res. Commun. 169, 346-351, 1990

A;Title: Structure of human monocyte chemotactic protein gene and its regulation by TPA.

A;Reference number: A35474; MUID:90290466; PMID:2357211

A;Accession: A35474

A;Molecule type: DNA

A;Residues: 1-99 <SH>

A;Cross-references: UNIPROT:P13500; UNIPARC:UPI00000000DC9; GB:M37719; NID:gl87447; PIDN:

R;Rollins, B.J.; Stier, P.; Ernst, T.; Wong, G.G.

Mol. Cell. Biol. 9, 4687-4695, 1989

A;Title: The human homolog of the JE gene encodes a monocyte secretory protein.

A;Reference number: A33476; MUID:90097880; PMID:2513477

A;Accession: A33476

A;Molecule type: mRNA

A;Residues: 1-99 <ROL>

A;Cross-references: UNIPARC:UPI00000000DC9; GB:M30816; GB:M31625; GB:M31626; NID:gl88701;

R;Yoshimura, T.; Yuhki, N.; Moore, S.K.; Appella, E.; Lerman, M.I.; Leonard, E.J.

FEBS Lett. 244, 487-493, 1989

A;Title: Human monocyte chemoattractant protein-1 (MCP-1). Full-length cDNA cloning, exp

A;Reference number: S03339; MUID:89153605; PMID:2465924

A;Accession: S03339

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-99 <YOS>

A;Cross-references: UNIPARC:UPI00000000DC9; GB:Y14768; NID:g34513; PIDN:CAA32876.1; PID:g

A;Experimental source: glioma cell line U-105MG

R;Yoshimura, T.; Leonard, E.J.

Adv. Exp. Med. Biol. 305, 47-56, 1991

A;Title: Human monocyte chemoattractant protein-1 (MCP-1).

A;Reference number: I51841; MUID:92095166; PMID:1661560

A;Accession: I51841

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-99 <YO2>

A;Cross-references: UNIPARC:UPI00000000DC9; GB:S71513; NID:g240867; PIDN:AAB20651.1; PID:g

R;Bottazzi, B.; Colotta, F.; Sica, A.; Nobili, N.; Mantovani, A.

Int. J. Cancer 45, 795-797, 1990

A;Title: A chemoattractant expressed in human sarcoma cells (tumor-derived chemotactic f

-1/MCAF).

A;Reference number: A60299; MUID:90216082; PMID:2182547

A;Accession: A60299

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

C:Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 09-Jul-2004  
C:Accession: J02136; S57498  
R:Hosang, K.; Knoke, I.; Klaudiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.  
Biochem. Biophys. Res. Commun. 199, 962-968, 1994  
A:Title: Porcine luteal cells express monocyte chemoattractant protein-1 (MCP-1): Analysis  
A:Reference number: J02136; MUID:94183284; PMID:7510962  
A:Accession: J02136  
A:Molecule type: mRNA  
A:Residues: 1-99 <HOS>  
A:Cross-references: UNIPROT:P42831; UNIPARC:UPI00001362C7; GB:248479; NID:G683716; PIDN:  
R:Zach, O.  
submitted to the EMBL Data Library, July 1994  
A:Reference number: S57497  
A:Accession: S57498  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-99 <ZAC>  
A:Cross-references: UNIPARC:UPI00001362C7; EMBL:X79416; NID:G872312; PIDN:CAA55945.1; PI  
C:Superfamily: macrophage inflammatory protein  
C:Keywords: glycoprotein  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-99/Product: monocyte chemoattractant protein-1 #status predicted <MAT>  
F:94/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 83.2%; Score 337; DB 2; Length 99;  
Best Local Similarity 80.0%; Pred. No. 1.9e-31;  
Matches 60; Conservative 8; Mismatches 7; Indels 0; Gaps 0;  
QY 1 QPDAINAPVTCYNTFNTRKISVQRILASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60  
DB 24 QPDAINSPVTCCTLTSTKISQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83  
QY 61 QDSMDHLDKQQTPTK 75  
DB 84 QDSISHLDDKKNQTPK 98  
RESULT 3  
monocyte chemoattractant protein 1 precursor - bovine  
N:Alternate names: monocyte chemotactic factor 1; seminal plasma protein P6  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A39296; B39296  
R:Wempe, F.; Henschen, A.; Scheit, K.H.  
DNA Cell Biol. 10, 671-679, 1991  
A:Title: Gene expression and cDNA cloning identified a major basic protein constituent  
A:Reference number: A39296; MUID:92096117; PMID:1721821  
A:Accession: A39296  
A:Molecule type: mRNA  
A:Residues: 1-99 <WEM>  
A:Cross-references: UNIPROT:P28291; UNIPARC:UPI000012EDA7; GB:M84602; NID:G16  
A:Accession: B39296  
A:Molecule type: protein  
A:Residues: 50-68, 'X', 70-74, 'X', 76 <WE2>  
A:Cross-references: UNIPARC:UPI00001736A1  
A:Experimental source: seminal vesicle  
C:Superfamily: macrophage inflammatory protein  
C:Keywords: glycoprotein  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-99/Product: monocyte chemoattractant protein 1 #status predicted <MAT>  
F:94/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 77.8%; Score 315; DB 1; Length 99;  
Best Local Similarity 73.3%; Pred. No. 6.4e-29;  
Matches 55; Conservative 13; Mismatches 7; Indels 0; Gaps 0;  
QY 1 QPDAINAPVTCYNTFNTRKISVQRILASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60  
DB 24 QPDAINSPVTCCTLTSTKISQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83  
QY 61 QDSMDHLDKQQTPTK 75  
DB 84 QDSISHLDDKKNQTPK 98  
RESULT 2  
monocyte chemoattractant protein-1 precursor - pig  
C:Species: Sus scrofa domestica (domestic pig)

A:Residues: 1-99 <BOT>  
A:Cross-references: UNIPARC:UPI00000000DC9  
R:Furutani, Y.; Nomura, H.; Nataka, M.; Oyamada, Y.; Fukui, T.; Yamada, M.; Larsen, C.G.  
Biochem. Biophys. Res. Commun. 159, 249-255, 1989  
A:Title: Cloning and sequencing of the cDNA for human monocyte chemoattractant and activatin  
A:Reference number: A32300; MUID:89165862; PMID:2323622  
A:Accession: A32300  
A>Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-99 <FUR>  
A:Cross-references: UNIPARC:UPI00000000DC9; GB:M24545; NID:G187434; PIDN:AAA18164.1; PID:  
R:Robinson, E.A.; Yoshimura, T.; Leonard, E.J.; Tanaka, S.; Griffin, P.R.; Shabanowitz,  
Proc. Natl. Acad. Sci. U.S.A. 86, 1850-1854, 1989  
A:Title: Complete amino acid sequence of a human monocyte chemoattractant, a putative me  
A:Reference number: A32396; MUID:89184525; PMID:2648385  
A:Accession: A32396  
A:Molecule type: protein  
A:Residues: 'X', 25-99 <ROB>  
A:Cross-references: UNIPARC:UPI00001429D5  
R:Decock, B.; Conings, R.; Lenaerts, J.P.; Billiau, A.; Van Damme, J.  
Biochem. Biophys. Res. Commun. 167, 904-909, 1990  
A:Title: Identification of the monocyte chemotactic protein from human osteosarcoma cell  
A:Reference number: A34561; MUID:90211336; PMID:2322286  
A:Accession: A34561  
A:Molecule type: protein  
A:Residues: 29-33, 'XX', 36-52; 82-92 <DEC>  
A:Cross-references: UNIPARC:UPI000017674D; UNIPARC:UPI0000017674E  
R:Li, Y.S.; Shyy, Y.J.; Wright, J.G.; Valente, A.J.; Cornhill, J.F.; Kolattukudy, P.E.  
Mol. Cell. Biochem. 126, 61-68, 1993  
A:Title: The expression of monocyte chemotactic protein (MCP-1) in human vascular endoth  
A:Reference number: I57488; MUID:94150478; PMID:8107690  
A:Accession: I57488  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-99 <LIY>  
A:Cross-references: UNIPARC:UPI00000000DC9; GB:S69738; NID:G545464; PIDN:AAB29926.1; PID:  
R:Ye, Q.N.; Su, G.F.; Yuan, Y.; Huang, C.F.  
Chinese J. Microbiol. Immunol. 14, 29-32, 1994  
A:Title: The PCR, cloning and sequencing of human monocyte chemoattractant protein-1 (MC  
A:Reference number: J01096  
A:Accession: J01096  
A:Molecule type: mRNA  
A:Residues: 24-28, 'Q', 30-99 <YEQ>  
A:Cross-references: UNIPARC:UPI0000017674F  
C:Genetics:  
A:Gene: GDB:SCVA2  
A:Cross-references: GDB:125279; OMIM:158105  
A:Map position: 17q11.2-17q12  
C:Superfamily: macrophage inflammatory protein  
C:Keywords: cytokine; glycoprotein; inflammation; pyroglutamic acid  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-99/Product: monocyte chemoattractant protein 1 #status experimental <MAT>  
F:29-99/Product: monocyte chemoattractant protein 1, short form #status experimental <MA  
F:37/Binding site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen  
F:37/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 100.0%; Score 405; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.2e-39;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QPDAINAPVTCYNTFNTRKISVQRILASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60  
DB 24 QPDAINAPVTCYNTFNTRKISVQRILASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83  
QY 61 QDSMDHLDKQQTPTK 76  
DB 84 QDSMDHLDKQQTPTK 99  
RESULT 2  
monocyte chemoattractant protein-1 precursor - pig  
C:Species: Sus scrofa domestica (domestic pig)





Qy 61 QDSMDHLDKQOTPK 75  
Db 94 QDFMKHLDDKKTQTPK 108

RESULT 8  
JC4912  
eotaxin precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
C:Accession: JC4912  
R:Bartels, J.; Schluster, C.; Richter, E.; Noso, N.; Kulke, R.; Christophers, E.; Schroe  
Biochem. Biophys. Res. Commun. 225, 1045-1051, 1996  
A:Title: Human dermal fibroblasts express eotaxin: Molecular cloning, mRNA expression, a  
A:Reference number: JC4912; MUID:96374440; PMID:8780731  
A:Accession: JC4912  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-97 <BAR>  
A:Cross-references: UNIPROT:P51671; UNIPARC:UPI000016A67B; EMBL:Z75668; NID:gl531982; PI  
A:Experimental source: dermal fibroblast  
C:Comment: This protein has eosinophil specific chemotactic activity.  
C:Superfamily: macrophage inflammatory protein  
C:Keywords: fibroblast  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-97/Product: eotaxin #status predicted <MAT>

Query Match 66.7%; Score 270; DB 2; Length 97;  
Best Local Similarity 67.1%; Pred. No. 8.8e-24;  
Matches 47; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

Qy 6 NAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWVDSMD 65  
Db 27 SVPTTCCFNLANRKIPQLRLESYRRITSGKCPKAVIFKTKLAKDICKADPKRWVDSMK 86

Qy 66 HLDKQOTPK 75  
Db 87 YLDQKSPTPK 96

RESULT 9  
JC5295  
monocyte chemotactic protein-2 precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 02-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 09-Jul-2004  
C:Accession: JC5295  
R:Van Coillie, E.; Froyen, G.; Nomiya, H.; Miura, R.; Fiten, P.; Van Aelst, I.; Van Da  
Biochem. Biophys. Res. Commun. 231, 726-730, 1997  
A:Title: Human monocyte chemotactic protein-2: cDNA cloning and regulated expression of  
A:Reference number: JC5295; MUID:97224420; PMID:9070881  
A:Accession: JC5295  
A:Molecule type: mRNA  
A:Residues: 1-99 <VAN>  
A:Cross-references: UNIPROT:P80075; UNIPARC:UPI0000030FC6; GB:Y10802; NID:g1924937; PIDN  
A:Experimental source: bone marrow  
C:Comment: This protein belongs to the beta-chemokine family which is one of the major H  
tis and in tumor biology, and contribute to the trafficking and recruitment of the respon  
C:Genetics:  
A:Gene: mcp-2  
C:Superfamily: macrophage inflammatory protein  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-99/Product: monocyte chemotactic protein-2 #status predicted <MAT>

Query Match 66.2%; Score 268; DB 2; Length 99;  
Best Local Similarity 62.7%; Pred. No. 1.5e-23;  
Matches 47; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 1 QPDAINAVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60  
Db 24 QPDSVSIPTCCFNINRKIPQLRLESYRRITNTIQCPKEAVIFKTKRQKGVADPKRWV 83

Qy 61 QDSMDHLDKQOTPK 75  
Db 94 QDFMKHLDDKKTQTPK 108

Db 84 RDSMKHLDDKQIFQNLK 98

RESULT 10  
JC2417  
monocyte chemoattractant protein-2 precursor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 24-Feb-1995 #sequence\_revision 24-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: JC2417  
R:Hosang, K.; Knoke, I.; Klaudiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.  
Biochem. Biophys. Res. Commun. 205, 148-153, 1994  
A:Title: Porcine luteal cells express monocyte chemoattractant protein-2 (MCP-2): Analy  
A:Reference number: JC2417; MUID:95091716; PMID:7999015  
A:Accession: JC2417  
A:Molecule type: mRNA  
A:Residues: 1-99 <HOS>  
A:Cross-references: UNIPROT:P49873; UNIPARC:UPI000001362D6; GB:Z48480; NID:g683718; PIDN:  
A:Experimental source: corpus luteum  
C:Superfamily: macrophage inflammatory protein  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-99/Product: monocyte chemoattractant protein-2 #status predicted <MAT>

Query Match 64.4%; Score 261; DB 2; Length 99;  
Best Local Similarity 60.0%; Pred. No. 9.6e-23;  
Matches 45; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Qy 1 QPDAINAVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60  
Db 24 QPDSVSIPTCCFNINRKIPQLRLESYRRITNTIQCPKEAVIFKTKRQKGVADPKQKWV 83

Qy 61 QDSMDHLDKQOTPK 75  
Db 84 QNSMKLLDQKSQTPK 98

RESULT 11  
A30209  
PDGF-inducible JE glycoprotein precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A30209; A44771; A30861  
R:Rollins, B.J.; Morrison, E.D.; Stiles, C.D.  
Proc. Natl. Acad. Sci. U.S.A. 85, 3738-3742, 1988  
A:Title: Cloning and expression of JE, a gene inducible by platelet-derived growth facto  
A:Reference number: A30209; MUID:98234501; PMID:3287374  
A:Accession: A30209  
A:Molecule type: DNA  
A:Residues: 1-148 <ROL>  
A:Cross-references: UNIPROT:P10148; UNIPARC:UPI0000020A69; GB:M19681; NID:g193486; PIDN:  
R:Kawahara, R.S.; Deuel, T.F.  
J. Biol. Chem. 264, 679-682, 1989  
A:Title: Platelet-derived growth factor-inducible gene JE is a member of a family of sma  
A:Reference number: A44771; MUID:89093129; PMID:2910859  
A:Accession: A44771  
A:Molecule type: DNA  
A:Residues: 1-148 <KAZ>  
A:Cross-references: UNIPARC:UPI0000020A69; GB:J04467; NID:g193488; PIDN:AAA37685.1; PID:  
C:Genetics:  
A:Gene: JE  
A:Introns: 26/1; 65/2  
C:Superfamily: macrophage inflammatory protein  
C:Keywords: cytokine; glycoprotein  
F:126/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 62.2%; Score 252; DB 1; Length 148;  
Best Local Similarity 60.9%; Pred. No. 1.5e-21;  
Matches 42; Conservative 17; Mismatches 10; Indels 0; Gaps 0;

Qy 1 QPDAINAVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60  
Db 24 QPDSVSIPTCCFNINRKIPQLRLESYRRITNTIQCPKEAVIFKTKRQKGVADPKRWV 83

Qy 61 QDSMDHLDK 69

Db 84 QTYIKNLD 92

RESULT 12

S07723

immediate-early serum-responsive protein JE precursor - rat

N;Alternate names: monocyte chemoattractant protein-1

C;Species: Rattus norvegicus (Norway rat)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C;Accession: S07723; JN0128

R;Timmers, H.T.M.; Pronk, G.J.; Bos, J.L.; van der Eb, A.J.

Nucleic Acids Res. 18, 23-34, 1990

A;Title: Analysis of the rat JE gene promoter identifies an AP-1 binding site essential

A;Reference number: S07723; MUID:90174947; PMID:2106664

A;Accession: S07723

A;Molecule type: DNA

A;Residues: 1-148 <TIM>

A;Cross-references: UNIPROT:P14844; UNIPARC:UPI0000000187; EMBL:X17053; NID:g55530; PIDN:R;Yoshimura, T.; Takeya, M.; Takahashi, K.

Biochem. Biophys. Res. Commun. 174, 504-509, 1991

A;Title: Molecular cloning of rat monocyte chemoattractant protein-1 (MCP-1) and its exp

A;Reference number: JN0128; MUID:91128376; PMID:1704226

A;Accession: JN0128

A;Molecule type: mRNA

A;Residues: 1-148 <YOS>

A;Cross-references: UNIPARC:UPI0000000187; GB:M57441; NID:g205333; PIDN:AAA63496.1; PID: A;Experimental source: spleen cells

A;Note: the authors translated the codon GAA for residue 62 as Lys and GCT for residue 6

C;Genetics:

A;Introns: 26/1; 65/2

C;Superfamily: macrophage inflammatory protein

F;1-23/Domain: signal sequence #status predicted <SIG>

F;23-148/Product: immediate-early serum-responsive protein JE #status predicted <MAT>

Query Match 59.5%; Score 241; DB 1; Length 148;

Best Local Similarity 55.3%; Pred. No. 2.8e-20;

Matches 42; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCVCYNFTNRKISVORLASYSRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

DB 24 QPDVAVNAPLCCVSPFGTKMIPMSRLNRYKRTISRCPEAVFVTKLKKEICADPNKEW 83

QY 61 QDSMDHLDKQOTQPKT 76

DB 84 QKVIRKLDQNVRSST 99

RESULT 13

I48147

monocyte chemoattractant protein-1 - guinea pig

C;Species: Cavia porcellus (guinea pig)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C;Accession: I48147

R;Yoshimura, T.

J. Immunol. 150, 5025-5032, 1993

A;Title: cDNA cloning of guinea pig monocyte chemoattractant protein-1 and expression of

A;Reference number: I48147; MUID:93267104; PMID:8496603

A;Accession: I48147

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-120 <RES>

A;Cross-references: UNIPROT:Q08782; UNIPARC:UPI00001362C6; GB:L04985; NID:g349820; PIDN: C;Genetics:

A;Gene: MCP-1

C;Superfamily: macrophage inflammatory protein

Query Match 58.3%; Score 236; DB 2; Length 120;

Best Local Similarity 59.7%; Pred. No. 8.4e-20;

Matches 43; Conservative 14; Mismatches 13; Indels 2; Gaps 2;

QY 1 QPDAINAPVTCVCYNFTNRKISVORLASYSRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Search completed: February 3, 2006, 09:59:42  
Job time : 6.68063 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:43:44 ; Search time 34.6863 Seconds  
(without alignments)  
1545.860 Million cell updates/sec

Title: US-10-644-277-149

Perfect score: 405

Sequence: 1 QPDAINAPVTCYCNFTNRKI.....QKVVQDSMDHLKQTQTPKT 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	405	100.0	99	1	CCL2_HUMAN
2	395	97.5	99	1	CCL2_PONPY
3	394	97.3	99	1	CCL2_MACFA
4	394	97.3	99	1	CCL2_MACMU
5	394	97.3	99	2	O6XV55_MACNE
6	394	97.3	99	2	O7LME7_MACMU
7	337	83.2	99	1	CCL2_PIG
8	331	81.7	101	1	CCL2_CANFA
9	330	81.5	99	1	CCL2_HORSE
10	315	77.8	99	1	MCPA_BOVIN
11	314	77.5	125	1	CCL2_RABIT
12	308	76.0	74	1	MCPB_BOVIN
13	297	73.3	99	2	O51F88_CANFA
14	297	73.3	109	2	O865F3_MACNE
15	292	72.1	99	2	O5K5U7_CANFA
16	287	70.9	99	1	CCL7_HUMAN
17	287	70.9	99	2	O569J6_HUMAN
18	287	70.9	109	2	O727Q8_HUMAN
19	284	70.1	104	1	CCL12_MOUSE
20	284	70.1	104	2	O5SVB4_MOUSE
21	277	68.4	99	2	O8MKC8_HORSE
22	274.5	67.8	98	1	CCL13_CANFA
23	274	67.7	99	2	O865F4_MACNE
24	273	67.4	97	1	CCL11_HUMAN
25	273	67.4	97	2	O619T4_HUMAN
26	273	67.4	99	1	CCL8_CANFA
27	271	66.9	99	2	O8HYQ0_MACMU
28	268	66.2	99	1	CCL8_HUMAN
29	261	64.4	97	1	CCL11_MACMU
30	261	64.4	97	2	O8HXZ5_MACMU
31	261	64.4	99	1	CCL8_PIG
32	260	64.2	150	2	O8CGM5_SIGHI
33	253.5	62.6	98	1	CCL13_HUMAN
34	253.5	62.6	98	2	O6ICQ6_HUMAN
35	252	62.2	100	1	CCL11_HORSE
36	252	62.2	148	1	CCL2_MOUSE
37	252	62.2	148	2	O5SVU3_MOUSE
38	249	61.5	97	2	O9Z318_CAVPO
39	247	61.0	99	1	CCL8_BOVIN
40	241	59.5	148	1	CCL5_RAT
41	241	59.5	148	2	O549R5_RAT
42	236	58.3	120	1	CCL2_CAVPO
43	235	58.0	97	2	O9TTS6_BOVIN
44	221	54.6	97	1	CCL11_RAT
45	218	53.8	97	1	CCL11_MOUSE

#### RESULT 1

ID	CCL2_HUMAN	STANDARD;	PRT;	99 AA.
AC	P13500; Q9UDF3;			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant protein 1) (MCP-1) (Monocyte chemoattractant protein 1) (Monocyte chemoattractant and activating factor) (MCAF) (Monocyte secretory protein JB) (HC11).			
GN	Names=CCL2; Synonyms=MCP1, SCYA2;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=89165862; PubMed=2923622;			
RA	Furutani Y., Nomura H., Notake M., Oyama Y., Fukui T., Yamada M., Larsen C.G., Oppenheim J.J., Matsushima K.;			
RT	"Cloning and sequencing of the cDNA for human monocyte chemoattractant and activating factor (MCAF).";			
RL	Biochem. Biophys. Res. Commun. 159:249-255(1989).			
RP	[2]			
RN	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=90097880; PubMed=2513477;			
RA	Rollins B.J., Stier P., Ernst T., Wong G.G.;			
RT	"The human homolog of the JB gene encodes a monocyte secretory protein.";			
RL	Mol. Cell. Biol. 9:4687-4695(1989).			
RP	[3]			
RN	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=89153605; PubMed=2465924; DOI=10.1016/0014-5793(89)80590-3;			
RA	Yoshimura T., Fukui N., Moore S.K., Appella E., Lerman M.I., Leonard E.J.;			
RT	"Human monocyte chemoattractant protein-1 (MCP-1). Full-length cDNA cloning, expression in mitogen-stimulated blood mononuclear leukocytes, and sequence similarity to mouse competence gene JB.";			
RL	FEBS Lett. 244:487-493(1989).			
RN	[4]			
RN	NUCLEOTIDE SEQUENCE.			
RP	MEDLINE=90290466; PubMed=2357211;			
RX	Shyy Y.J., Li Y.S., Kolattukudy P.E.;			
RA	"Structure of human monocyte chemoattractant protein gene and its regulation by TPA.";			
RT	Biochem. Biophys. Res. Commun. 169:346-351(1990).			
RN	[5]			
RN	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=91207938; PubMed=2518726;			
RA	Chang H.C., Hsu F., Freeman G.J., Griffin J.D., Reinherz E.L.;			
RT	"Cloning and expression of a gamma-interferon-inducible gene in monocytes: a new member of a cytokine gene family.";			

RL Int. Immunol. 1:388-399(1989).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=94150478; PubMed=8107690;  
 RA Li Y.S., Shyy Y.J., Wright J.G., Valente A.J., Cornhill J.F.,  
 RA Kolattukudy P.E.;  
 RT "The expression of monocyte chemotactic protein (MCP-1) in human  
 RT vascular endothelium in vitro and in vivo.";  
 RL Mol. Cell. Biochem. 126:61-68(1993).  
 RN [7]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92095166; PubMed=1661560;  
 RA Yoshimura T., Leonard E.J.;  
 RT "Human monocyte chemoattractant protein-1 (MCP-1).";  
 RL Adv. Exp. Med. Biol. 305:47-56(1991).  
 RN [8]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=91301709; PubMed=2071154;  
 RA Rollins B.J., Morton C.C., Ledbetter D.H., Eddy R.L. Jr., Shows T.B.;  
 RT "Assignment of the human small inducible cytokine A2 gene, SCYA2  
 RT (encoding JE or MCP-1), to 17q11.2-12: evolutionary relatedness of  
 RT cytokines clustered at the same locus.";  
 RL Genomics 10:489-492(1991).  
 RN [9]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20374005; PubMed=10918580; DOI=10.1038/sj.onc.1203643;  
 RA Finzer P., Soto U., Delius H., Patzelt A., Poustka A., Coy J.F.,  
 RA zur Hausen H., Roess F.;  
 RT "Differential transcriptional regulation of the monocyte-  
 RT chemoattractant protein-1 (MCP-1) gene in tumorigenic and non-  
 RT tumorigenic HPV 18 positive cells: the role of the chromatin structure  
 RT and AP-1 composition.";  
 RL Oncogene 19:3235-3244(2000).  
 RN [10]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,  
 RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,  
 RA Phelan M., Farmer A.;  
 RT "Cloning of human full-length CDSs in BD Creator(TM) system donor  
 RT vector.";  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
 RN [11]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,  
 RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;  
 RT "SeattleSNPs: NHLBI HL66682 program for genomic applications, UW-  
 RT FHCR, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [12]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC TISSUE=Pancreas;  
 RX MEDLINE=22382257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Berger J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
 RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fanej J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Tringwood J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Gough J., Schmutz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [13]  
 RP PROTEIN SEQUENCE OF 24-99.  
 RX MEDLINE=89184525; PubMed=2648385;  
 RA Robinson E.A., Yoshimura T., Leonard E.J., Tanaka S., Griffin P.R.,  
 RA Shabanowitz J., Hunt D.F., Appella E.;  
 RT "Complete amino acid sequence of a human monocyte chemoattractant, a  
 RT putative mediator of cellular immune reactions.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1850-1854(1989).  
 RN [14]  
 RP PROTEIN SEQUENCE OF 29-53 AND 82-92.  
 RX MEDLINE=90211336; PubMed=2322286;  
 RA Decock B., Conings R., Lenaerts J.-P., Biliau A., van Damme J.;  
 RT "Identification of the monocyte chemotactic protein from human  
 RT osteosarcoma cells and monocytes: detection of a novel N-terminally  
 RT processed form.";  
 RL Biochem. Biophys. Res. Commun. 167:904-909(1990).  
 RN [15]  
 RP 3D-STRUCTURE MODELING.  
 RX MEDLINE=91312872; PubMed=1857712;  
 RA Gronenborn A.M., Clore G.M.;  
 RT "Modeling the three-dimensional structure of the monocyte chemo-  
 RT attractant and activating protein MCP-1 on the basis of the  
 RT solution structure of interleukin-8.";  
 RL Protein Eng. 4:263-269(1991).  
 RN [16]  
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).  
 RX MEDLINE=97143315; PubMed=8989326;  
 RA Lubkowski J., Bujacz G., Domaille P.J., Handel T.M., Wlodawer A.;  
 RT "The structure of MCP-1 in two crystal forms provides a rare example  
 RT of variable quaternary interactions.";  
 RL Nat. Struct. Biol. 4:64-69(1997).  
 RN [17]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=96234959; PubMed=8639605; DOI=10.1021/bi9602270;  
 RA Handel T.M., Domaille P.J.;  
 RT "Heteronuclear (1H, 13C, 15N) NMR assignments and solution structure  
 RT of the monocyte chemoattractant protein-1 (MCP-1) dimer.";  
 RL Biochemistry 35:6569-6584(1996).  
 RN [18]  
 RP EFFECT OF DELETION OF N-TERMINAL RESIDUES.  
 RX MEDLINE=96195223; PubMed=8627182; DOI=10.1084/jem.183.2.681;  
 RA Weber M., Uguccioni M., Baggiolini M., Clark-Lewis I., Dahinden C.A.;  
 RT "Deletion of the NH2-terminal residue converts monocyte chemotactic  
 RT protein 1 from an activator of basophil mediator release to an  
 RT eosinophil chemoattractant.";  
 RL J. Exp. Med. 183:681-685(1996).  
 RN [19]  
 RP MUTAGENESIS.  
 RX MEDLINE=94253189; PubMed=8195247;  
 RA Zhang Y.J., Rutledge B.J., Rollins B.J.;  
 RT "Structure/activity analysis of human monocyte chemoattractant  
 RT protein-1 (MCP-1) by mutagenesis. Identification of a mutated protein  
 RT that inhibits MCP-1-mediated monocyte chemotaxis.";  
 RL J. Biol. Chem. 269:15918-15924(1994).  
 RN [20]  
 RP SUBUNIT.  
 RX MEDLINE=97053697; PubMed=8898111; DOI=10.1016/0014-5793(96)01024-1;  
 RA Kim K.-S., Rajaratnam K., Clark-Lewis I., Sykes B.D.;  
 RT "Structural characterization of a monomeric chemokine: monocyte  
 RT chemoattractant protein-3.";  
 RL FEBS Lett. 395:277-282(1996).  
 CC -1- FUNCTION: Chemotactic factor that attracts monocytes and basophils  
 CC but not neutrophils or eosinophils. Augments monocyte anti-tumor  
 CC activity. Has been implicated in the pathogenesis of diseases  
 CC characterized by monocyte infiltrates, like psoriasis, rheumatoid  
 CC arthritis or atherosclerosis. May be involved in the recruitment  
 CC of monocytes into the arterial wall during the disease process of  
 CC atherosclerosis. Binds to CCR2 and CCR4.  
 CC -1- SUBUNIT: Monomer or homodimer; in equilibrium.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: Processing at the N-terminus can regulate receptor and target  
 CC cell selectivity. Deletion of the N-terminal residue converts it  
 CC from an activator of basophil to an eosinophil chemoattractant.  
 CC -1- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.

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CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC
Query Match 100.0%; Score 405; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 7.6e-38;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCYNTNRKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

Qy 61 QDSMDHLKQQTPTK 76
Db 84 QDSMDHLKQQTPTK 99

RESULT 2
CCL2_PONPY STANDARD; PRT; 99 AA.
AC Q5RA36;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DE Small inducible cytokine A2 precursor (CCL2).
DE Small inducible cytokine A2 precursor (CCL2).
GN Name=CCL2;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC Tissue=Kidney;
RG The German cDNA consortium;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Chemotactic factor that attracts monocytes and basophils
CC but not neutrophils or eosinophils. Binds to CCR2 and CCR4 (By
CC similarity).
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
DR EMBL; CR859186; CAH91374.1; -, mRNA.
DR SMR; Q5RA36; 24-94.
DR InterPro; IPR000827; CC chemokine sm1.
DR InterPro; IPR001811; Chemokine IL8.
DR Pfam; PF000048; IL8; 1.
DR PRINTS; PR01721; FRACTALKINE.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL CYTOKINES CC; 1.
KW Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;
KW Pyrilidone carboxylic acid; Sensory transduction; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 99 Small inducible cytokine A2.
FT MOD_RES 24 24 Pyrilidone carboxylic acid (By
FT similarity).
FT CARBOHYD 37 37 N-linked (GlcNAc...) (Potential).
FT DISULFID 34 59 By similarity.
FT DISULFID 35 75 By similarity.
SQ SEQUENCE 99 AA; 11015 MW; 45FCA8CC64FF8A4F CRC64;

Query Match 97.5%; Score 395; DB 1; Length 99;
Best Local Similarity 98.7%; Pred. No. 1e-36;
Matches 75; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCYNTNRKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

Qy 61 QDSMDHLKQQTPTK 75
Db 84 QDSMDHLKQQTPTK 99
```

```
Db 24 QPDAINAPVTCYNTNRKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

Qy 61 QDSMDHLKQQTPTK 76
Db 84 QDSMDHLKQQTPTK 99

RESULT 3
CCL2_MACFA STANDARD; PRT; 99 AA.
AC P61274; Q9MYN4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
DE protein 1) (MCP-1) (Monocyte chemoattractant protein 1).
GN Name=CCL2; Synonyms=MCPI, SCY2;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopitheinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Studer C., Ufer R.;
RT "Cloning and expression of cynomolgus monkey chemoattractant protein-
RT 1.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Chemotactic factor that attracts monocytes and basophils
CC but not neutrophils or eosinophils. Binds to CCR2 and CCR4 (By
CC similarity).
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
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removed.
DR EMBL; AF276081; AAP81899.1; -, mRNA.
DR HSP; P13500; IDOK.
DR SMR; P61274; 24-93.
DR InterPro; IPR000827; CC chemokine sm1.
DR InterPro; IPR001811; Chemokine IL8.
DR InterPro; IPR008097; Fractalkine.
DR Pfam; PF000048; IL8; 1.
DR PRINTS; PR01721; FRACTALKINE.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL CYTOKINES CC; 1.
KW Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;
KW Pyrilidone carboxylic acid; Sensory transduction; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 99 Small inducible cytokine A2.
FT MOD_RES 24 24 Pyrilidone carboxylic acid (By
FT similarity).
FT CARBOHYD 37 37 N-linked (GlcNAc...) (Potential).
FT DISULFID 34 59 By similarity.
FT DISULFID 35 75 By similarity.
SQ SEQUENCE 99 AA; 11007 MW; 433CB88C64EE7A4F CRC64;

Query Match 97.3%; Score 394; DB 1; Length 99;
Best Local Similarity 98.7%; Pred. No. 1.3e-36;
Matches 74; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCYNTNRKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83

Qy 61 QDSMDHLKQQTPTK 75
Db 84 QDSMDHLKQQTPTK 99
```

06XVNS MACNE









Best Local Similarity 73.3%; Pred. No. 1.1e-27;  
Matches 55; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

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Qy 1 OPDAINAPVTCYNTNFKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
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Db 24 QPDAVNSPVTCCYFTNKTISVKRLMSYRRINSTKCPKEAVIFMTKLAKGICADPKQKWV 83
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 QDSMDHLDKOTQTPKT 75
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 84 QDSINYLKKNQTPK 98
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

## RESULT 11

```
CCL2_RABIT
ID _CCL2_RABIT STANDARD; PRT; 125 AA.
AC P28292;
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
protein 1) (MCP-1) (Monocyte chemoattractant protein 1).
GN Name=CCL2; Synonyms=SCYA2;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]
```

## NUCLEOTIDE SEQUENCE.

```
RP STRAIN=New Zealand white; TISSUE=Spleen;
RX MEDLINE=91225489; PubMed=2026877;
RA Yoshimura T., Yuhki N.;
RT "Neutrophil attractant/activation protein-1 and monocyte
chemoattractant protein-1 in rabbit. cDNA cloning and their expression
in spleen cells."
RL J. Immunol. 146:3483-3488 (1991).
CC -1- FUNCTION: Chemotactic factor that attracts monocytes, but not
neutrophils.
CC -1- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
```

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use as long as its content is in no way modified and this statement is not  
removed.

```
DR EMBL; M57440; AAA31386.1; -; mRNA.
DR PIR; I46857; I46857.
DR HSSP; P13500; IDOM.
DR SMR; P28292; 24-99.
DR InterPro; IPR000827; CC chemokine sm1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;
KW Pyrrolidone carboxylic acid; Sensory transduction; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 125 Small inducible cytokine A2. (By
FT MOD_RES 24 24 Pyrrolidone carboxylic acid (By
FT CARBOHYD 40 40 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 55 55 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 112 112 N-linked (GlcNAc... ) (Potential).
FT DISULFID 34 59 By similarity.
FT DISULFID 35 75 By similarity.
SQ SEQUENCE 125 AA; 13776 MW; 24C3A542CB6A47EE CRC64;
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Query Match 77.5%; Score 314; DB 1; Length 125;

Best Local Similarity 75.0%; Pred. No. 1.9e-27;  
Matches 57; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

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Qy 1 OPDAINAPVTCYNTNFKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 24 QPDAVNSPVTCCYFTNKTISVKRLMSYRRINSTKCPKEAVIFMTKLAKGICADPKQKWV 83
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 QDSMDHLDKOTQTPKT 76
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 84 QDAIANLDDKKMQTPKT 99
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

## RESULT 12

```
MCPB_BOVIN
ID _MCPB_BOVIN STANDARD; PRT; 74 AA.
AC P80343;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Monocyte chemotactic protein 1B (MCP-1B) (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP PROTEIN SEQUENCE.
RX TISSUE=Kidney;
RX MEDLINE=95034774; PubMed=7947749;
RA Proost P., Wuyts A., Lenaerts J.-P., van Damme J.;
RT "Purification, sequence analysis, and biological characterization of a
second bovine monocyte chemotactic protein-1 (Bo MCP-1B).";
RL Biochemistry 33:13406-13412 (1994).
CC -1- FUNCTION: Chemotactic factor that attracts monocytes, but not
neutrophils. Augments monocyte anti-tumor activity. Also induces
the release of gelatinase B. This protein can bind heparin.
CC -1- PTM: The N-terminus is blocked.
CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
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removed.

```
DR HSSP; P13500; IDOK.
DR SMR; P80343; 1-68.
DR InterPro; IPR000827; CC chemokine sm1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Direct protein sequencing; Heparin-binding;
KW Sensory transduction.
FT DISULFID 9 34 By similarity.
FT DISULFID 10 50 By similarity.
FT NON_TER 1 1
SQ SEQUENCE 74 AA; 8363 MW; FAAF72B970EB16E3 CRC64;
```

Query Match 76.0%; Score 308; DB 1; Length 74;

Best Local Similarity 75.3%; Pred. No. 5.2e-27;  
Matches 55; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

```
Qy 3 DAINAPVTCYNTNFKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWVD 62
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DAINSPVTCYTTSTKSKMORLMSYRRVTSKCPKEAVIFKTIAGKEICAEPPKXWVD 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 63 SMDHLDKOTQTPK 75
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SISHLDKKNQXPX 73
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

## RESULT 13

Q516F8\_CANFA

ID Q516F8\_CANFA PRELIMINARY; PRT; 99 AA.

Search completed: February 3, 2006, 09:57:26  
Job time : 36.6863 secs

Search completed: February 3, 2006, 09:57:26  
Job time : 36.6863 secs